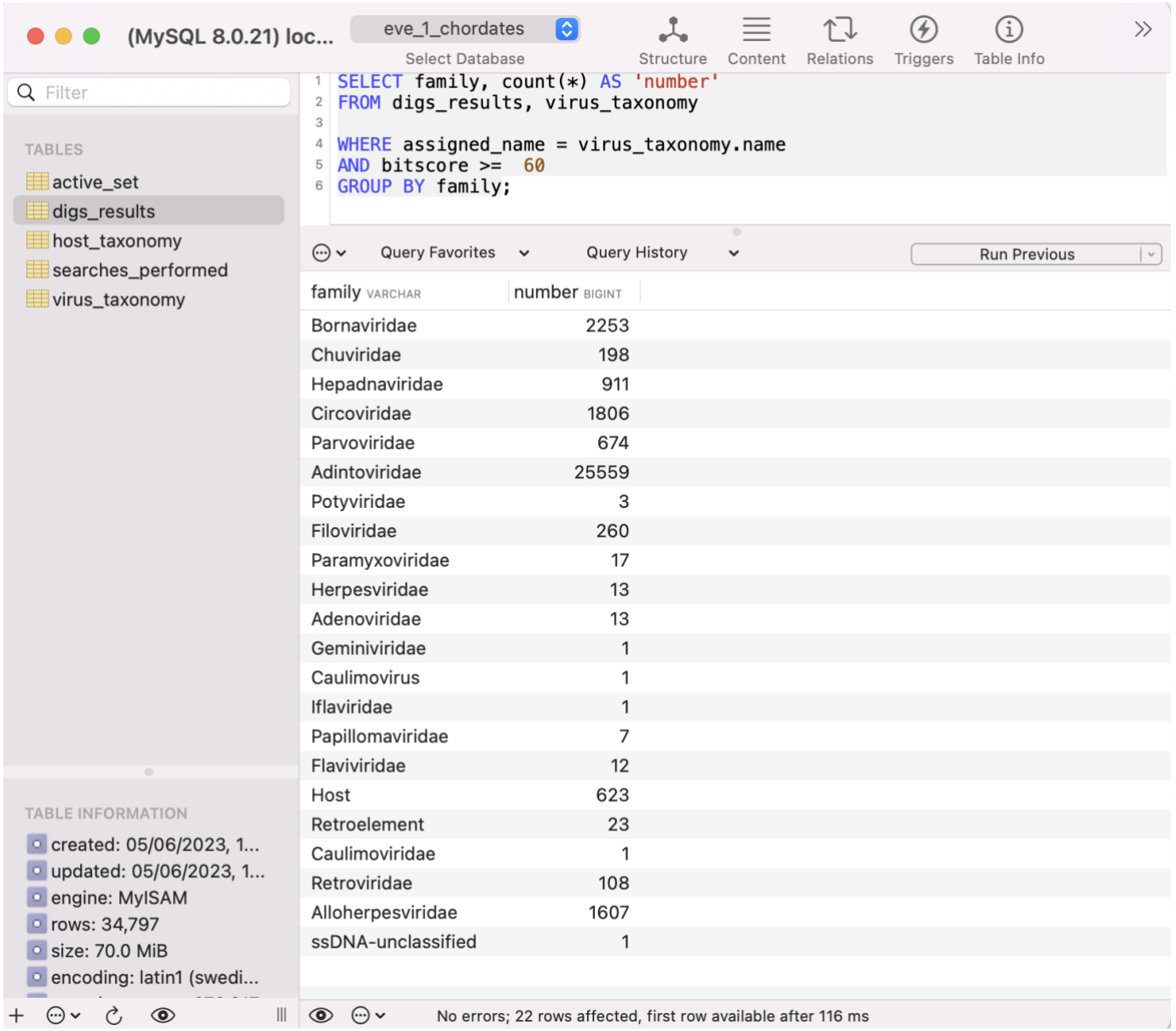
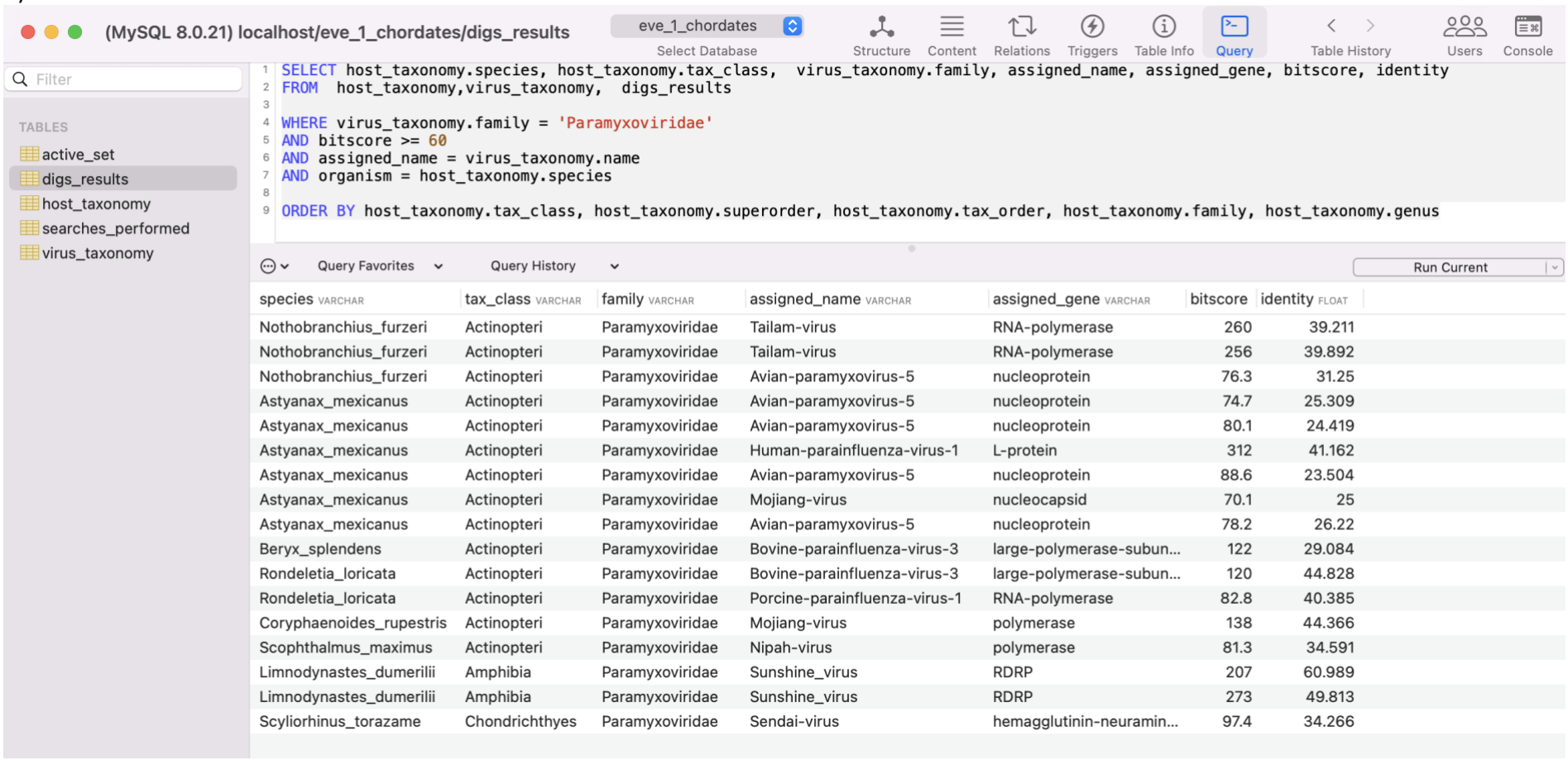
a)

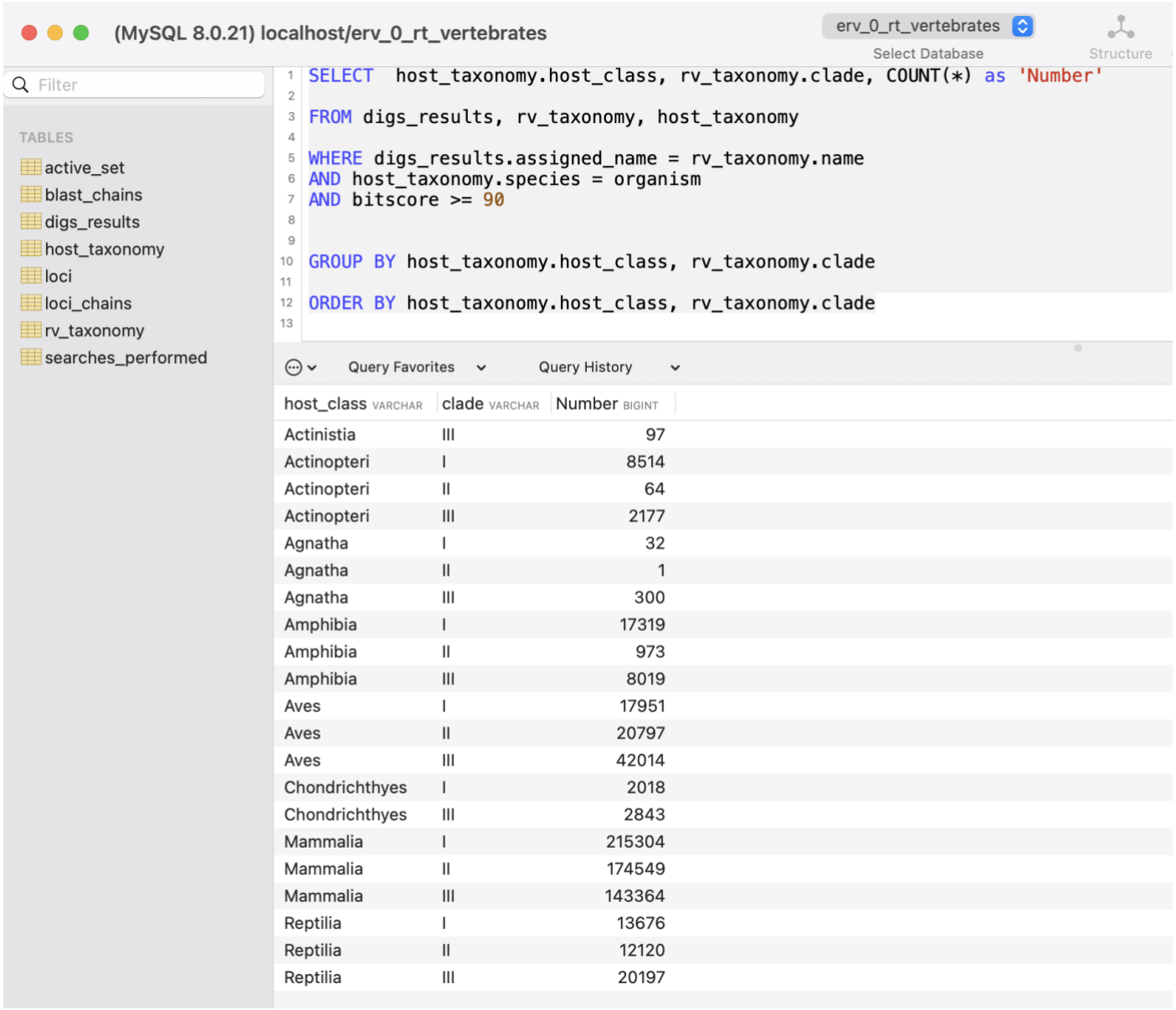

(MySQL 8.0.21) loc...
eve_1_chordates
Select Database
Structure
Content
Relations
Triggers
Table Info
Filter
TABLES
active_set
digs_results
host_taxonomy
searches_performed
virus_taxonomy
1 SELECT family, count(*) AS 'number'
2 FROM digs_results, virus_taxonomy
3
4 WHERE assigned_name = virus_taxonomy.name
5 AND bitscore >= 60
6 GROUP BY family;
Query Favorites
Query History
Run Previous
family VARCHAR
number BIGINT
Bornaviridae 2253
Chuviridae 198
Hepadnaviridae 911
Circoviridae 1806
Parvoviridae 674
Adintoviridae 25559
Potyviridae 3
Filoviridae 260
Paramyxoviridae 17
Herpesviridae 13
Adenoviridae 13
Geminiviridae 1
Caulimovirus 1
Iflaviridae 1
Papillomaviridae 7
Flaviviridae 12
Host 623
Retroelement 23
Caulimoviridae 1
Retroviridae 108
Alloherpesviridae 1607
ssDNA-unclassified 1
TABLE INFORMATION
created: 05/06/2023, 1...
updated: 05/06/2023, 1...
engine: MyISAM
rows: 34,797
size: 70.0 MiB
encoding: latin1 (swedi...
No errors; 22 rows affected, first row available after 116 ms

b)



species VARCHAR	tax_class VARCHAR	family VARCHAR	assigned_name VARCHAR	assigned_gene VARCHAR	bitscore	identity FLOAT
Nothobranchius_furzeri	Actinopteri	Paramyxoviridae	Tailam-virus	RNA-polymerase	260	39.211
Nothobranchius_furzeri	Actinopteri	Paramyxoviridae	Tailam-virus	RNA-polymerase	256	39.892
Nothobranchius_furzeri	Actinopteri	Paramyxoviridae	Avian-paramyxovirus-5	nucleoprotein	76.3	31.25
Astyanax_mexicanus	Actinopteri	Paramyxoviridae	Avian-paramyxovirus-5	nucleoprotein	74.7	25.309
Astyanax_mexicanus	Actinopteri	Paramyxoviridae	Avian-paramyxovirus-5	nucleoprotein	80.1	24.419
Astyanax_mexicanus	Actinopteri	Paramyxoviridae	Human-parainfluenza-virus-1	L-protein	312	41.162
Astyanax_mexicanus	Actinopteri	Paramyxoviridae	Avian-paramyxovirus-5	nucleoprotein	88.6	23.504
Astyanax_mexicanus	Actinopteri	Paramyxoviridae	Mojiang-virus	nucleocapsid	70.1	25
Astyanax_mexicanus	Actinopteri	Paramyxoviridae	Avian-paramyxovirus-5	nucleoprotein	78.2	26.22
Beryx_splendens	Actinopteri	Paramyxoviridae	Bovine-parainfluenza-virus-3	large-polymerase-subun...	122	29.084
Rondeletia_loricata	Actinopteri	Paramyxoviridae	Bovine-parainfluenza-virus-3	large-polymerase-subun...	120	44.828
Rondeletia_loricata	Actinopteri	Paramyxoviridae	Porcine-parainfluenza-virus-1	RNA-polymerase	82.8	40.385
Coryphaenoides_rupestris	Actinopteri	Paramyxoviridae	Mojiang-virus	polymerase	138	44.366
Scophthalmus_maximus	Actinopteri	Paramyxoviridae	Nipah-virus	polymerase	81.3	34.591
Limnodynastes_dumerilii	Amphibia	Paramyxoviridae	Sunshine_virus	RDRP	207	60.989
Limnodynastes_dumerilii	Amphibia	Paramyxoviridae	Sunshine_virus	RDRP	273	49.813
Scyliorhinus_torazame	Chondrichthyes	Paramyxoviridae	Sendai-virus	hemagglutinin-neuramin...	97.4	34.266

c)



host_class VARCHAR	clade VARCHAR	Number BIGINT
Actinistia	III	97
Actinopteri	I	8514
Actinopteri	II	64
Actinopteri	III	2177
Agnatha	I	32
Agnatha	II	1
Agnatha	III	300
Amphibia	I	17319
Amphibia	II	973
Amphibia	III	8019
Aves	I	17951
Aves	II	20797
Aves	III	42014
Chondrichthyes	I	2018
Chondrichthyes	III	2843
Mammalia	I	215304
Mammalia	II	174549
Mammalia	III	143364
Reptilia	I	13676
Reptilia	II	12120
Reptilia	III	20197

Figure S3. Examples of SQL-based querying of DIGS results.

Panels show screenshots of a MySQL client program (Sequel Ace) connected to a screening database generated using the database-integrated genome screening (DIGS) tool. Structured query language (SQL) can be used to interrogate and manipulate screening databases. Each panel shows a distinct SQL query (upper window) and its results (lower window).

(a) Deriving stratified counts of non-retroviral EVE loci. The query shown here uses a custom table ('virus taxonomy',) linked via the 'assigned name' field (see **Fig. S2a)**, to group hits according to virus family. A 'digs results' table field, 'bit score', is used to restrict results to higher confidence hits - it is derived from the 'reverse' BLAST-step, in which a sequence hit identified from a 'forward' BLAST (i.e. probe versus target database file) is compared to the reference sequence library (RSL). It thereby provides an index showing how similar individual hits are to sequences included in the RSL.

(b) Retrieving information about paramyxovirus-derived EVEs recovered via DIGS. The query shown here provides an overview of paramyxovirus EVEs, showing the vertebrate class in which they were identified, which paramyxovirus species and genes they disclose similarity to (based on comparison to RSL sequences), and fields that show the closeness of the match. It uses two custom tables: (i) 'virus taxonomy' and (ii) 'host taxonomy,' which is linked via the 'organism' field (see **Fig. S2**). A bitscore cut-off is used to filter hits, and an order statement is used to sort results by the taxonomic designations of host species.

(c) An SQL query used to retrieve individual counts of high confidence endogenous retrovirus (ERV) reverse transcriptase (RT). RT hits were recovered by screening a target database comprising whole genome sequence data of 874 vertebrate species. We empirically determined that a bit score of >=90 eliminates false positive RT hits. Host and virus taxonomy tables, linked as described above for non-retroviral viruses, are used to stratify results.