

CORRECTION

Correction: DeltaBreed: A BrAPI-centric breeding data information system

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The images for [Figs 2–7](#) and [9](#) and [10](#) are incorrectly switched. The image that appears as [Fig 6](#) should be [Fig 2](#), the image that appears as [Fig 4](#) should be [Fig 3](#), the image that appears as [Fig 5](#) should be [Fig 4](#), the image that appears as [Fig 7](#) should be [Fig 5](#), the image that appears as [Fig 2](#) should be [Fig 6](#), the image that appears as [Fig 3](#) should be [Fig 7](#), the image that appears as [Fig 10](#) should be [Fig 9](#) and the image that appears as [Fig 9](#) should be [Fig 10](#). The figure captions appear in the correct order. The authors have provided a corrected version of figures here.

Reference

- Yarnes SC, Palladino N, Meidlinger DJ, Philips DR, Sweeney HM, Mustafa SA, et al. DeltaBreed: A BrAPI-centric breeding data information system. PLoS One. 2025;20(12):e0324104. <https://doi.org/10.1371/journal.pone.0324104> PMID: 41385557



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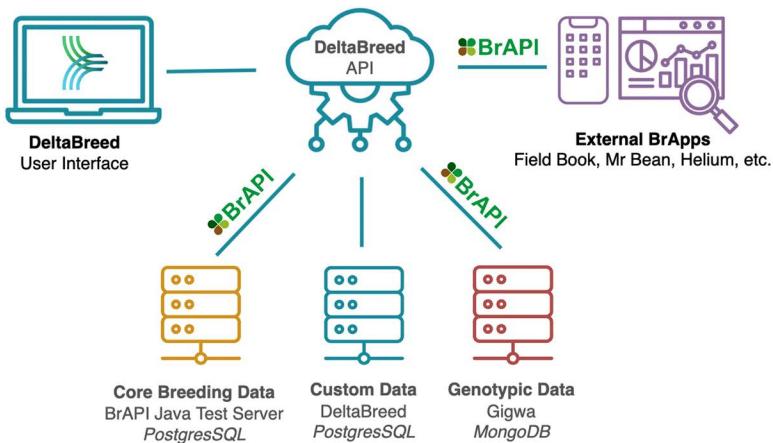


Fig 2. DeltaBreed v1.0 modular software architecture. Users can interact with DeltaBreed v1.0 data through the web interface and via external BrApps. REST APIs, primarily BrAPI, are used to communicate breeding data among various web services, including DeltaBreed-associated databases. DeltaBreed v1.0 communicates with two BrAPI databases and uses a custom database to handle data not supported by BrAPI, like user account management. Disparate data types are handled by connected subsystems with optimized data architectures suitable to the data storage needs. BrAPI logo republished under a CC BY license, with permission from Peter Selby, original copywrite 2016.

<https://doi.org/10.1371/journal.pone.0341691.g002>

ⓘ Error(s) detected in file, Error Message Feature.xls. (See details below.) Import cannot proceed. ×

Import File

Germplasm Ontology **Experiments & Observations** Genotypic Data Genotype Samples

Importing...

Before You Import...
 Experimental germplasm and ontology terms must be created in the system before experiments can be created via import. See the import template for more information about data requirements. Importing phenotypic observations into existing experiments requires only Observation Unit IDs to match with the experimental design.

[Download the Experiments & Observations Import Template](#)
Template version placeholder

Select workflow
 Create new experiment ▼

Choose a file...

⚠ File contains data errors

Row	Field	Error
3	X length	Non-numeric text detected detected
4	X Disease Rate	Undefined ordinal category detected
6	Germplasm GID	A non-existing GID
6	X Date	Incorrect date format detected. Expected YYYY-MM-DD
8	X Disease Rate	Undefined ordinal category detected
9	Germplasm GID	A non-existing GID
9	X Disease Rate	Undefined ordinal category detected

Fig 3. A screenshot of DeltaBreed v1.0 experiment and observation file import module displaying data validation and error messaging. DeltaBreed v1.0 has clear and actionable UI error messaging, as demonstrated in the experiment import module. Error messages appear as a banner across the top of the windowpane. In this example, there are several data errors detected in the Experiment and Observation import file. An error table indicates to users to the exact row(s) in the import file that needs correction.

<https://doi.org/10.1371/journal.pone.0341691.g003>

DELTA BREED ABC ⌂

Ontology Term Active

Term Type* Phenotype

Name* PltHght

Full Name Plant Height (cm)

Description* assessed by meter stick from ground to flag leaf at maturity (cm)

Synonyms PltHght, Plant Height (cm)

Tags morphological Start typing to see suggestions

Trait = Entity + Attribute = Plant Height

Entity* Plant

Attribute* Height

Method = Description + Class = Meter Stick Measurement

Description Meter Stick

Class* Measurement

Scale

Class* Numerical

Note: additional options for this field will appear after selection

Unit* cm

Can be any measurable unit.

Min Minimum Valid Enter integer value only.

Max Maximum Valid Enter integer value only.

Decimals Decimal Places Leave blank for integer type.

Save Cancel

Fig 4. DeltaBreed v1.0 ontology module screenshot of a Plant Height observation variable.

<https://doi.org/10.1371/journal.pone.0341691.g004>

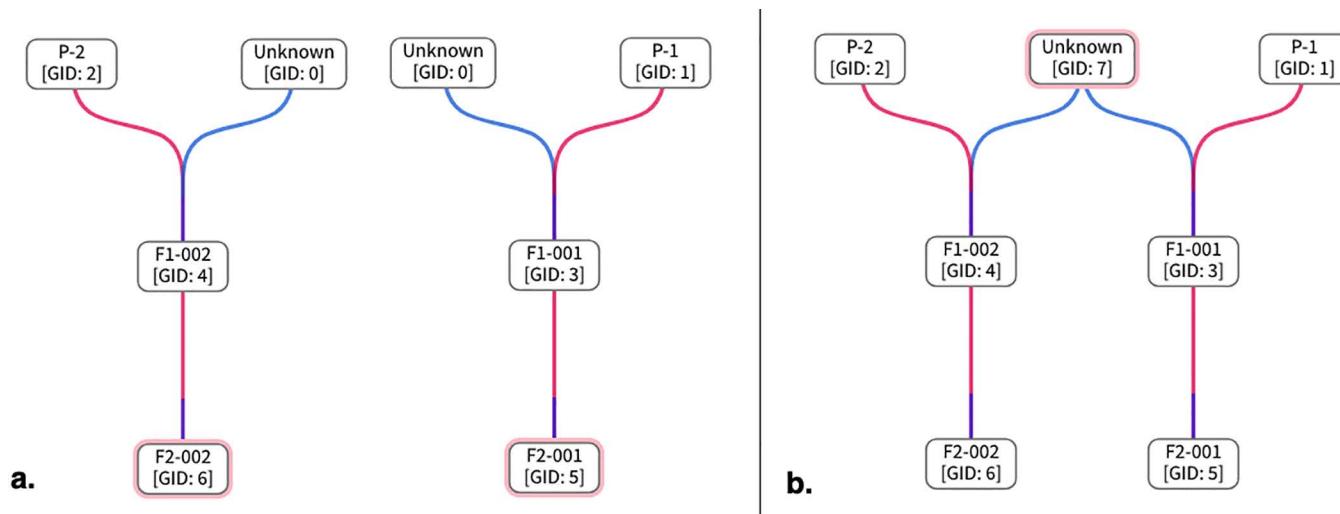


Fig 5. Screenshots of DeltaBreed v1.0 pedigree viewer module when there is an unknown parent in germplasm records.

<https://doi.org/10.1371/journal.pone.0341691.g005>

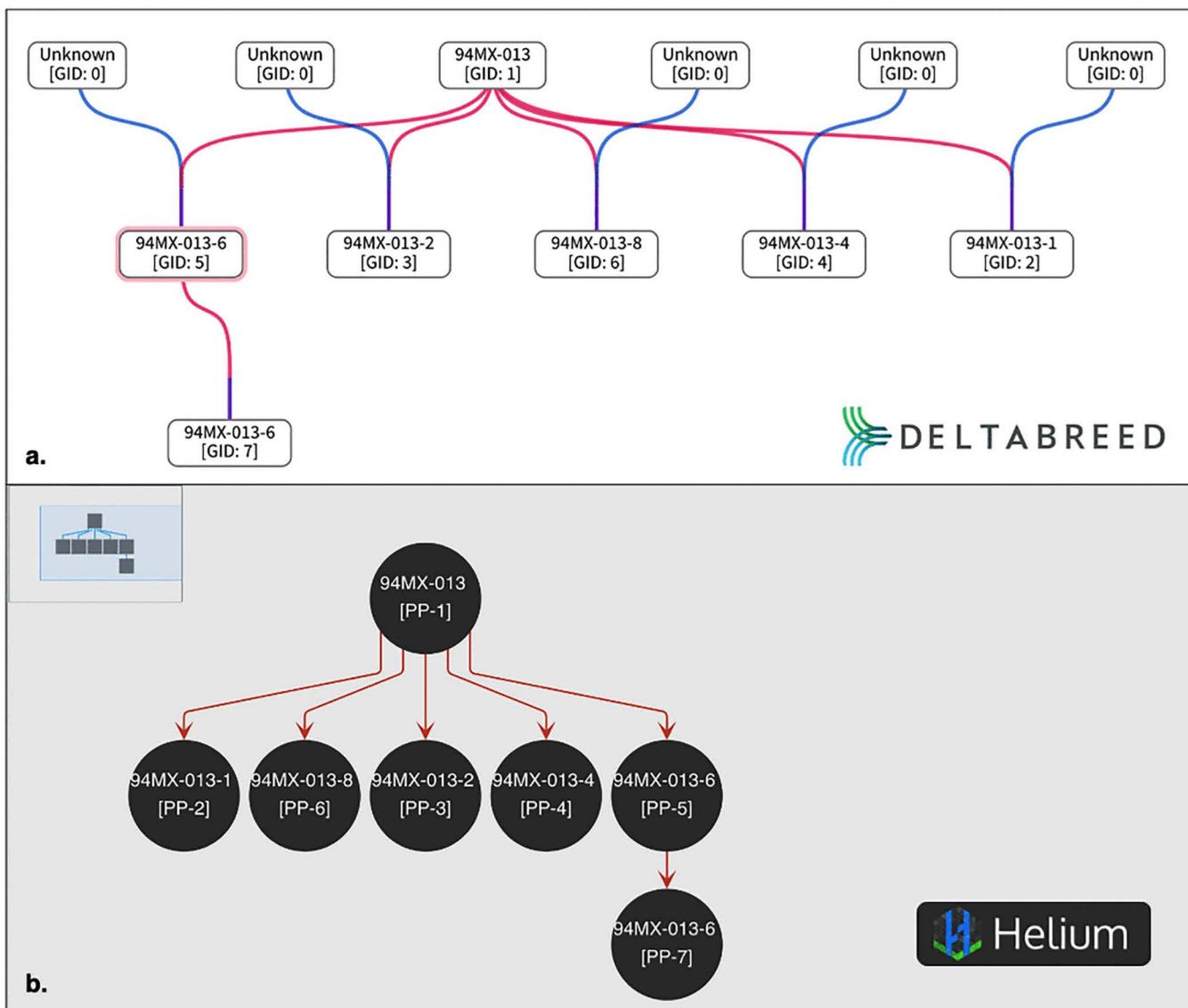


Fig 6. Screenshots of a pedigree view comparing DeltaBreed v1.0 and Helium for the same pecan individual.

<https://doi.org/10.1371/journal.pone.0341691.g006>

ABC

Home

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System Administration

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webv1.1+e53/splv1.1.1+995

< All Experiments

2025 Disease Screen 001

Description: Disease resistance evaluation - fictional
Experimental unit: Plot
Type: RCBD
User: BI-DEV Admin
Creation Date: 2025-06-10
Experimental design: Externally generated

Germplasm: 100
Collaborators:
Manage Experiment

Plot

Observation Variables: 6
Total observations: 0

Germplasm Name	GID	Test(T) or Check (C)	Env	Env Location	Env Year	Exp Unit ID	Exp Replicate #	Exp Block #	Row	Column	Lat	Long	Elevation	RTK	Treatment Factors	ObsUnitID	X Disease Rate	X Length
Mood	418	TEST	Ith23	Ithaca, NY	2023	1	1	1	1	1	-76.537262	42.407916	125	500 cfu	894fb0c0-3628-4f15-8723-a2d6403b315b			
Pop	90	TEST	Ith23	Ithaca, NY	2023	2	1	1	1	2	-76.537262	42.407916	125	500 cfu	c020416a-0c0e-4b3c-bdca-0db6e75d8ff1			
Farm	498	TEST	Ith23	Ithaca, NY	2023	3	1	1	1	3	-76.537262	42.407916	125	500 cfu	6db1bf97-b0fe-44c9-af09-24a36b3b9fa2			
Polished	779	TEST	Ith23	Ithaca, NY	2023	4	1	1	1	4	-76.537262	42.407916	125	500 cfu	5518c06c-f965-44cd-963a-f8fe4a8e726e			
Hunt	1220	TEST	Ith23	Ithaca, NY	2023	5	1	1	1	5	-76.537262	42.407916	125	500 cfu	92e486ff-be27-4d91-b886-a299da5582d4			
Bus	637	CHECK	Ith23	Ithaca, NY	2023	6	1	1	1	6	-76.537262	42.407916	125	500 cfu	423464fc-d534-42de-991d-6ceca514e69f			
Greedy	592	TEST	Ith23	Ithaca, NY	2023	7	1	1	1	7	-76.537262	42.407916	125	500 cfu	0f7188f9-f91e-409d-bb7a-63398f36626b			
				Ithaca,														

Fig 7. Screenshot of DeltaBreed v1.0 experiments and observations user interface. Displayed is an experiment view in DeltaBreed v1.0 before observations have been made (see S5 File for data). Each table row represents an observation unit, in this case a plot, with its unique ObsUnitID and associated human-readable germplasm record (GID). The grey cells represent pending observations with no recorded values. Experimental observation variables (e.g., “XLength”) are defined in the DeltaBreed v1.0 ontology module.

<https://doi.org/10.1371/journal.pone.0341691.g007>

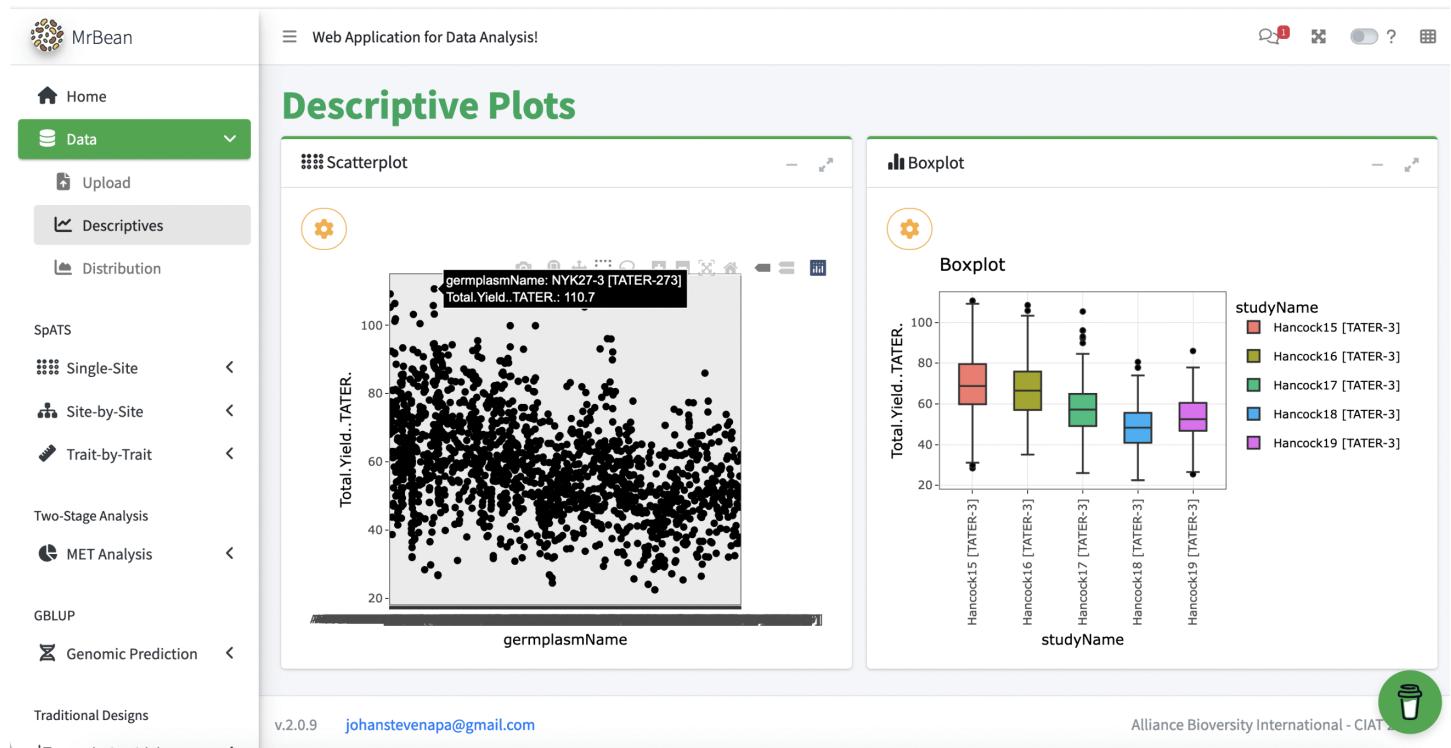


Fig 9. Screenshot of MrBean's UI for descriptive plots using potato data pulled from DeltaBreed v1.0 via QBMS and BrAPI. The center-left panel displays a scatterplot of all germplasm evaluated for total yield in the Vignette1 potato dataset [34]. The center-right panel displays a boxplot of total yield across five environments (the location “Hancock” across years 2015–2019). Notice in the scatter plot that the selected germplasmName is appended with program code and GID, [TATER-273]. Similarly, studyName in the boxplot is appended with program code and experiment ID. These appends are hidden from users on the DeltaBreed v1.0 UI and are artifacts of DeltaBreed v1.0 interoperability logic, also described with Helium integration (see Fig 4). See S6 File for data. MrBean logo republished under a CC BY license, with permission from Johan Aparicio, original copyright 2023.

<https://doi.org/10.1371/journal.pone.0341691.g009>

< All Germplasm

Germplasm Details

Preferred Name: Dixo
GID: 104
Breeding Method: Unknown
Source: UNK
Pedigree:
Pedigree GID(s):
Synonyms:

External UID:
User: BI-DEV Admin
Creation Date: 2024-11-19

Pedigrees

Genotype

Callsets: Dixo_89.001_S10.05.1-2024-11-19T20:46:05.737681

Chromosome	Position	Ref	Alt(s)	Genotype(s)	
VaccDscaff1	188466	GACAGAGTAACACCAATTCTCTATCATACTGAAACGAGCTCAACCCATGAAATTTTGCTCCAGGCTCAGATTG	GACAGAAAGTACACCAATTCTCTATCATACTGAAACGAGCTCAACCCATGAAATTTTGCTCCAGGCTCAGATTG GACAGAAAGTACACCAATTCTCTATCATACTGAAACGAGCTCAACCCATGAAATTTTGCTCCAGGCTCAGATTG	GACAGAAAGTACACCAATTCTCTATCATACTGAAACGAGCTCAACCCATGAAATTTTGCTCCAGGCTCAGATTG GACAGAAAGTACACCAATTCTCTATCATACTGAAACGAGCTCAACCCATGAAATTTTGCTCCAGGCTCAGATTG GACAGAAAGTACACCAATTCTCTATCATACTGAAACGAGCTCAACCCATGAAATTTTGCTCCAGGCTCAGATTG	Details >
VaccDscaff1	255524	GACATGATGCTCACTGCAACCTTGGATGCACTGCTCTCTGTTACACACACTCCATGACCGAAGCATTG	GACATGATGCTCACTGCAACCTTGGATGCACTGCTCTCTGTTACACACACTCCATGACCGAAGCATTG GACATGATGCTCACTGCAACCTTGGATGCACTGCTCTCTGTTACACACACTCCATGACCGAAGCATTG GACATGATGCTCACTGCAACCTTGGATGCACTGCTCTCTGTTACACACACTCCATGACCGAAGCATTG GACATGATGCTCACTGCAACCTTGGATGCACTGCTCTCTGTTACACACACTCCATGACCGAAGCATTG GACATGATGCTCACTGCAACCTTGGATGCACTGCTCTCTGTTACACACACTCCATGACCGAAGCATTG	GACATGATGCTCACTGCAACCTTGGATGCACTGCTCTCTGTTACACACACTCCATGACCGAAGCATTG GACATGATGCTCACTGCAACCTTGGATGCACTGCTCTCTGTTACACACACTCCATGACCGAAGCATTG GACATGATGCTCACTGCAACCTTGGATGCACTGCTCTCTGTTACACACACTCCATGACCGAAGCATTG GACATGATGCTCACTGCAACCTTGGATGCACTGCTCTCTGTTACACACACTCCATGACCGAAGCATTG	Details >
VaccDscaff1	332115	CCCCAAAGACCACTGAAAGTAAGTACAAATTAGCTTAAAGCTGAGGAAGAGTTTCAGGAAGAAAGCAGTTA	CCCCAAAGACCACTGAAAGTAAGTACAAATTAGCTTAAAGCTGAGGAAGAGTTTCAGGAAGAAAGCAGTTA CCCCAAAGACCACTGAAAGTAAGTACAAATTAGCTTAAAGCTGAGGAAGAGTTTCAGGAAGAAAGCAGTTA CCCCAAAGACCACTGAAAGTAAGTACAAATTAGCTTAAAGCTGAGGAAGAGTTTCAGGAAGAAAGCAGTTA	CCCCAAAGACCACTGAAAGTAAGTACAAATTAGCTTAAAGCTGAGGAAGAGTTTCAGGAAGAAAGCAGTTA CCCCAAAGACCACTGAAAGTAAGTACAAATTAGCTTAAAGCTGAGGAAGAGTTTCAGGAAGAAAGCAGTTA CCCCAAAGACCACTGAAAGTAAGTACAAATTAGCTTAAAGCTGAGGAAGAGTTTCAGGAAGAAAGCAGTTA	Details >

Fig 10. Screenshot of DeltaBreed v1.1 prototype visualization of microhaplotypes in the germplasm record view for a blueberry accession called “Dixi”. The Germplasm Details viewer shows the genotype of an autotetraploid blueberry ($2n=4x=48$) accession called ‘Dixi’ [GID:104]. The accession was genotyped on the 3K DArTag Blueberry panel (Blackberry_DArTag_BI_Cornell_University (1.0), [9]) and microhaplotypes were discovered, curated, and displayed at each targeted locus (only 3 loci are shown in this example). At each marker locus, the “Ref” column shows the microhaplotype allele that matches the reference genome exactly for the target sequence and surrounding sequence, the “Alt(s)” column shows the microhaplotype allele that matches known alternative alleles at the target locus by design, and the “Genotype(s)” displays the four microhaplotypes detected at on each of the four homologous chromosomes at the indicated locus in the genome. The ‘Dixi’ cultivar harbors four copies of “Alt” alleles at locus VaccDscaff1_188466, one copy of the “Ref” and three copies of the “Alt” alleles at locus VaccDscaff1_255524, and three copies of “Ref” and one copy of the “Alt” alleles at locus VaccDscaff1_332115.

<https://doi.org/10.1371/journal.pone.0341691.g010>