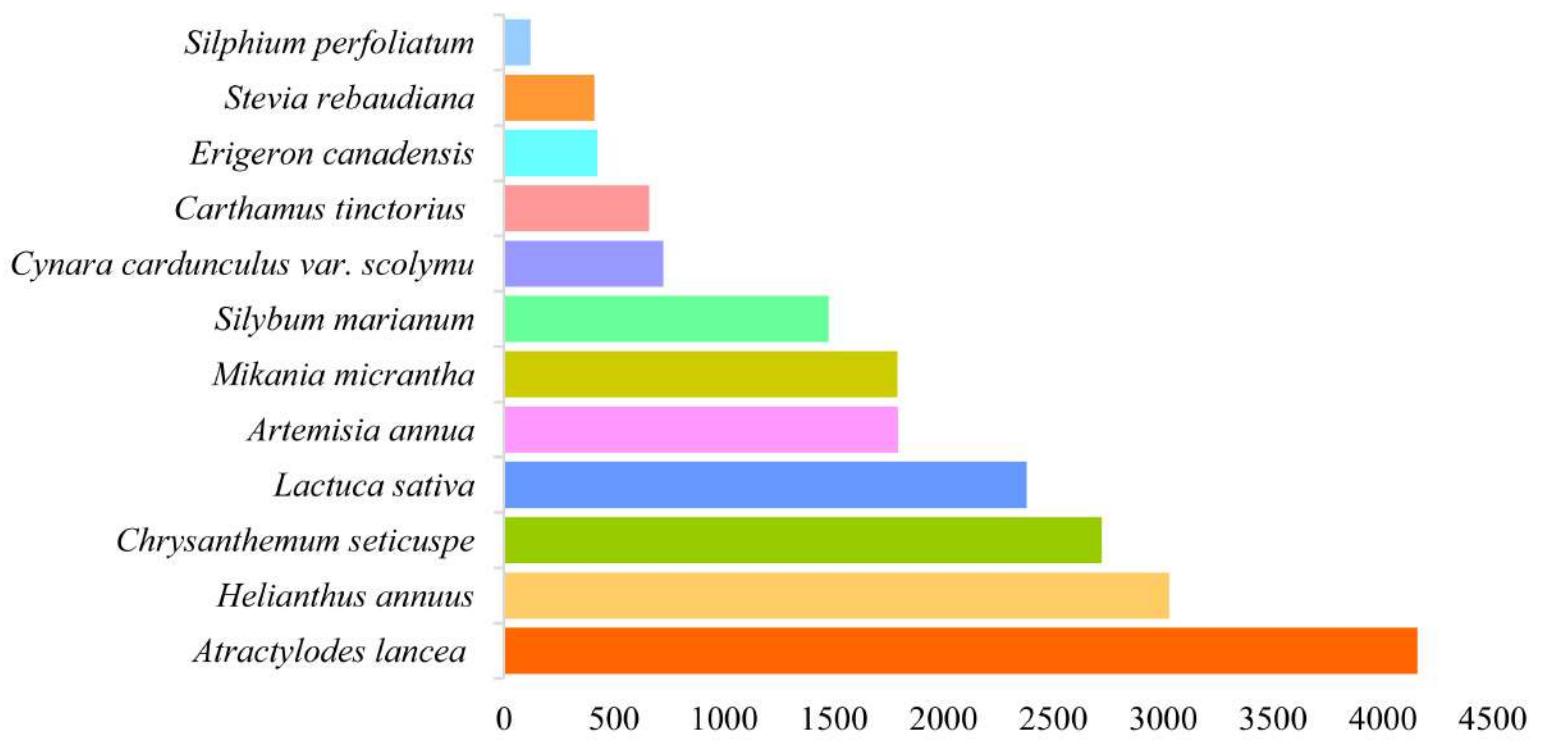
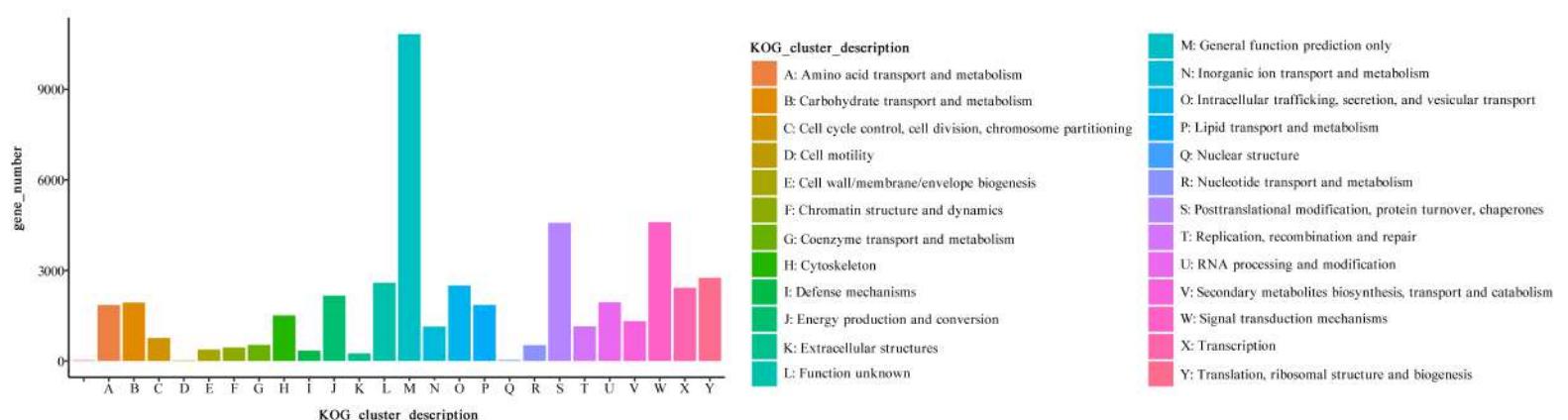




Supplementary Figure S1. Plants and rhizome of *A.lancea*



Supplementary Figure S2. Comparison the genome size of 12 species of Compositae



Supplementary Figure S3.KOG functional classification of *A. lanceaunigenes*.

NR_annotation_stats

species

Cynara:0.51
Lactuca:0.1
Homo:0.1
Rhizoctonia:0.08
Helianthus:0.06
Artemisia:0.05
Phialocephala:0.03
Rhizophagus:0.03
Stagonospora:0.02
Parastagonospora:0.01

NR_annotation_ratio

Supplementary Figure S4. NR annotated homologous species distributions

Supplementary Table S1. Statistics of filtering data

Lib id	Length	Raw data	Clean data	GC rate
190626_I9_V300022484_L3_RHIs hvDAAAA-573	150	14,518,852,200	14,249,431,800	38.98
190626_I9_V300022484_L3_RHIs hvDAAAA-574	150	16,785,220,500	16,471,137,000	38.91
190626_I9_V300022484_L3_RHIs hvDAAAA-575	150	14,729,106,000	14,448,511,200	38.9
190626_I9_V300022484_L3_RHIs hvDAAAA-576	150	13,615,597,500	13,348,510,200	38.93
190626_I9_V300022484_L3_RHIs hvDAAAA-577	150	15,861,435,600	15,566,351,400	38.89
190626_I9_V300022484_L3_RHIs hvDAAAA-578	150	16,151,568,000	15,851,755,800	38.94
190626_I9_V300022484_L3_RHIs hvDAAAA-579	150	17,966,042,100	17,646,709,500	38.87
190626_I9_V300022484_L3_RHIs hvDAAAA-580	150	14,990,523,000	14,716,546,800	38.94
190626_I9_V300022484_L4_RHIs hvDAAAA-573	150	15,333,206,400	14,993,685,600	38.88
190626_I9_V300022484_L4_RHIs hvDAAAA-574	150	17,745,398,100	17,352,470,700	38.8
190626_I9_V300022484_L4_RHIs hvDAAAA-575	150	15,459,255,300	15,108,670,500	38.81
190626_I9_V300022484_L4_RHIs hvDAAAA-576	150	14,491,109,700	14,161,733,400	38.8
190626_I9_V300022484_L4_RHIs hvDAAAA-577	150	16,822,270,200	16,451,535,000	38.78
190626_I9_V300022484_L4_RHIs hvDAAAA-578	150	17,067,861,600	16,689,940,500	38.84
190626_I9_V300022484_L4_RHIs hvDAAAA-579	150	18,935,608,800	18,532,550,100	38.77
190626_I9_V300022484_L4_RHIs hvDAAAA-580	150	15,874,163,700	15,529,107,600	38.84

Supplementary Table S2. Genome assembly statistics of *A. lancea* and comparisons to 11 genomes of Compositae

Species	Gene size (Mb)	Number of protein-coding genes	GC content (%)	Hetero zygosity (%)	Repeat (%)	References
<i>Actractylodes lancea</i>	4159.24	n.c	38.4	2.28	89.2	This study
<i>Carthamus tinctorius</i> (safflower)	661.938	n.c	37.3	n.c	n.c	Bower, J.E, 2016
<i>Stevia rebaudiana</i>	411.38	n.c	34.6	n.c	n.c	n.c
<i>Chrysanthemum seticuspe</i>	2721.84	n.c	36.1	n.c	72.5	Hideki, 2019
<i>Silphium perfoliatum</i>	121.712	n.c	36.7	n.c	n.c	n.c
<i>Silybum marianum</i>	1477.58	n.c	37.2	n.c	n.c	n.c
<i>Erigeron canadensis</i>	425.611	n.c	34	0.203	42.9	Laforest et al., 2020 Peng et al., 2014
<i>Mikania micrantha</i>	1790.64	46329	36.2	n.c	n.c	n.c
<i>Cynara cardunculus</i> var. <i>scolymus</i>	725.198	38406	36.75	n.c	n.c	Caglione et al., 2016
<i>Lactuca sativa</i>	2380	38919	37.75	n.c	n.c	Verwaaijen et al., 2017 Reye et al., 2016
<i>Artemisia annua</i>	1792.86	66918	34.1	1.0-1.5	60.1	Shen et al., 2018
<i>Helianthus annuus</i>	3027.84	73839	38.91	n.c	n.c	Bock et al., 2014 Badouin et al., 2017

Supplementary Table S3. Statistics of gene functional annotation

Data_base	annotated_number	annotated_ratio
GO	33896	24%
KEGG	34929	24%
KOG	48493	34%
nr	91165	64%
pfam	58121	41%
swiss_prot	60411	42%
TrEMBL	92046	65%
Total	93434	66%