

# CDCB Genomic Nominators Workshop

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Maritime Conference Center – Linthicum Heights, MD

May 17, 2017



# Introductions

## NAAB

- ABS Global
- Accelerated Genetics
- *Alta Genetics*
- Genex
- NAAB
- *New Generation Genetics*
- Select Sires

## PDCA

- Ayrshire (ABA)
- Brown Swiss (BSCBA)
- Holstein (HAUSA)
- Guernsey (AGA)
- Jersey (AJCA)

## Genomic laboratories

- BioGenesys
- Genetic Visions
- Neogen
- *VHL*
- Zoetis

## PRPs

- NDHIA

## Canada

- *CDN*
- *Holstein Canada*
- Semex

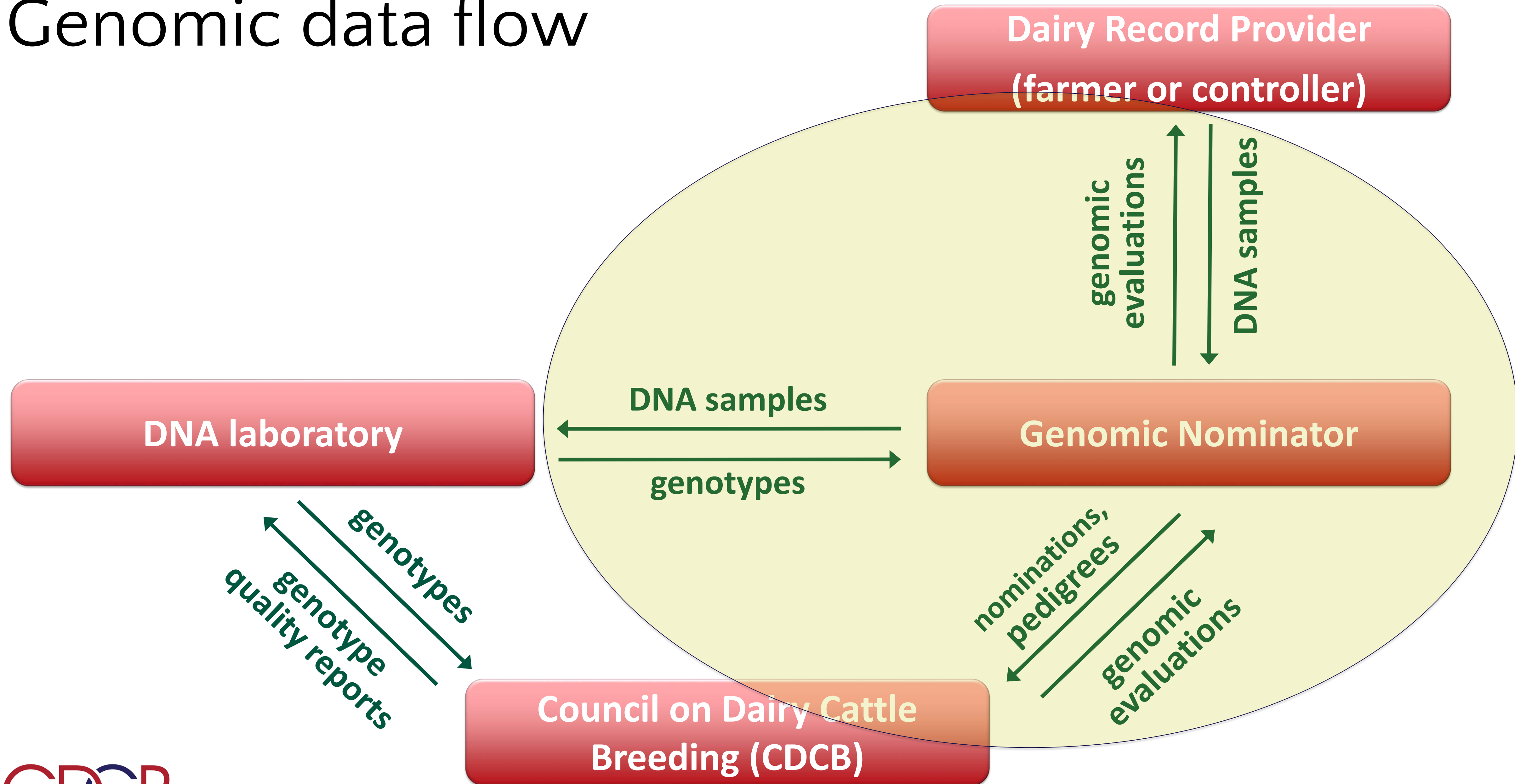
# CDCB Genomic Nominators Workshop Program

- 8:00 – Introductions
- 8:30 – CDCB Genomic Nomination Review
  - Genomic nominator – roles and responsibilities
  - Genomic nomination process
    - Common reasons for not receiving genomic evaluations
    - Genomic nominator queries
    - Data corrections
    - CDCB service fees
  - Excluding animals with unlikely grandsires from genomic evaluation
- 10:30 – Milk break

- 10:50 – CDCB Genomic Nominator Customer Support
  - Using Redmine for documentation and issue tracking
  - FAQ
- 12:00 – Lunch
- 1:00 – CDCB Genomic Nominator Quality Certification Program Review
  - Genomic nominator SOPs
  - QC Metrics
  - QC Audits
- 3:00 – Milk break
- 3:20 – Wrap up discussion
- 4:00 – Adjourn

# CDCB GENOMIC NOMINATION REVIEW

# Genomic data flow



# Genomic Nominators Main Tasks & Responsibilities

1. Upload information for nominated animals into the CDCB system
2. Resolve errors such as sampling and pedigree errors
3. Work with genomic laboratory and farms to resolve problems that prevent animals from getting evaluations
4. Distribute evaluation results to the requesters

# Genomic Nominators Requirements

1. Supply unique animal identification, including sire and dam if available.
2. Assign unique IDs to the biological sample linked to the animal ID
3. Provide the DNA laboratory with samples that are reliably identified
4. Nominate animals before genotypes are received by CDCB
5. Perform necessary corrections to nominations prior to deadline
6. Report genomic conflicts back to customer/owner in timely manner
7. Deliver genomic evaluations to customers
8. Collect CDCB fees according to the fee structure and herd class supplied by CDCB, and pay CDCB invoices by the due date
9. Notify CDCB staff (~30 d) of changes in ownership, location address, billing address, and any issue that could affect quality of services

# CDCB SERVICE FEES



# CDCB Fee Schedule

## (Updated March 2, 2015)

Rate Code	Participation type	Female fee (\$)	Initial male fee (\$)		AI service fee for males (\$)
1	Total program	0,00	15,00		575,00
2	Member	1,00	22,00		575,00
3	Non-member	3,00	150,00		575,00
			<15 mo	> 15 mo	
4	Canada	6,00	150,00	575,00	575,00
5	Approved partners	7,00	15,00	575,00	575,00
6	All others	7,00	150,00	1200,00	1200,00

# CDCB Fee Schedule – Decision Tree

[https://www.uscdcb.com/fee\\_schedule\\_main.htm](https://www.uscdcb.com/fee_schedule_main.htm)

Secure | https://www.uscdcb.com/fee\_schedule\_main.htm

C Council on Dairy Cattl | Imported | Choice Strategies | Governance | CDCB-Survey | https://www.cdc.us/j | The Council of Dairy C | COUNCIL ON DAIRY C | Fee schedule » | Other bookmarks

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CDCB Fee Schedule

Animal has unique permanent ID?

Yes

No

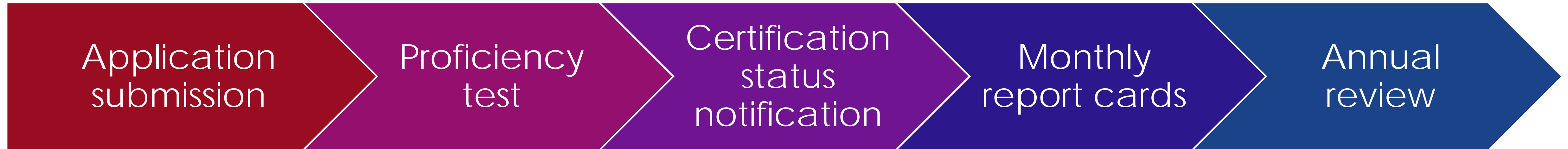
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# CDCB GENOMIC NOMINATOR QUALITY CERTIFICATION PROGRAM REVIEW

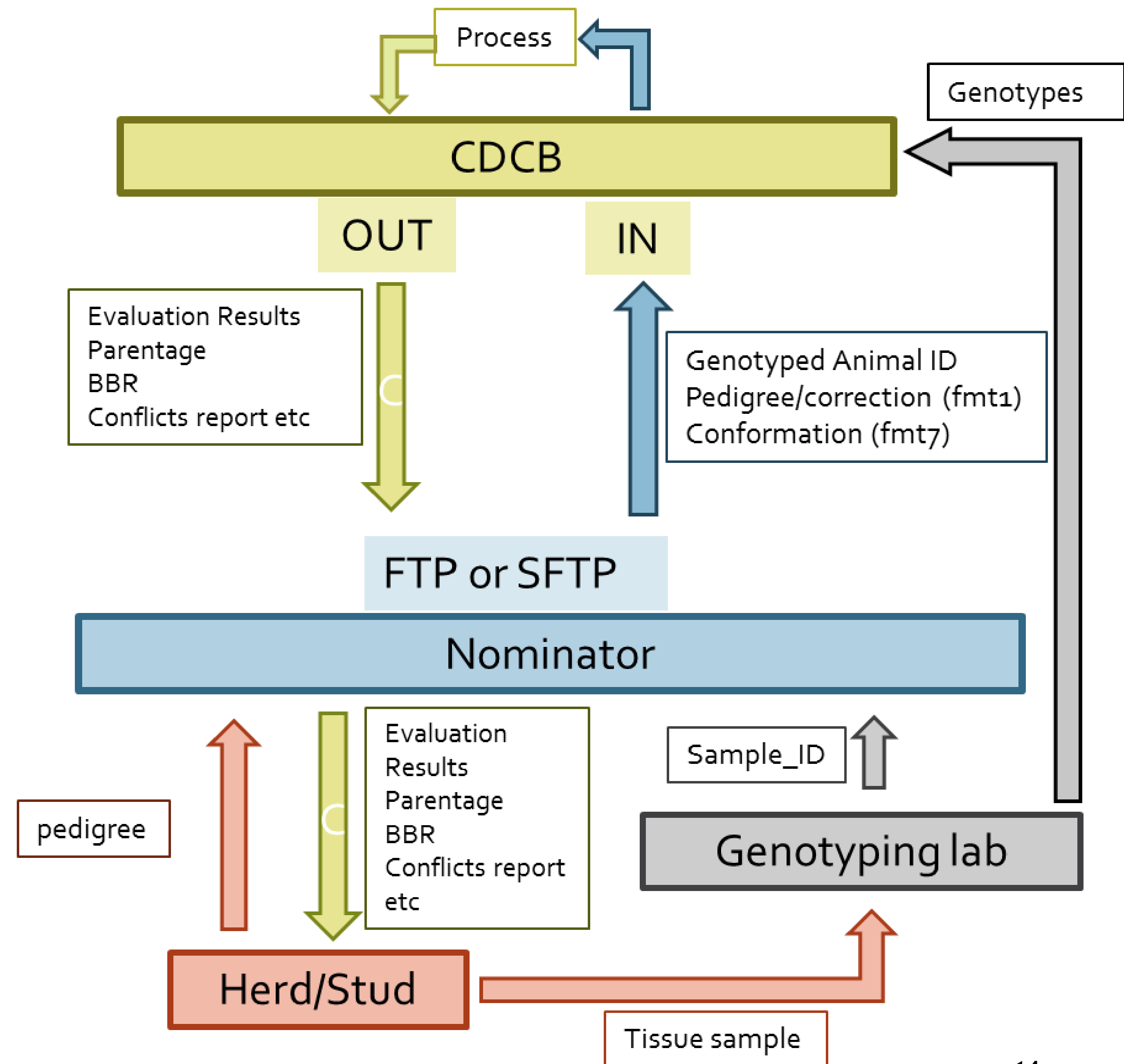
# CDCB Genomic Nominator QC Program

- Purpose
  - Ensure the accuracy and uniformity of all records included in the national genomic evaluation program so that the impact of contributed resources and efficiency of the system are maximized.
- Resources
  - [Quality Certification Requirements for Genomic Nominators](#)
  - [CDCB Nominator Guidelines](#)

# Certification Process



# Nomination flow chart



# Standard Operating Procedures

- Background
- Purpose
- Scope
- Definitions
- Responsibilities
- Procedure
- Effective criteria
- References
- Revisions

# Items of the process that need to be covered by the Genomic Nomination SOPs

- Animal Identification
- Pedigrees
- Sample collection
- Sample identification
- Sample submission to genomic laboratory
- Nomination procedures (Format 1, online forms)
- Data conflicts management
  - Communication with requesters
  - Corrections to submitted data
- CDCB service fees
- Delivery of CDCB results to requesters



# Genomic Nominators Quality Performance Metrics

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July 15, 2016 revision
- » New Queries
- » General Queries
- » Industry Queries
- » Active AI Lists
- » Top Bull Lists
- » Elite Cow List
- » Password
- » Data Exchange
- » Contact CDCB
- » Genotype Counts
- » Lab/Nominator Qs
- » ID Range Query

## [How Do I ?](#)

This query is used to ADD/REMOVE/UPDATE nominations and UPDATE genotype information.

[CDCB-Nomination\\_Q](#)

Genotype reports based on requester  
[affiliate specific genotype reports](#)

Check ~~FMT1~~ records.

[Check FMT1 records](#)

Get 116 parentage SNP

[Get 116 parentage SNP for a list of animal IDs](#)

This is used to show (and fix) the usability/error status of received genotypes.

[Genotype Query\(30 SNP\)](#)

This is used by the DNA labs to look up SAMPLE\_IDs.

[Genotype Lab Query](#)

This is the CDCB Fee (by herdcode) Query

[GT\\_Fee](#)

Retrieve Parentage Validation Record

[parentage.cfm](#)

This is for correcting bad genotype to animal assignments.

[Genotype Move/Swap APP](#)

Provides herd code and CDCB Fee for specified animal ID

[getfee](#)

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## Affiliate specific genotype reports

Select desired report :

Select affiliate to build report for :

Submit

- » [CDCB Fee Schedule](#)
- » [July 15, 2016 revision](#)
- » [New Queries](#)
- » [General Queries](#)
- » [Industry Queries](#)
- » [Active AI Lists](#)
- » [Top Bull Lists](#)
- » [Elite Cow List](#)
- » [Password](#)
- » [Data Exchange](#)
- » [Contact CDCB](#)
- » [Genotype Counts](#)
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- » [ID Range Query](#)

## Affiliate specific genotype reports

### Nominator Cumulative Report Card - AIPL

	November 2016	December 2016	January 2017	February 2017	March 2017	April 2017	May 2017
Total genotypes	1863	2328	823	954	993	1013	1024
Genotypes missing nomination when loaded	2	5	8	30	50	100	200
Genotypes with unknown animal ID	0	0	0	0	0	0	0
Sire pedigree missing	11	15	20	29	55	120	60
Dam pedigree missing	10	100	100	200	200	100	10
Dam blanked due to conflict	400	200	100	50	50	50	50
Group_Name not found as a herd of animal or dam	203	755	200	164	150	100	50
Usability code = N	200	200	100	60	100	150	50
Fee code = N	200	100	200	100	30	100	40
Genotype withdrawn	200	300	80	150	20	150	250
Genotype reassigned	100	300	50	200	100	70	40
Changes in pedigree	150	250	50	80	250	150	250

## **Definitions:**

**Total number of genotypes submitted by the nominator** - This number is provided each month based on the 4 to 5-week period, determined by monthly release dates.

### **Number of genotypes by each chip type**

**Number of genotypes missing a nomination when loaded** - Nominators are required to submit a record for each animal nominated to the CDCB database (including the animals pedigrees if known) so the information arrives preceding the genotype from the laboratory to satisfy Metric 4 of the Quality Certification Requirements for Genomic Nominators ([https://www.uscdcb.com/quality\\_certification/Quality%20Certification%20Requirements%20for%20Genomic%20Nominators.pdf](https://www.uscdcb.com/quality_certification/Quality%20Certification%20Requirements%20for%20Genomic%20Nominators.pdf)). The standard states that the nominators submissions of pedigree data precede arrivals of genotypes from the laboratory 99% of the time.

**Number of genotypes with unknown animal identification (ID)** - This occurs when the animal has not been nominated and the genotype submission is missing the animals ID or the animal ID has not been entered in the CDCB database. The requirement for Metric 2 states genotypes should have an animal ID associated with the sample at least 99% of the time.

**Number of genotypes with sires pedigree missing** - This shows the frequency when there is no pedigree information in the CDCB database for the sire ID. This can occur when the sire ID is invalid, if a herd bull is not enrolled with a breed association, or if a foreign bulls pedigree has not been provided. The nominator may have to provide it.

**Number of genotypes with dams pedigree missing** - This shows the frequency when there is no pedigree information in the CDCB database for the dam. Unfortunately, this information is not always available on the farm, but Metric 3 states that the nominator should make the effort to request this whenever possible, and supply it when available. Metric 3 indicates animals with known dams will have pedigree requested at least 95% of the time. Determining whether this is being met cannot be determined from the Report Card only, but high percentage may suggest that additional work with customers is needed.

**Number of genotypes with dams blanked due to conflict** - Information on the dam was supplied but the information was not stored due to a conflict. Common reasons for blanking are because the animals birth date did not agree with the dams calving date or a maternal sibling has a birth date within 9 months of the animal submitted. These checks are bypassed for animals coded as having resulted from an embryo transfer birth.

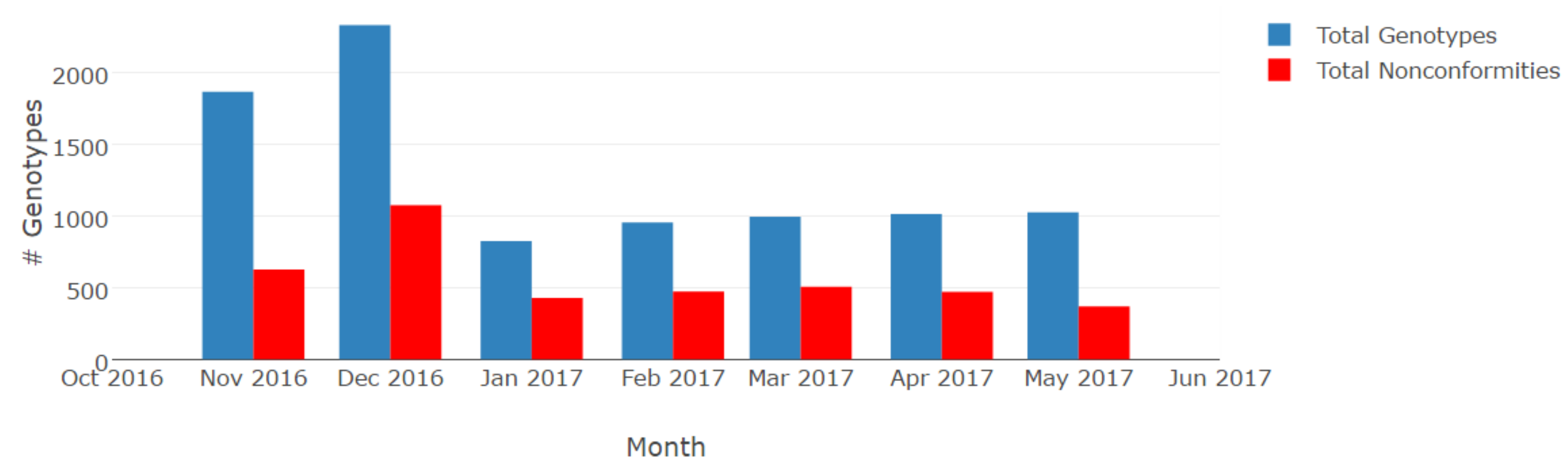
**Number of genotypes having IDs starting with 573 or 574** - IDs starting with these digits are assigned by the nominator and typically not attached to the animal. The preferred solution is to identify the animal by a tag attached to the animal.

**Number of genotypes where group name (basis for fee designated) not found in fee table for codes 1 or 2** - The DHI herd code supplied was not found among the herd codes that have a fee code assigned. This can be expected to occur for those herds that have begun testing recently.

**Number of genotypes where group name (herd code) not found as a herd of the animal or dam** - The herd code assigned by the nominator does not agree with the one in the database which came through DHI.

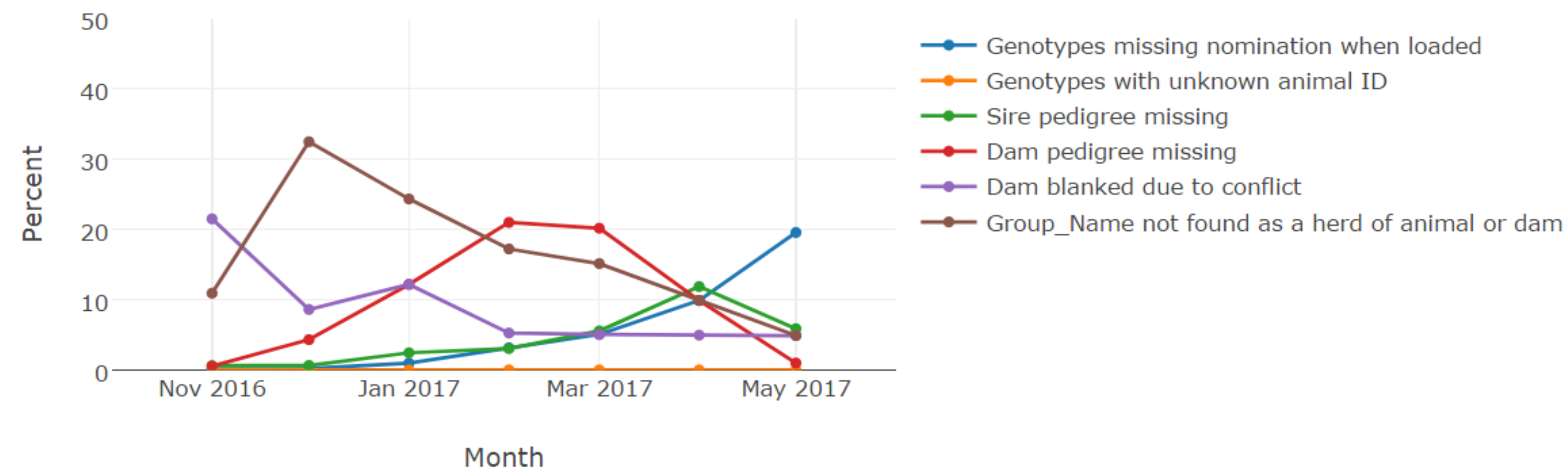


AIPL total number of genotypes vs. total number of non-conformity



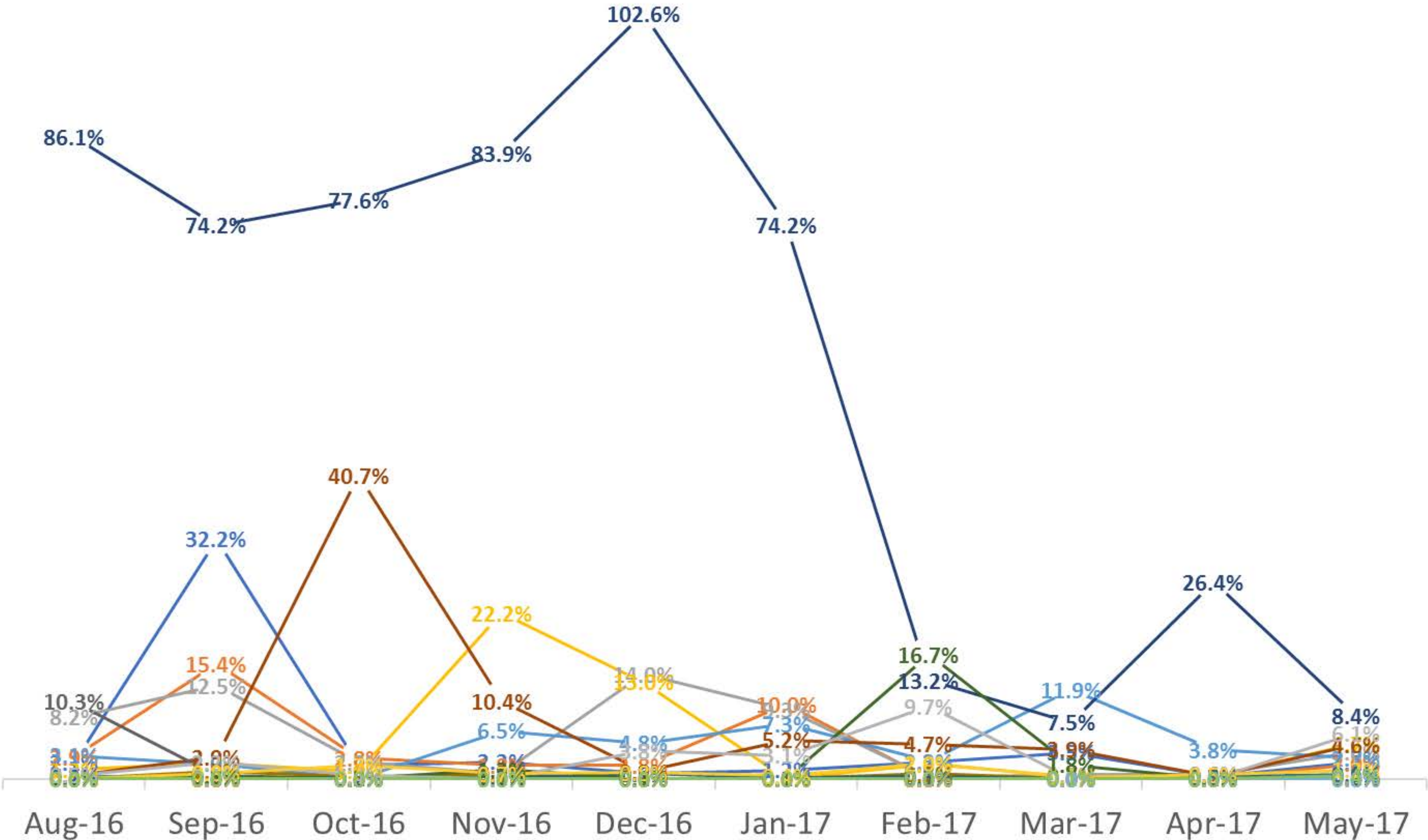
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AIPL relative frequency of each type of non-conformity compared to total number of genotypes

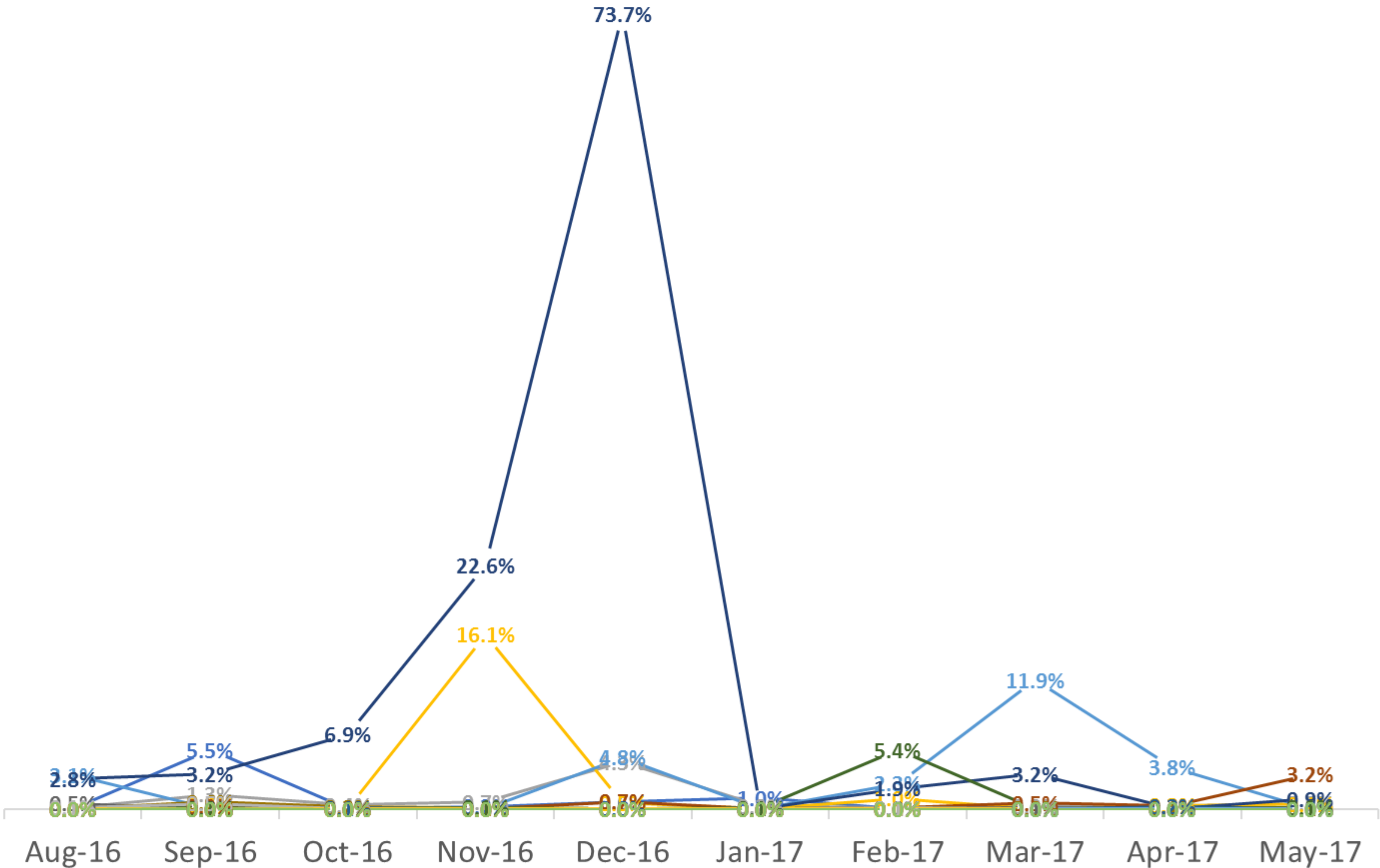


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GENOTYPES MISSING NOMINATION WHEN LOADED

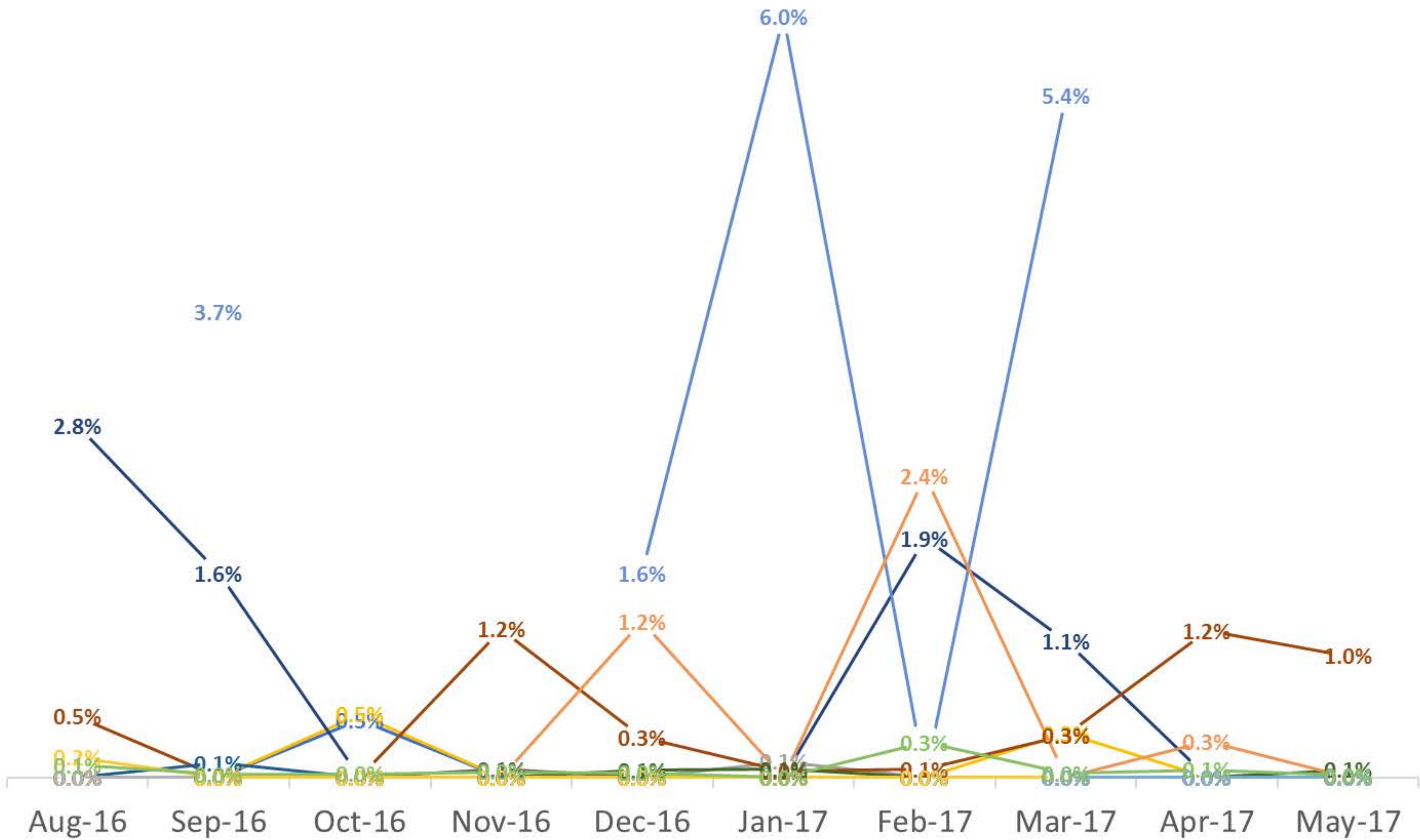


GENOTYPES WITH UNKNOWN ANIMAL ID

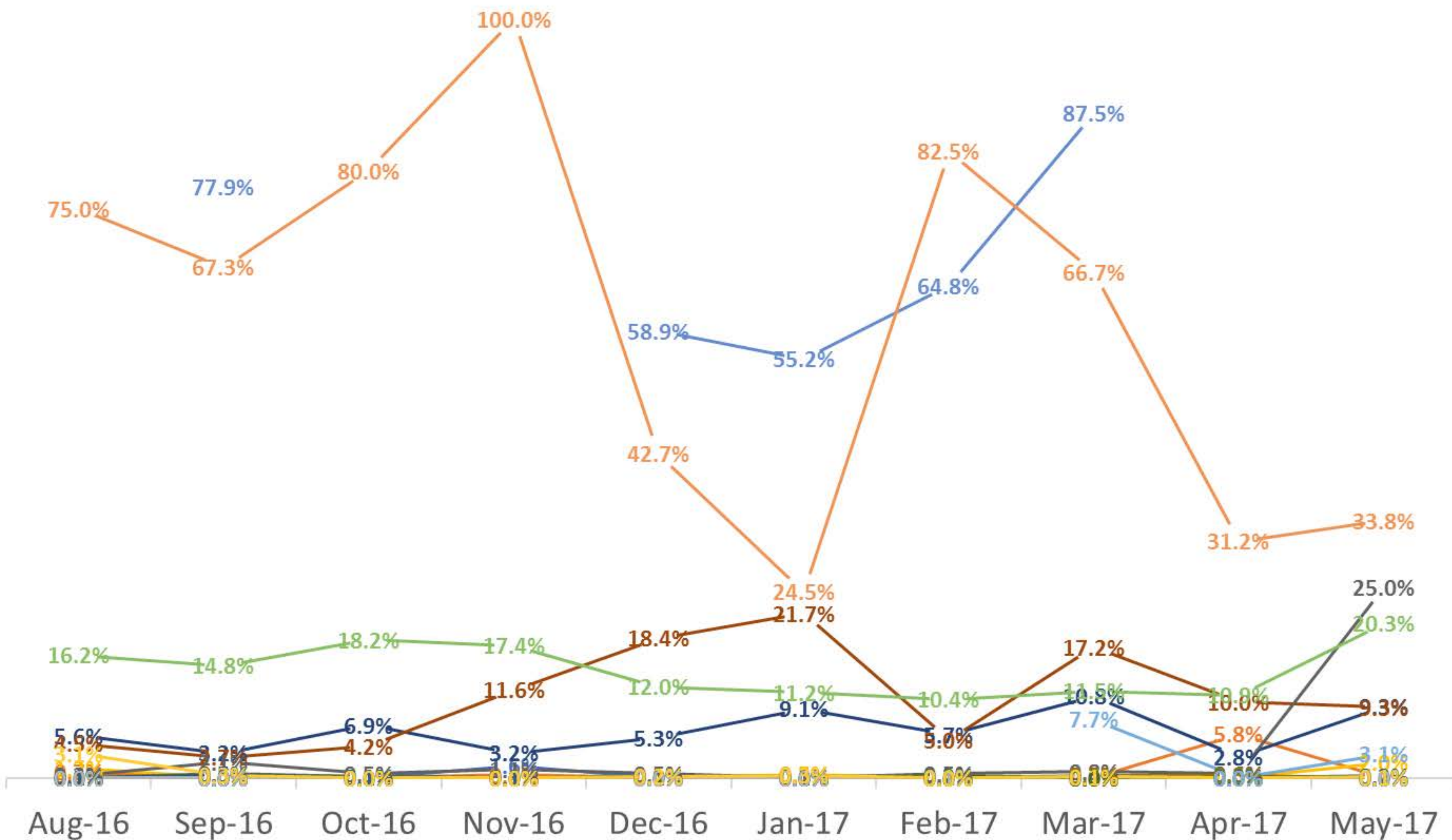




SIRE PEDIGREE MISSING

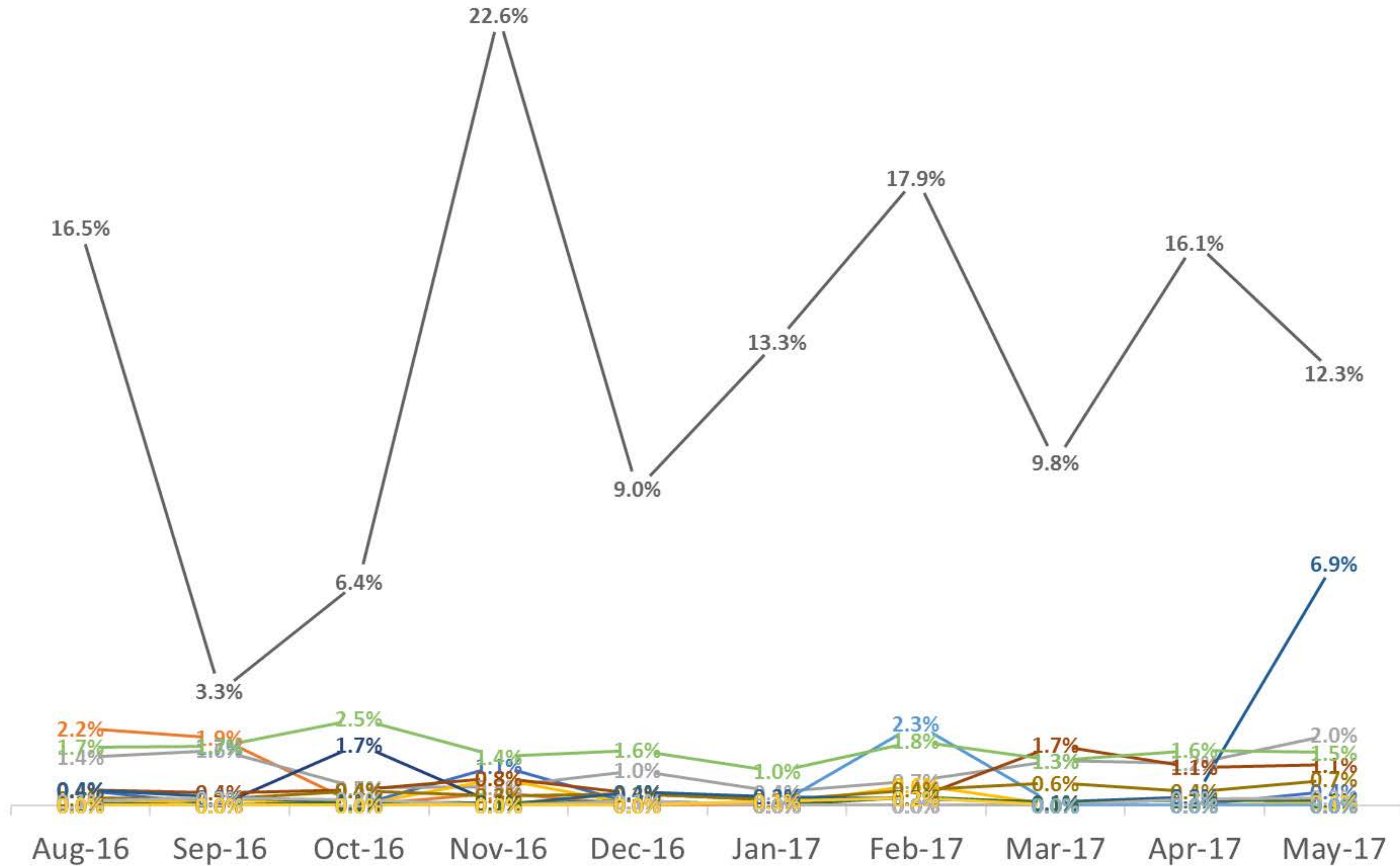


DAM PEDIGREE MISSING



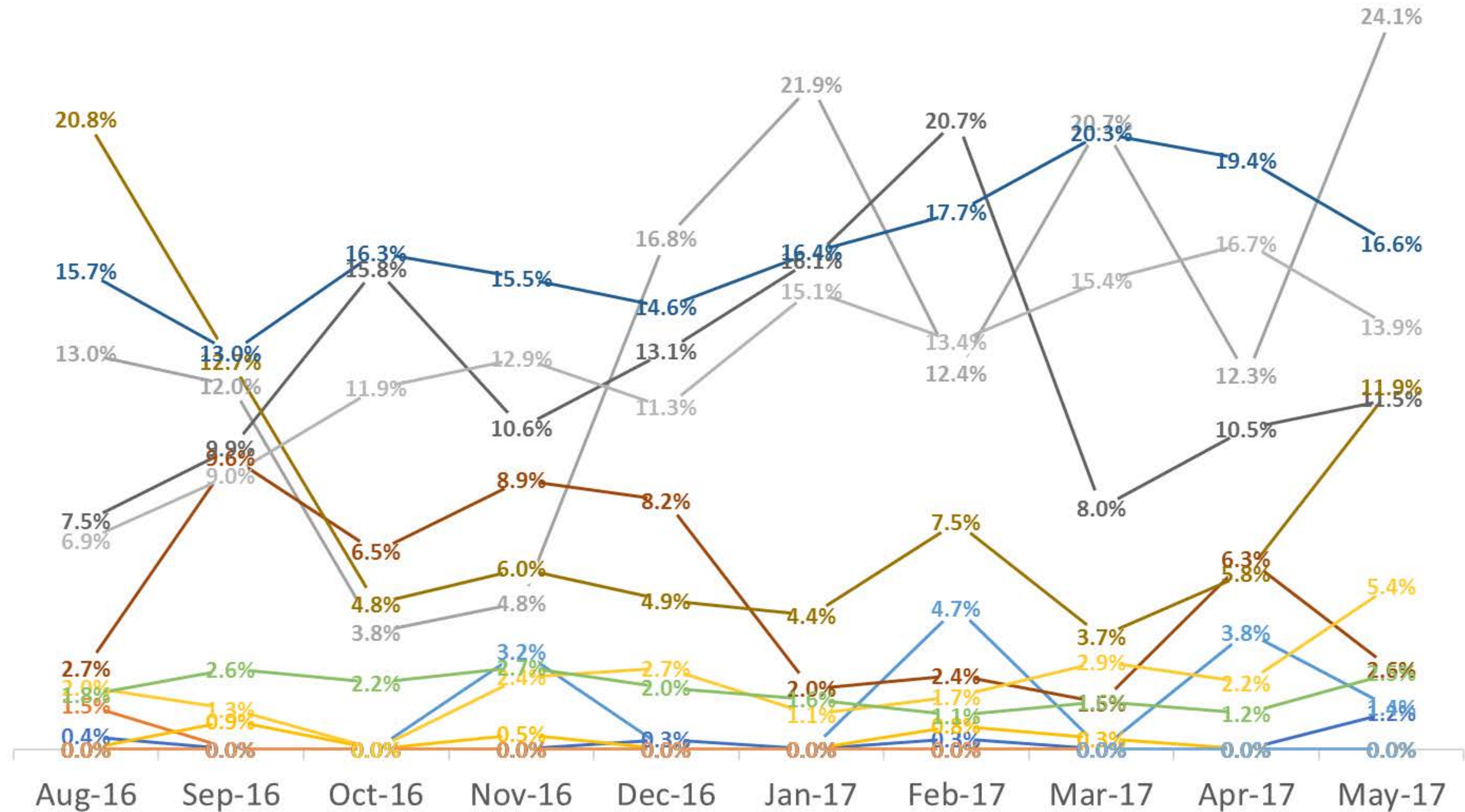


# DAM BLANKED DUE TO CONFLICT

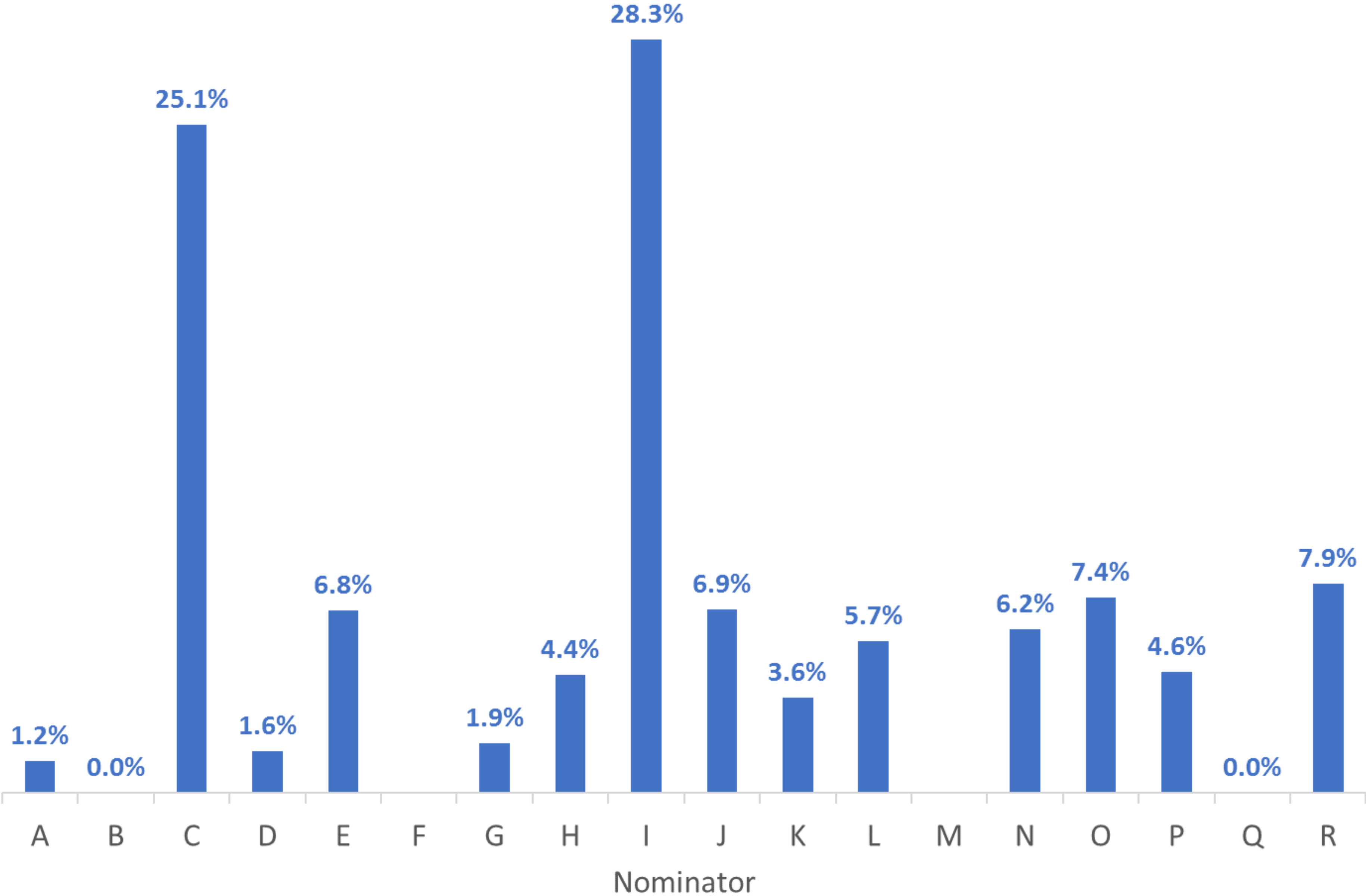




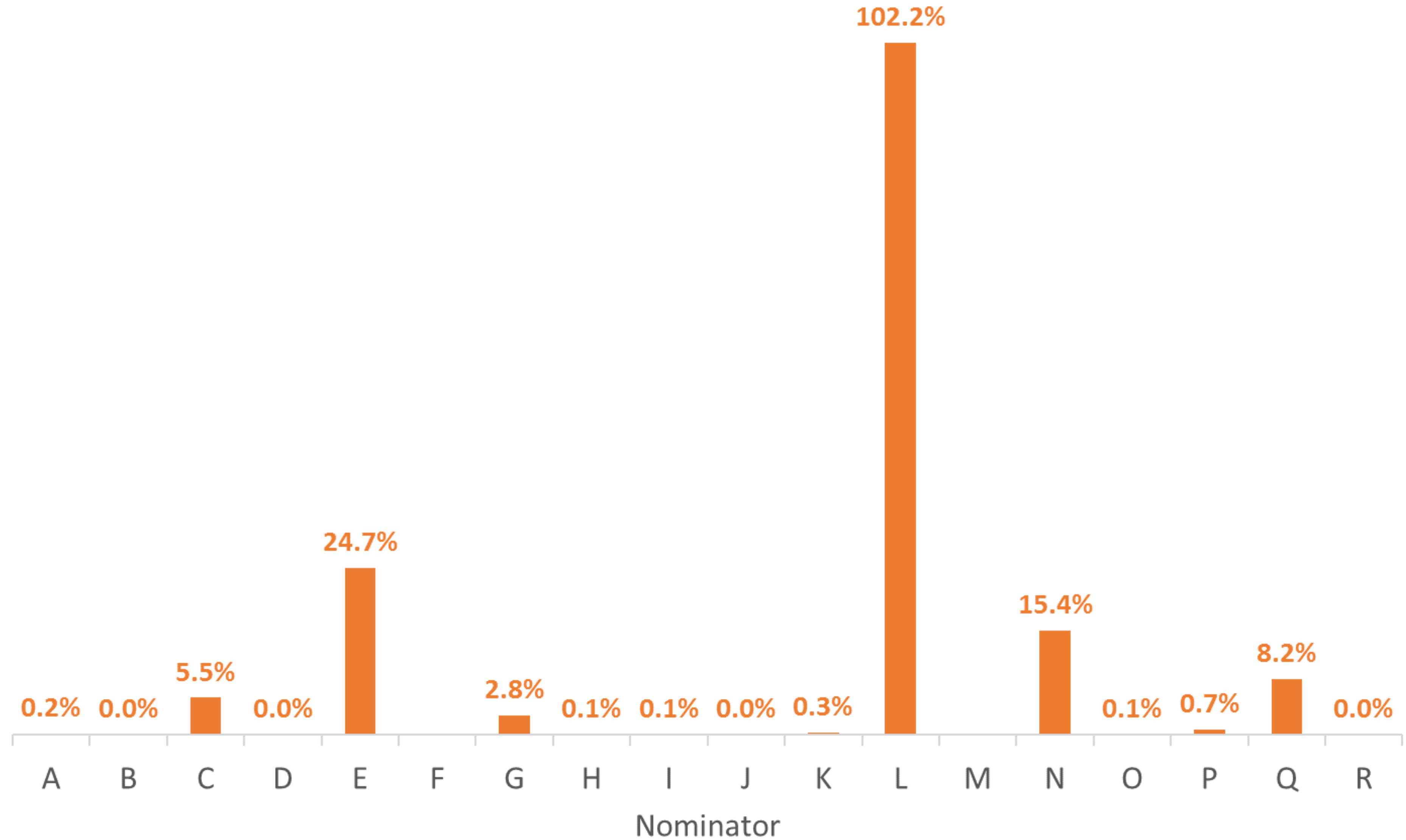
# GROUP\_NAME NOT FOUND AS A HERD OF ANIMAL OR DAM



USABILITY CODE = N (MAY 2017)



## FEE CODE = N (MAY 2017)

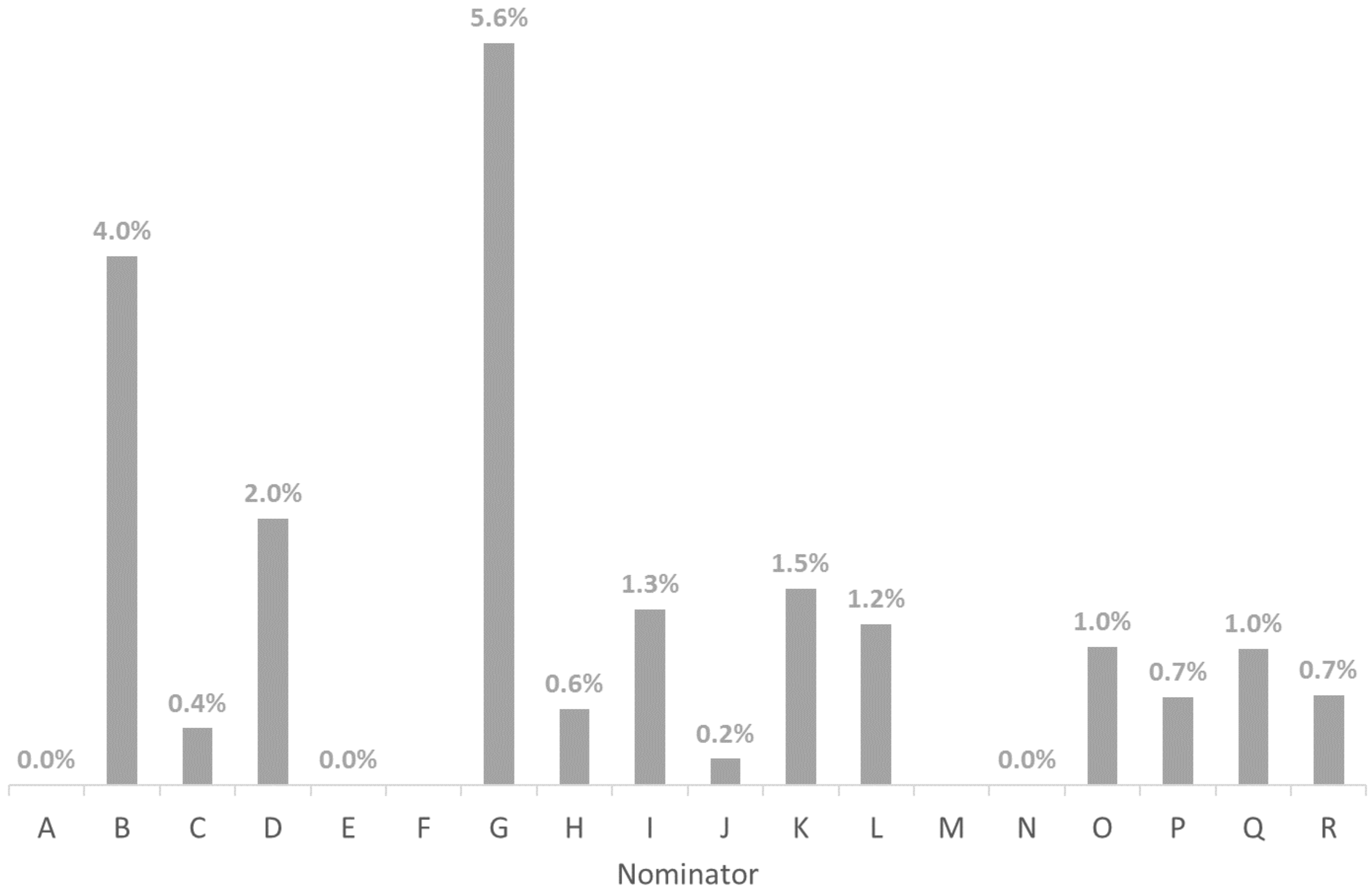


## GENOTYPE WITHDRAWN (MAY 2017)



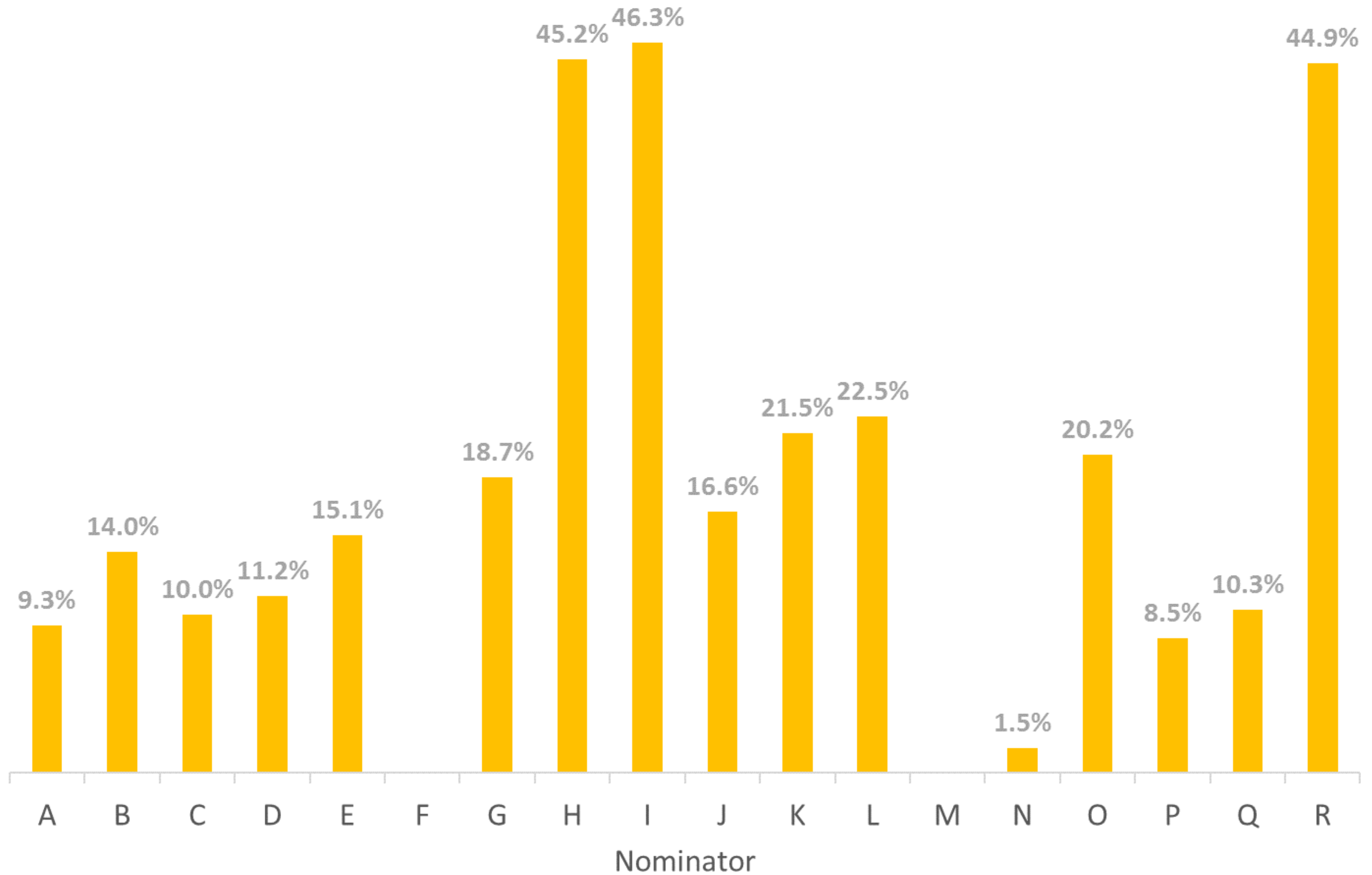


## GENOTYPE REASSIGNED (MAY 2017)





## CHANGES IN PEDIGREE (MAY 2017)



# Proposed threshold values for monitoring nominators' metrics

Metric	Threshold
Genotypes missing nomination when loaded	1%
Genotypes with unknown animal ID	1%
Sire pedigree missing	1%
Dam pedigree missing	5%
Dam blanked due to conflict	1%
Group_Name not found as a herd of animal or dam	5%
Usability code = N	5%
Fee code = N	N.A.
Genotype withdrawn	0.5%
Genotype reassigned	1%
Changes in pedigree	15%

# Action plan for 2017

- Immediate
  - Graphs to monitor performance
  - Redmine
  - Monthly comments from CDCB staff
- September 15
  - Submission of Nominators SOPs
- December 1<sup>st</sup>
  - Annual fee invoices will be sent out
  - 2017 review process starts

# Annual Review Plan







# Questions?