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file name: DAV_5_melpomene_a-scaffolds.fasta_1kb.fa
sequences: 12179
total length: 289529429 bp (289477054 bp excl N/X-runs)
GC level: 32.74 %
bases masked: 42390139 bp ( 14.64 %)
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	number of elements*	length occupied	percentage of sequence
Retroelements	18032	4390549 bp	1.52 %
SINEs:	684	34049 bp	0.01 %
Penelope	2	155 bp	0.00 %
LINEs:	12167	3257088 bp	1.12 %
CRE/SLACS	0	0 bp	0.00 %
L2/CR1/Rex	6128	1511859 bp	0.52 %
R1/LOA/Jockey	2340	674824 bp	0.23 %
R2/R4/NeSL	1459	468411 bp	0.16 %
RTE/Bov-B	1740	483943 bp	0.17 %
L1/CIN4	12	624 bp	0.00 %
LTR elements:	5181	1099412 bp	0.38 %
BEL/Pao	633	144481 bp	0.05 %
Ty1/Copia	178	40374 bp	0.01 %
Gypsy/DIRS1	3862	807954 bp	0.28 %
Retroviral	0	0 bp	0.00 %
DNA transposons	231972	30820377 bp	10.64 %
hobo-Activator	8196	1506936 bp	0.52 %
Tc1-IS630-Pogo	123631	15828698 bp	5.47 %
En-Spm	0	0 bp	0.00 %
MuDR-IS905	0	0 bp	0.00 %
PiggyBac	88	35700 bp	0.01 %
Tourist/Harbinger	11	1563 bp	0.00 %
Other (Mirage, P-element, Transib)	146	7447 bp	0.00 %
Rolling-circles	0	0 bp	0.00 %
Unclassified:	1997	282672 bp	0.10 %
Total interspersed repeats:		35493598 bp	12.26 %
Small RNA:	790	49738 bp	0.02 %
Satellites:	331	18247 bp	0.01 %
Simple repeats:	128725	5687070 bp	1.96 %
Low complexity:	25791	1246843 bp	0.43 %

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

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The query species was assumed to be hexapoda
RepeatMasker version open-4.0.5 , default mode

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