De novo transcriptome assembly for the spiny mouse (*Acomys cahirinus*)

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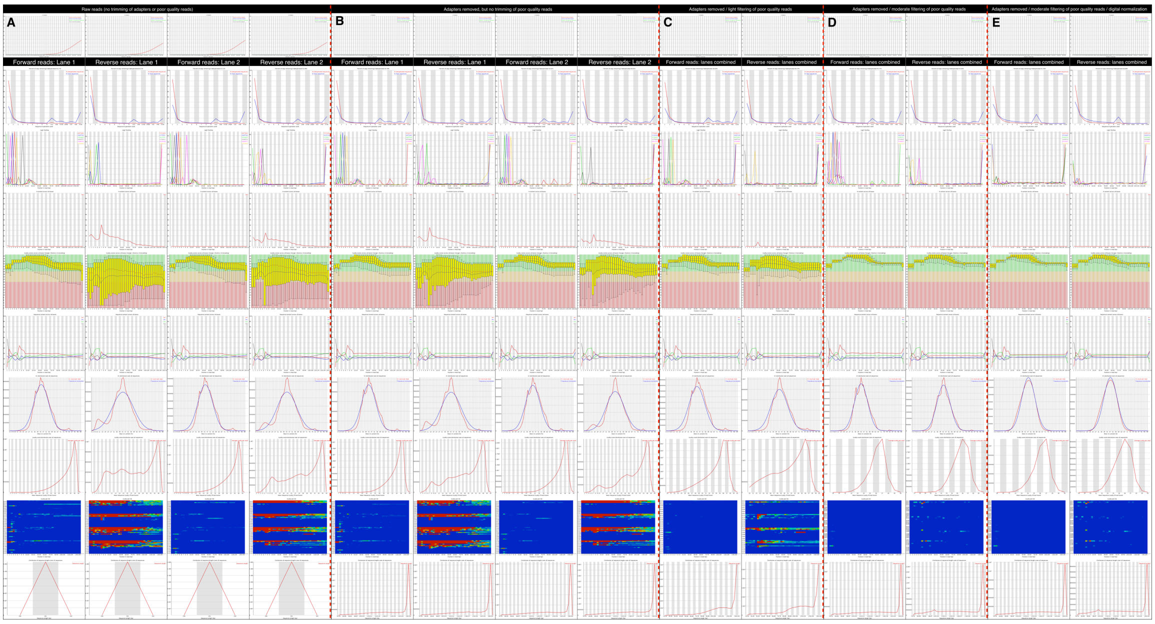
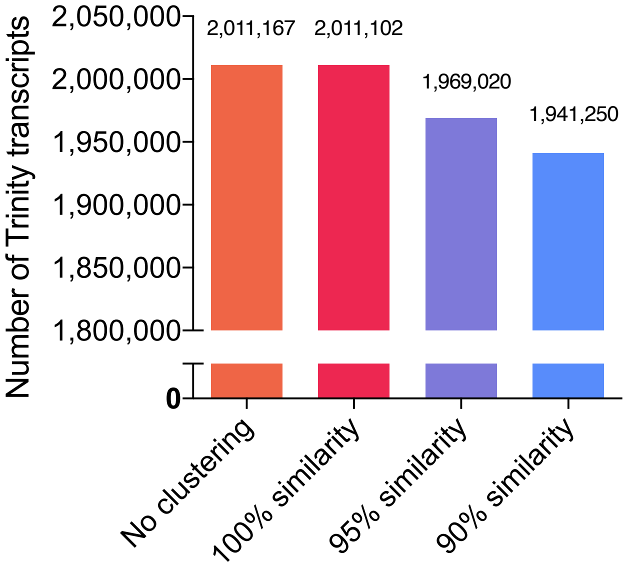
Supplementary Figures

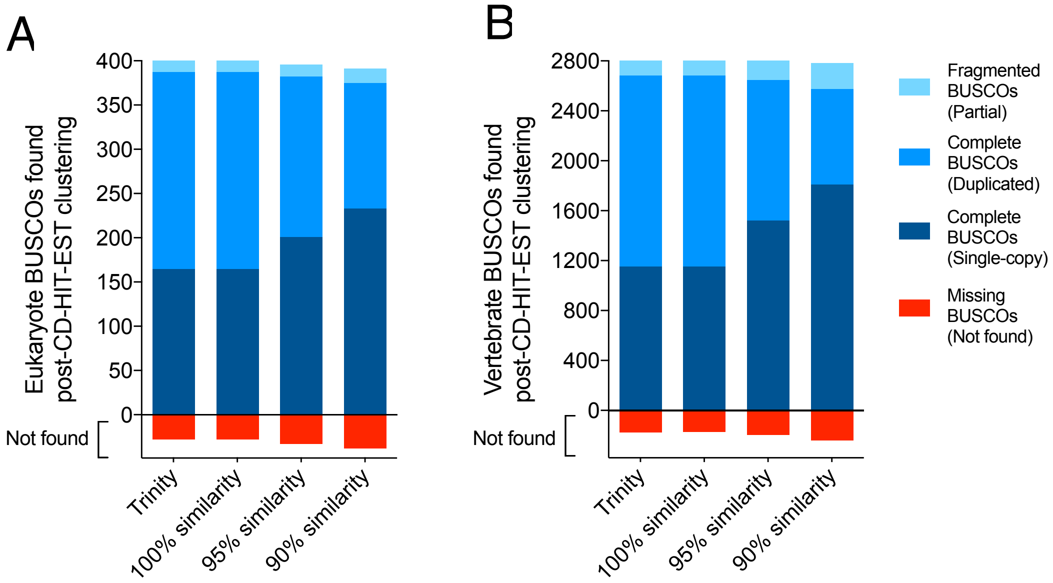


Supplementary Figure S1: FastQC reports for RNA-Seq reads: (A) unfiltered, (B) light filtering of poor quality reads, (C) moderate filtering of concatenated reads, (D) Strict quality filtering, (E) In silico normalization.

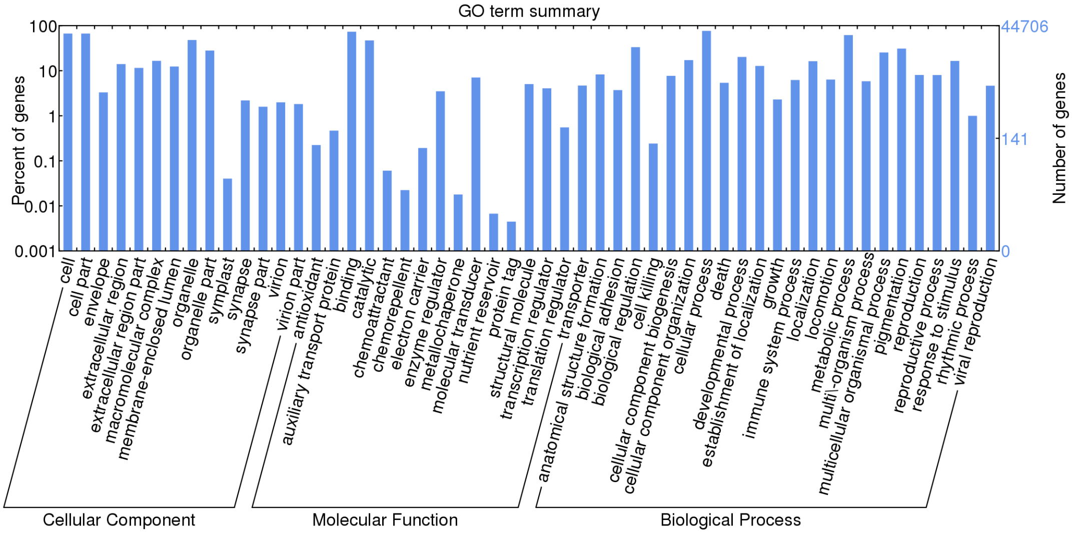
Full resolution image: https://doi.org/10.6084/m9.figshare.5170783.v1



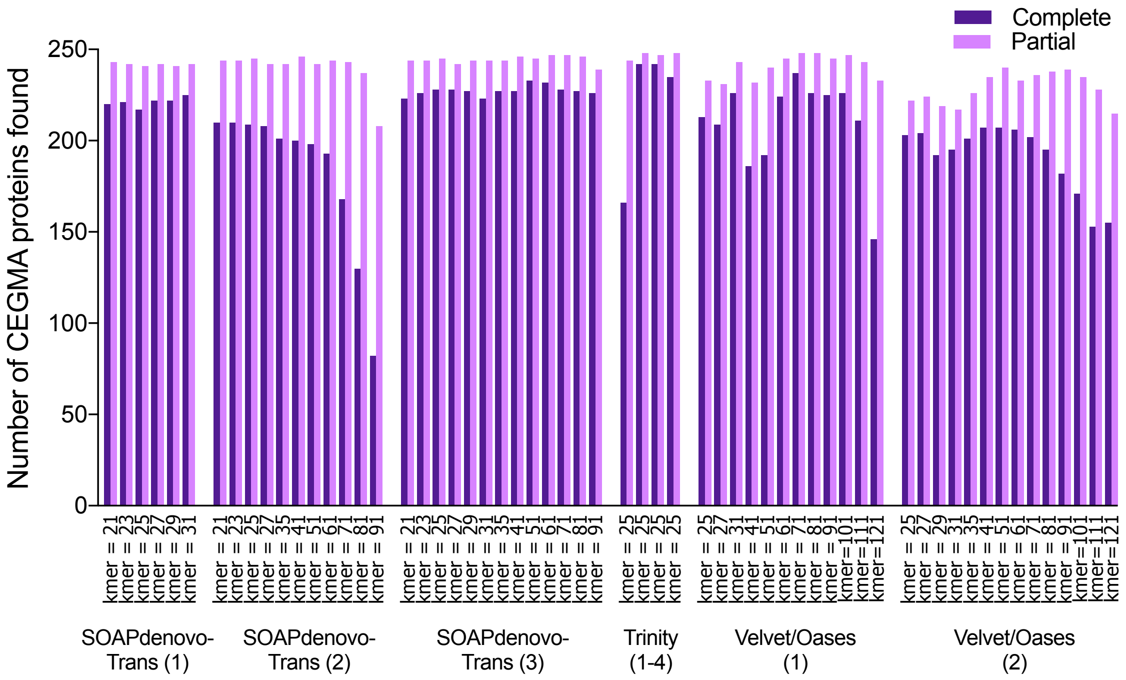
Supplementary Figure S2: Number of Trinity transcripts after CD-HIT-EST clustering at specified thresholds (100%, 95%, 90%).



Supplementary Figure S3: BUSCO analysis after CD-HIT-EST clustering at specified thresholds (100%, 95%, 90%). (A) Eukaryota, (B) Vertebrata



Supplementary Figure S4: Summary of gene ontology (GO) terms associated with SwissProt/UniProt blast hits.



Supplementary Figure S5: Number of complete/partial CEGMA proteins found in each assembly.

Table S1. Summary statistics for RNASeq runs.

	Forward reads		Reverse reads		Total
Yield Total (G)	45.9		45.9		91.77617
Aligned (%)	0.45		0.25		0.3509741
Error Rate (%)	0.62		1.6		1.003602
Intensity Cycle 1	3255		3054		3154.379
% >= Q30	80.5		46.5		63.47869
Lane	1	2	1	2	
Tiles	64	64	64	64	
Density (K/mm2)	1209 ± 78	1242 ± 72	1209 ± 78	1242 ± 72	
Clusters PF (%)	64.69 ± 14	69.66 ± 10	64.69 ± 14	69.66 ± 10	
Phas/Prephas (%)	0.157 / 0.202	0.151 / 0.209	0.076 / 0.121	0.100 / 0.164	
Reads (M)	222.79	228.94	222.79	228.94	
Reads PF (M)	145.46	160.46	145.46	160.46	
% >= Q30	80.2	80.7	42.1	50.4	
Yield(G)	22	24	22	24	
Cycles Err Rated	150	150	0 150 0 150		
Aligned (%)	0.44 ± 0.06	0.46 ± 0.05	0.22 ± 0.20	0.28 ± 0.20	
Error Rate (%)	0.65 ± 0.30	0.59 ± 0.24	1.59 ± 0.51	1.61 ± 0.90	
Error Rate 35 cycle	0.33 ± 0.26	0.24 ± 0.21	0.89 ± 0.39	0.95 ± 0.61	
Error Rate 75 cycle	0.38 ± 0.27	0.31 ± 0.22	1.27 ± 0.51	1.18 ± 0.60	
Error Rate 100 cycle	0.44 ± 0.27	0.38 ± 0.29	1.35 ± 0.52	1.30 ± 0.69	
Intensity Cycle 1	3285 ± 266	3225 ± 264	2995 ± 1829	3113 ± 1678	

Supplementary Table S2: EvidentialGene tr2aacds pipeline output (class tables)

Class Table for Tr2aacds_v1

```
class           okay      drop      okay      drop
althi           11.2      1.2       112390    12098
althi1          6.1       1.5       61522     15135
althia2         0         0         0         629
altmfrag        0.2       0         2272      364
altmfraga2      0         0         171       21
altmid          0.8       0         8259      856
altmida2        0.1       0         1276      84
main            11.1      0.6       112092    6870
maina2          0.2       0         2865      629
noclass         58.5      6.1       587241    61278
noclassa2       0         0         372       98
parthi          0         1.2       0         12337
parthi1         0         0.3       0         3918
parthia2        0         0         0         511
-------------------------------------------------------------------------------------------
total       88.5          11.4      888460    114828
=======================================================
# AA-quality for okay set (no okalt): all and longest 1000 summary
                n         average   median    min,max       sum         gaps
okay.top        1000      2138      1837      1397, 29738   2138352     110, 0.1
okay.all        702570    100       83        40, 29738     70957577    224333, 0.3
```

Class Table for Tr2aacds_v2

```
class           okay      drop      okay      drop
althi           1.9       18.2      239423    2211673
althi1          1.1       17        133676    2065173
althia2         0         0.2       0         26395
altmfrag        0         0.2       3396      27243
altmfraga2      0         0         324       1285
altmid          0.1       1         16618     122236
altmida2        0         0.1       3081      13216
main            3.3       15.7      406187    1916052
maina2          0         0.5       10564     63529
noclass         1.8       29.1      221430    3532448
noclassa2       0         0         425       4697
parthi          0         6.5       0         790178
parthi1         0         2.3       0         279538
parthia2        0         0.3       0         43112
---------------------------------------------------------------------------------------------
total           8.5       91.4      1035124   11096775
=======================================================
# AA-quality for okay set (no okalt): all and longest 1000 summary
            n         average   median    min,max         sum         gaps
okay.top    1000      2096      1799      1372, 29738     2096967     344, 0.3
okay.all    638606    104       91        40, 29738       66481461    211449, 0.3
```