

```

=====
file name: Homo_sapiens.all_chromosomes.fasta
sequences: 24
total length: 3095677412 bp (2858660140 bp excl N/X-runs)
GC level: Unknown %
bases masked: 1412780617 bp ( 45.64 %)
=====

```

	number of elements*	length occupied	percentage of sequence
SINEs:	1658864	385270856 bp	12.45 %
ALUs	1136457	306395826 bp	9.90 %
MIRs	517233	78244089 bp	2.53 %
LINEs:	913889	609952196 bp	19.70 %
LINE1	539553	503348534 bp	16.26 %
LINE2	319303	93411598 bp	3.02 %
L3/CR1	42713	10009516 bp	0.32 %
LTR elements:	487433	259122242 bp	8.37 %
ERV	108675	55875700 bp	1.80 %
ERV-MaLRs	247590	108138874 bp	3.49 %
ERV_classI	109816	82706444 bp	2.67 %
ERV_classII	7480	8820605 bp	0.28 %
DNA elements:	383832	95646896 bp	3.09 %
hAT-Charlie	214295	43419001 bp	1.40 %
TcMar-Tigger	82218	33550442 bp	1.08 %
Unclassified:	9962	5418573 bp	0.18 %
Total interspersed repeats:		1355410763 bp	43.78 %
Small RNA:	13482	1443809 bp	0.05 %
Satellites:	4502	12381861 bp	0.40 %
Simple repeats:	403012	25937716 bp	0.84 %
Low complexity:	393080	17947554 bp	0.58 %

```

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

```

```

The query species was assumed to be homo sapiens
RepeatMasker version open-3.3.0 , default mode

```

```

run with rmbblastn version : 2.2.23+
RepBase Update 20110419, RM database version 20110419

```

```
=====
file name: Pan_troglodytes.all_chromosomes.fasta
sequences: 23
total length: 2996268118 bp (2600126684 bp excl N/X-runs)
GC level: Unknown %
bases masked: 1252612466 bp ( 41.81 %)
=====
```

	number of elements*	length occupied	percentage of sequence
-----			
SINEs:	1540783	352119302 bp	11.75 %
ALUs	1052868	278634631 bp	9.30 %
MIRs	483094	72891245 bp	2.43 %
LINEs:	844282	533798830 bp	17.82 %
LINE1	495441	436591232 bp	14.57 %
LINE2	297810	85062747 bp	2.84 %
L3/CR1	39406	9155649 bp	0.31 %
LTR elements:	448170	227050774 bp	7.58 %
ERV	100464	50462825 bp	1.68 %
ERV-MaLRs	228482	97666971 bp	3.26 %
ERV_classI	99719	68464694 bp	2.28 %
ERV_classII	6557	7151882 bp	0.24 %
DNA elements:	356780	88453616 bp	2.95 %
hAT-Charlie	198814	40151218 bp	1.34 %
TcMar-Tigger	76949	31016233 bp	1.04 %
Unclassified:	9202	4303678 bp	0.14 %
Total interspersed repeats:		1205726200 bp	40.24 %
Small RNA:	12314	1313626 bp	0.04 %
Satellites:	4140	8625270 bp	0.29 %
Simple repeats:	363359	21414870 bp	0.71 %
Low complexity:	361561	15848659 bp	0.53 %

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

```
The query species was assumed to be pan troglodytes
RepeatMasker version open-3.3.0 , default mode
```

```
run with rmbblastn version : 2.2.23+
RepBase Update 20110419, RM database version 20110419
```

```

=====
file name: Rattus_norvegicus.all_chromosomes.fasta
sequences: 21
total length: 2718881021 bp (2480263085 bp excl N/X-runs)
GC level: Unknown %
bases masked: 1091908110 bp ( 40.16 %)
=====

```

	number of elements*	length occupied	percentage of sequence
SINEs:	1263875	171456178 bp	6.31 %
Alu/B1	363997	40167632 bp	1.48 %
B2-B4	645210	106369568 bp	3.91 %
IDs	164347	14240236 bp	0.52 %
MIRs	88048	10431394 bp	0.38 %
LINEs:	651753	526328158 bp	19.36 %
LINE1	597796	517447372 bp	19.03 %
LINE2	42555	7328069 bp	0.27 %
L3/CR1	8717	1189896 bp	0.04 %
LTR elements:	647364	240357739 bp	8.84 %
ERV	75249	23844377 bp	0.88 %
ERV-MaLRs	323153	103526707 bp	3.81 %
ERV_classI	44796	24155357 bp	0.89 %
ERV_classII	202270	88450609 bp	3.25 %
DNA elements:	124355	25517898bp	0.94 %
hAT-Charlie	84117	16331880 bp	0.60 %
TcMar-Tigger	23610	5666832 bp	0.21 %
Unclassified:	59738	47824283 bp	1.76 %
Total interspersed repeats:		1011484256 bp	37.20 %
Small RNA:	56584	5324859 bp	0.20 %
Satellites:	12685	3548588 bp	0.13 %
Simple repeats:	839985	55040729 bp	2.02 %
Low complexity:	324419	16623671 bp	0.61 %

```

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

```

The query species was assumed to be rattus norvegicus  
RepeatMasker version open-3.3.0 , default mode

run with rmbblastn version : 2.2.23+  
RepBase Update 20110419, RM database version 20110419

```
=====
file name: Mus_musculus.all_chromosomes.fasta
sequences: 21
total length: 2654895218 bp (2558512666 bp excl N/X-runs)
GC level: Unknown %
bases masked: 1119810346 bp ( 42.18 %)
=====
```

	number of elements*	length occupied	percentage of sequence
SINEs:	1384717	194323459 bp	7.32 %
Alu/B1	537834	63432364 bp	2.39 %
B2-B4	694930	115288287 bp	4.34 %
IDs	51903	3697061 bp	0.14 %
MIRs	97621	11642470 bp	0.44 %
LINEs:	669956	512121108 bp	19.29 %
LINE1	610880	502148388 bp	18.91 %
LINE2	46945	8297283 bp	0.31 %
L3/CR1	9220	1273507 bp	0.05 %
LTR elements:	735764	297112207 bp	11.19 %
ERV	83501	30696616 bp	1.16 %
ERV-MaLRs	356897	118282327 bp	4.46 %
ERV_classI	47646	24584511 bp	0.93 %
ERV_classII	245507	123121567 bp	4.64 %
DNA elements:	133702	27528140bp	1.04 %
hAT-Charlie	89912	17472765 bp	0.66 %
TcMar-Tigger	25558	6169778 bp	0.23 %
Unclassified:	19788	8510525 bp	0.32 %
Total interspersed repeats:		1039595439 bp	39.16 %
Small RNA:	19064	1597592 bp	0.06 %
Satellites:	21505	3314029 bp	0.12 %
Simple repeats:	949926	55694579 bp	2.10 %
Low complexity:	380938	19729301 bp	0.74 %

```
=====
* 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-3.3.0 , default mode

run with rmblastn version : 2.2.23+  
RepBase Update 20110419, RM database version 20110419

```
=====
file name: Canis_familiaris.all_chromosomes.fasta
sequences: 39
total length: 2445110183 bp (2309889441 bp excl N/X-runs)
GC level: 41.02 %
bases masked: 919863057 bp ( 37.62 %)
=====
```

	number of elements*	length occupied	percentage of sequence
-----			
SINEs:	1479262	243251071 bp	9.95 %
Alu/B1	1	54 bp	0.00 %
MIRs	426185	62853107 bp	2.57 %
LINEs:	806552	461321498 bp	18.87 %
LINE1	502746	378401441 bp	15.48 %
LINE2	258187	72394829 bp	2.96 %
L3/CR1	35171	7980538 bp	0.33 %
RTE	10099	2460440 bp	0.10 %
LTR elements:	272475	107148389 bp	4.38 %
ERV_L	81342	36565136 bp	1.50 %
ERV_L-MaLRs	136904	47707485 bp	1.95 %
ERV_classI	44143	20449608 bp	0.84 %
ERV_classII	0	0 bp	0.00 %
DNA elements:	275219	59867636 bp	2.45 %
hAT-Charlie	173050	33315882 bp	1.36 %
TcMar-Tigger	39070	13427048 bp	0.55 %
Unclassified:	5918	1256194 bp	0.05 %
Total interspersed repeats:		872844788 bp	35.70 %
Small RNA:	44087	3429628 bp	0.14 %
Satellites:	507	595668 bp	0.02 %
Simple repeats:	546529	25808328 bp	1.06 %
Low complexity:	432457	17513633 bp	0.72 %

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

The query species was assumed to be canis lupus familiaris  
RepeatMasker version open-3.3.0 , default mode

run with rmblastn version : 2.2.23+  
RepBase Update 20110419, RM database version 20110419

```
=====
file name: Tetraodon_nigroviridis.all_chromosomes.fasta
sequences:      21
total length:  240984470 bp (208710104 bp excl N/X-runs)
GC level:      45.98 %
bases masked:  5459400 bp ( 2.27 %)
=====
```

	number of elements*	length occupied	percentage of sequence
-----	-----	-----	-----
Retroelements	2174	472843 bp	0.20 %
SINEs:	645	85839 bp	0.04 %
Penelope	1273	204285 bp	0.08 %
LINEs:	1529	387004 bp	0.16 %
CRE/SLACS	0	0 bp	0.00 %
L2/CR1/Rex	0	0 bp	0.00 %
R1/L0A/Jockey	0	0 bp	0.00 %
R2/R4/NeSL	212	145557 bp	0.06 %
RTE/Bov-B	0	0 bp	0.00 %
L1/CIN4	9	9847 bp	0.00 %
LTR elements:	0	0 bp	0.00 %
BEL/Pao	0	0 bp	0.00 %
Ty1/Copia	0	0 bp	0.00 %
Gypsy/DIRS1	0	0 bp	0.00 %
Retroviral	0	0 bp	0.00 %
DNA transposons	0	0 bp	0.00 %
hobo-Activator	0	0 bp	0.00 %
Tc1-IS630-Pogo	0	0 bp	0.00 %
En-Spm	0	0 bp	0.00 %
MuDR-IS905	0	0 bp	0.00 %
PiggyBac	0	0 bp	0.00 %
Tourist/Harbinger	0	0 bp	0.00 %
Other (Mirage, P-element, Transib)	0	0 bp	0.00 %
Rolling-circles	0	0 bp	0.00 %
Unclassified:	1	62 bp	0.00 %
Total interspersed repeats:		472905 bp	0.20 %
Small RNA:	384	35627 bp	0.01 %
Satellites:	1	243 bp	0.00 %
Simple repeats:	80923	3657582 bp	1.52 %
Low complexity:	29876	1297249 bp	0.54 %

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

The query species was assumed to be tetraodon nigroviridis  
RepeatMasker version open-3.3.0 , default mode

run with rmblastn version : 2.2.23+  
RepBase Update 20110419, RM database version 20110419

```
=====
file name: Danio_rerio.all_chromosomes.fasta
sequences: 25
total length: 1357035047 bp (1354638161 bp excl N/X-runs)
GC level: 36.60 %
bases masked: 709285840 bp ( 52.27 %)
=====
```

	number of elements*	length occupied	percentage of sequence
Retroelements	353163	136796341 bp	10.08 %
SINEs:	138450	31911777 bp	2.35 %
Penelope	0	0 bp	0.00 %
LINEs:	96375	36984466 bp	2.73 %
CRE/SLACS	0	0 bp	0.00 %
L2/CR1/Rex	75981	26518990 bp	1.95 %
R1/L0A/Jockey	6913	2320797 bp	0.17 %
R2/R4/NeSL	251	123592 bp	0.01 %
RTE/Bov-B	7179	3265441 bp	0.24 %
L1/CIN4	6603	3837725 bp	0.28 %
LTR elements:	118338	67900098 bp	5.00 %
BEL/Pao	2006	2536536 bp	0.19 %
Ty1/Copia	151	150050 bp	0.01 %
Gypsy/DIRS1	49749	40339466 bp	2.97 %
Retroviral	12816	4797089 bp	0.35 %
DNA transposons	1779603	473157323 bp	34.87 %
hobo-Activator	641989	151210764 bp	11.14 %
Tc1-IS630-Pogo	197955	63335983 bp	4.67 %
En-Spm	169887	29231900 bp	2.15 %
MuDR-IS905	4215	2136789 bp	0.16 %
PiggyBac	66816	26535626 bp	1.96 %
Tourist/Harbinger	83096	29095596 bp	2.14 %
Other (Mirage, P-element, Transib)	4863	1261810 bp	0.09 %
Rolling-circles	0	0 bp	0.00 %
Unclassified:	80740	12475619 bp	0.92 %
Total interspersed repeats:		622429283 bp	45.87 %
Small RNA:	28006	2751619 bp	0.20 %
Satellites:	119326	28101508 bp	2.07 %
Simple repeats:	520471	41852231 bp	3.08 %
Low complexity:	401429	21535007 bp	1.59 %

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

The query species was assumed to be danio rerio  
RepeatMasker version open-3.3.0 , default mode

run with rmblastn version : 2.2.23+  
RepBase Update 20110419, RM database version 20110419

```
=====
file name: Ciona_intestinalis.all_chromosomes.fasta
sequences: 20
total length: 93809953 bp (87650325 bp excl N/X-runs)
GC level: 35.56 %
bases masked: 13621411 bp ( 14.52 %)
=====
```

	number of elements*	length occupied	percentage of sequence
-----	-----	-----	-----
Retroelements	39649	5247405 bp	5.59 %
SINEs:	26935	3843839 bp	4.10 %
Penelope	1226	104124 bp	0.11 %
LINEs:	12573	1347787 bp	1.44 %
CRE/SLACS	0	0 bp	0.00 %
L2/CR1/Rex	2905	450431 bp	0.48 %
R1/L0A/Jockey	4825	504765 bp	0.54 %
R2/R4/NeSL	17	10943 bp	0.01 %
RTE/Bov-B	0	0 bp	0.00 %
L1/CIN4	3600	277524 bp	0.30 %
LTR elements:	141	55779 bp	0.06 %
BEL/Pao	0	0 bp	0.00 %
Ty1/Copia	0	0 bp	0.00 %
Gypsy/DIRS1	141	55779 bp	0.06 %
Retroviral	0	0 bp	0.00 %
DNA transposons	35688	6478041 bp	6.91 %
hobo-Activator	2717	731169 bp	0.78 %
Tc1-IS630-Pogo	31004	5108347 bp	5.45 %
En-Spm	0	0 bp	0.00 %
MuDR-IS905	0	0 bp	0.00 %
PiggyBac	249	99928 bp	0.11 %
Tourist/Harbinger	0	0 bp	0.00 %
Other (Mirage, P-element, Transib)	821	345186 bp	0.37 %
Rolling-circles	0	0 bp	0.00 %
Unclassified:	1	53 bp	0.00 %
Total interspersed repeats:		11725499 bp	12.50 %
Small RNA:	48	5061 bp	0.01 %
Satellites:	1700	412792 bp	0.44 %
Simple repeats:	3960	241484 bp	0.26 %
Low complexity:	29391	1240042 bp	1.32 %

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

The query species was assumed to be *ciona intestinalis*  
RepeatMasker version open-3.3.0 , default mode

run with rmblastn version : 2.2.23+  
RepBase Update 20110419, RM database version 20110419



```
=====
file name: Caenorhabditis_elegans.all_chromosomes.fasta
sequences: 6
total length: 100272276 bp (100272276 bp excl N/X-runs)
GC level: 35.44 %
bases masked: 13162235 bp ( 13.13 %)
=====
```

	number of elements*	length occupied	percentage of sequence
-----	-----	-----	-----
Retroelements	1489	883137 bp	0.88 %
SINEs:	512	87172 bp	0.09 %
Penelope	0	0 bp	0.00 %
LINEs:	577	396882 bp	0.40 %
CRE/SLACS	0	0 bp	0.00 %
L2/CR1/Rex	428	262087 bp	0.26 %
R1/L0A/Jockey	27	17795 bp	0.02 %
R2/R4/NeSL	0	0 bp	0.00 %
RTE/Bov-B	85	90551 bp	0.09 %
L1/CIN4	0	0 bp	0.00 %
LTR elements:	400	399083 bp	0.40 %
BEL/Pao	236	306952 bp	0.31 %
Ty1/Copia	0	0 bp	0.00 %
Gypsy/DIRS1	128	84108 bp	0.08 %
Retroviral	0	0 bp	0.00 %
DNA transposons	31955	6845259 bp	6.83 %
hobo-Activator	3324	508622 bp	0.51 %
Tc1-IS630-Pogo	6955	1686339 bp	1.68 %
En-Spm	0	0 bp	0.00 %
MuDR-IS905	1107	335613 bp	0.33 %
PiggyBac	3911	762360 bp	0.76 %
Tourist/Harbinger	11	17714 bp	0.02 %
Other (Mirage, P-element, Transib)	92	56599 bp	0.06 %
Rolling-circles	0	0 bp	0.00 %
Unclassified:	11315	2477999 bp	2.47 %
Total interspersed repeats:		10206395 bp	10.18 %
Small RNA:	7	7936 bp	0.01 %
Satellites:	3672	800017 bp	0.80 %
Simple repeats:	6357	572486 bp	0.57 %
Low complexity:	39601	1627503 bp	1.62 %

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

The query species was assumed to be *caenorhabditis elegans*  
RepeatMasker version open-3.3.0 , default mode

run with rmblastn version : 2.2.23+  
RepBase Update 20110419, RM database version 20110419

```

=====
file name: Anopheles_gambiae.all_chromosomes.fasta
sequences: 5
total length: 230466657 bp (225028590 bp excl N/X-runs)
GC level: 44.55 %
bases masked: 23387492 bp ( 10.15 %)
=====

```

	number of elements*	length occupied	percentage of sequence
Retroelements	23810	11470301 bp	4.98 %
SINEs:	9990	1553186 bp	0.67 %
Penelope	0	0 bp	0.00 %
LINEs:	9514	5294400 bp	2.30 %
CRE/SLACS	0	0 bp	0.00 %
L2/CR1/Rex	2985	2218213 bp	0.96 %
R1/L0A/Jockey	3117	1230819 bp	0.53 %
R2/R4/NeSL	47	14902 bp	0.01 %
RTE/Bov-B	3212	1701779 bp	0.74 %
L1/CIN4	86	79901 bp	0.03 %
LTR elements:	4306	4622715 bp	2.01 %
BEL/Pao	1224	1780843 bp	0.77 %
Ty1/Copia	301	292026 bp	0.13 %
Gypsy/DIRS1	2677	2529766 bp	1.10 %
Retroviral	0	0 bp	0.00 %
DNA transposons	28306	7544355 bp	3.27 %
hobo-Activator	3552	816457 bp	0.35 %
Tc1-IS630-Pogo	8865	2769130 bp	1.20 %
En-Spm	0	0 bp	0.00 %
MuDR-IS905	0	0 bp	0.00 %
PiggyBac	620	124559 bp	0.05 %
Tourist/Harbinger	1898	414380 bp	0.18 %
Other (Mirage, P-element, Transib)	5895	1256585 bp	0.55 %
Rolling-circles	0	0 bp	0.00 %
Unclassified:	1233	224768 bp	0.10 %
Total interspersed repeats:		19239424 bp	8.35 %
Small RNA:	28	9812 bp	0.00 %
Satellites:	1000	416997 bp	0.18 %
Simple repeats:	54866	2457431 bp	1.07 %
Low complexity:	28974	1278785 bp	0.55 %

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

The query species was assumed to be anopheles gambiae  
RepeatMasker version open-3.3.0 , default mode

run with rmblastn version : 2.2.23+  
RepBase Update 20110419, RM database version 20110419

```
=====
file name: Drosophila_melanogaster.all_chromosomes.fasta
sequences: 6
total length: 120381546 bp (120290946 bp excl N/X-runs)
GC level: 42.41 %
bases masked: 10974817 bp ( 9.12 %)
=====
```

	number of elements*	length occupied	percentage of sequence
Retroelements	3811	6490381 bp	5.39 %
SINEs:	0	0 bp	0.00 %
Penelope	0	0 bp	0.00 %
LINEs:	1407	1893670 bp	1.57 %
CRE/SLACS	0	0 bp	0.00 %
L2/CR1/Rex	222	240708 bp	0.20 %
R1/L0A/Jockey	1168	1625651 bp	1.35 %
R2/R4/NeSL	2	110 bp	0.00 %
RTE/Bov-B	0	0 bp	0.00 %
L1/CIN4	0	0 bp	0.00 %
LTR elements:	2404	4596711 bp	3.82 %
BEL/Pao	808	1400644 bp	1.16 %
Ty1/Copia	109	250073 bp	0.21 %
Gypsy/DIRS1	1487	2945994 bp	2.45 %
Retroviral	0	0 bp	0.00 %
DNA transposons	1761	733485 bp	0.61 %
hobo-Activator	113	52699 bp	0.04 %
Tc1-IS630-Pogo	577	302985 bp	0.25 %
En-Spm	0	0 bp	0.00 %
MuDR-IS905	3	3536 bp	0.00 %
PiggyBac	13	5581 bp	0.00 %
Tourist/Harbinger	0	0 bp	0.00 %
Other (Mirage, P-element, Transib)	1047	366105 bp	0.30 %
Rolling-circles	0	0 bp	0.00 %
Unclassified:	3771	769910 bp	0.64 %
Total interspersed repeats:		7993776 bp	6.64 %
Small RNA:	102	13624 bp	0.01 %
Satellites:	553	311520 bp	0.26 %
Simple repeats:	29352	1390902 bp	1.16 %
Low complexity:	32650	1278435 bp	1.06 %

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

The query species was assumed to be drosophila melanogaster  
RepeatMasker version open-3.3.0 , default mode

run with rmblastn version : 2.2.23+  
RepBase Update 20110419, RM database version 20110419

```
=====
file name: Zea_all_chromosomes.fasta
sequences: 10
total length: 2058582553 bp (2045698570 bp excl N/X-runs)
GC level: 46.90 %
bases masked: 1607479856 bp ( 78.09 %)
=====
```

	number of elements*	length occupied	percentage of sequence
Retroelements	593337	1507035339 bp	73.21 %
SINEs:	2611	327593 bp	0.02 %
Penelope	0	0 bp	0.00 %
LINEs:	20492	17400689 bp	0.85 %
CRE/SLACS	0	0 bp	0.00 %
L2/CR1/Rex	0	0 bp	0.00 %
R1/L0A/Jockey	0	0 bp	0.00 %
R2/R4/NeSL	0	0 bp	0.00 %
RTE/Bov-B	3862	2116445 bp	0.10 %
L1/CIN4	16630	15284244 bp	0.74 %
LTR elements:	570234	1489307057 bp	72.35 %
BEL/Pao	0	0 bp	0.00 %
Ty1/Copia	242338	537882801 bp	26.13 %
Gypsy/DIRS1	320602	949779542 bp	46.14 %
Retroviral	0	0 bp	0.00 %
DNA transposons	133611	77376548 bp	3.76 %
hobo-Activator	40647	12891618 bp	0.63 %
Tc1-IS630-Pogo	3123	553191 bp	0.03 %
En-Spm	49048	44430178 bp	2.16 %
MuDR-IS905	16821	13331806 bp	0.65 %
PiggyBac	0	0 bp	0.00 %
Tourist/Harbinger	16898	5196483 bp	0.25 %
Other (Mirage, P-element, Transib)	0	0 bp	0.00 %
Rolling-circles	0	0 bp	0.00 %
Unclassified:	33059	9841018 bp	0.48 %
Total interspersed repeats:		1594252905 bp	77.44 %
Small RNA:	4116	2790630 bp	0.14 %
Satellites:	2939	4316900 bp	0.21 %
Simple repeats:	61510	3055605 bp	0.15 %
Low complexity:	87719	4039077 bp	0.20 %

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

The query species was assumed to be zea  
RepeatMasker version open-3.3.0 , default mode

run with rmblastn version : 2.2.23+  
RepBase Update 20110419, RM database version 20110419

```
=====
file name: Sorghum_bicolor.all_chromosomes.fasta
sequences:      10
total length:  659229367 bp (625636247 bp excl N/X-runs)
GC level:      43.80 %
bases masked:  116688255 bp ( 17.70 %)
=====
```

	number of elements*	length occupied	percentage of sequence
Retroelements	116859	89629527 bp	13.60 %
SINEs:	78	9088 bp	0.00 %
Penelope	0	0 bp	0.00 %
LINEs:	11105	4940006 bp	0.75 %
CRE/SLACS	0	0 bp	0.00 %
L2/CR1/Rex	0	0 bp	0.00 %
R1/L0A/Jockey	0	0 bp	0.00 %
R2/R4/NeSL	0	0 bp	0.00 %
RTE/Bov-B	471	62192 bp	0.01 %
L1/CIN4	10634	4877814 bp	0.74 %
LTR elements:	105676	84680433 bp	12.85 %
BEL/Pao	0	0 bp	0.00 %
Ty1/Copia	32306	26373597 bp	4.00 %
Gypsy/DIRS1	72198	58095317 bp	8.81 %
Retroviral	0	0 bp	0.00 %
DNA transposons	64231	19145019 bp	2.90 %
hobo-Activator	7621	2024183 bp	0.31 %
Tc1-IS630-Pogo	11423	2135656 bp	0.32 %
En-Spm	20478	11006199 bp	1.67 %
MuDR-IS905	2046	810032 bp	0.12 %
PiggyBac	0	0 bp	0.00 %
Tourist/Harbinger	22359	3101410 bp	0.47 %
Other (Mirage, P-element, Transib)	0	0 bp	0.00 %
Rolling-circles	0	0 bp	0.00 %
Unclassified:	3241	773589 bp	0.12 %
Total interspersed repeats:		109548135 bp	16.62 %
Small RNA:	143	68967 bp	0.01 %
Satellites:	366	57388 bp	0.01 %
Simple repeats:	47050	2677604 bp	0.41 %
Low complexity:	98633	4371416 bp	0.66 %

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

The query species was assumed to be zea  
RepeatMasker version open-3.3.0 , default mode

run with rmblastn version : 2.2.23+  
RepBase Update 20110419, RM database version 20110419

```

=====
file name: Arabidopsis_thaliana.all_chromosomes.fasta
sequences: 5
total length: 119146348 bp (118960744 bp excl N/X-runs)
GC level: 36.03 %
bases masked: 19423425 bp ( 16.30 %)
=====

```

	number of elements*	length occupied	percentage of sequence
-----	-----	-----	-----
Retroelements	7283	9185573 bp	7.71 %
SINEs:	625	113434 bp	0.10 %
Penelope	0	0 bp	0.00 %
LINEs:	1494	1186326 bp	1.00 %
CRE/SLACS	0	0 bp	0.00 %
L2/CR1/Rex	0	0 bp	0.00 %
R1/L0A/Jockey	0	0 bp	0.00 %
R2/R4/NeSL	0	0 bp	0.00 %
RTE/Bov-B	0	0 bp	0.00 %
L1/CIN4	1426	1165614 bp	0.98 %
LTR elements:	5164	7885813 bp	6.62 %
BEL/Pao	0	0 bp	0.00 %
Ty1/Copia	1531	1694946 bp	1.42 %
Gypsy/DIRS1	2965	6115312 bp	5.13 %
Retroviral	0	0 bp	0.00 %
DNA transposons	7907	5188644 bp	4.35 %
hobo-Activator	1157	469562 bp	0.39 %
Tc1-IS630-Pogo	798	215960 bp	0.18 %
En-Spm	738	976950 bp	0.82 %
MuDR-IS905	3481	3016543 bp	2.53 %
PiggyBac	0	0 bp	0.00 %
Tourist/Harbinger	380	161707 bp	0.14 %
Other (Mirage, P-element, Transib)	0	0 bp	0.00 %
Rolling-circles	0	0 bp	0.00 %
Unclassified:	3406	2175285 bp	1.83 %
Total interspersed repeats:		16549502 bp	13.89 %
Small RNA:	354	60201 bp	0.05 %
Satellites:	1120	1022137 bp	0.86 %
Simple repeats:	9597	397721 bp	0.33 %
Low complexity:	31308	1447609 bp	1.21 %

```

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

```

The query species was assumed to be arabidopsis thaliana  
RepeatMasker version open-3.3.0 , default mode

run with rmblastn version : 2.2.23+  
RepBase Update 20110419, RM database version 20110419

```

=====
file name: Arabidopsis_lyrata.all_chromosomes.fasta
sequences:      8
total length: 194182311 bp (173245969 bp excl N/X-runs)
GC level:      35.98 %
bases masked:  34476087 bp ( 17.75 %)
=====

```

	number of elements*	length occupied	percentage of sequence
-----			
Retroelements	16497	18954941 bp	9.76 %
SINEs:	2100	489705 bp	0.25 %
Penelope	0	0 bp	0.00 %
LINEs:	3722	3503282 bp	1.80 %
CRE/SLACS	0	0 bp	0.00 %
L2/CR1/Rex	0	0 bp	0.00 %
R1/L0A/Jockey	0	0 bp	0.00 %
R2/R4/NeSL	0	0 bp	0.00 %
RTE/Bov-B	0	0 bp	0.00 %
L1/CIN4	3626	3473992 bp	1.79 %
LTR elements:	10675	14961954 bp	7.71 %
BEL/Pao	0	0 bp	0.00 %
Ty1/Copia	4610	5541842 bp	2.85 %
Gypsy/DIRS1	5618	9237653 bp	4.76 %
Retroviral	0	0 bp	0.00 %
DNA transposons	19684	7188652 bp	3.70 %
hobo-Activator	3473	1052035 bp	0.54 %
Tc1-IS630-Pogo	2673	537572 bp	0.28 %
En-Spm	1958	1197364 bp	0.62 %
MuDR-IS905	8903	3628893 bp	1.87 %
PiggyBac	0	0 bp	0.00 %
Tourist/Harbinger	673	293304 bp	0.15 %
Other (Mirage, P-element, Transib)	0	0 bp	0.00 %
Rolling-circles	0	0 bp	0.00 %
Unclassified:	10570	3441746 bp	1.77 %
Total interspersed repeats:		29585339 bp	15.24 %
Small RNA:	1277	298680 bp	0.15 %
Satellites:	1880	515210 bp	0.27 %
Simple repeats:	19531	824259 bp	0.42 %
Low complexity:	69858	3555824 bp	1.83 %

```

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

```

The query species was assumed to be arabidopsis  
RepeatMasker version open-3.3.0 , default mode

run with rmblastn version : 2.2.23+  
RepBase Update 20110419, RM database version 20110419