

# Summary of 2017 QC Audit Review

5/10/2018

---

---

Kaori Tokuhisa, CDCB Genomic Data Analyst

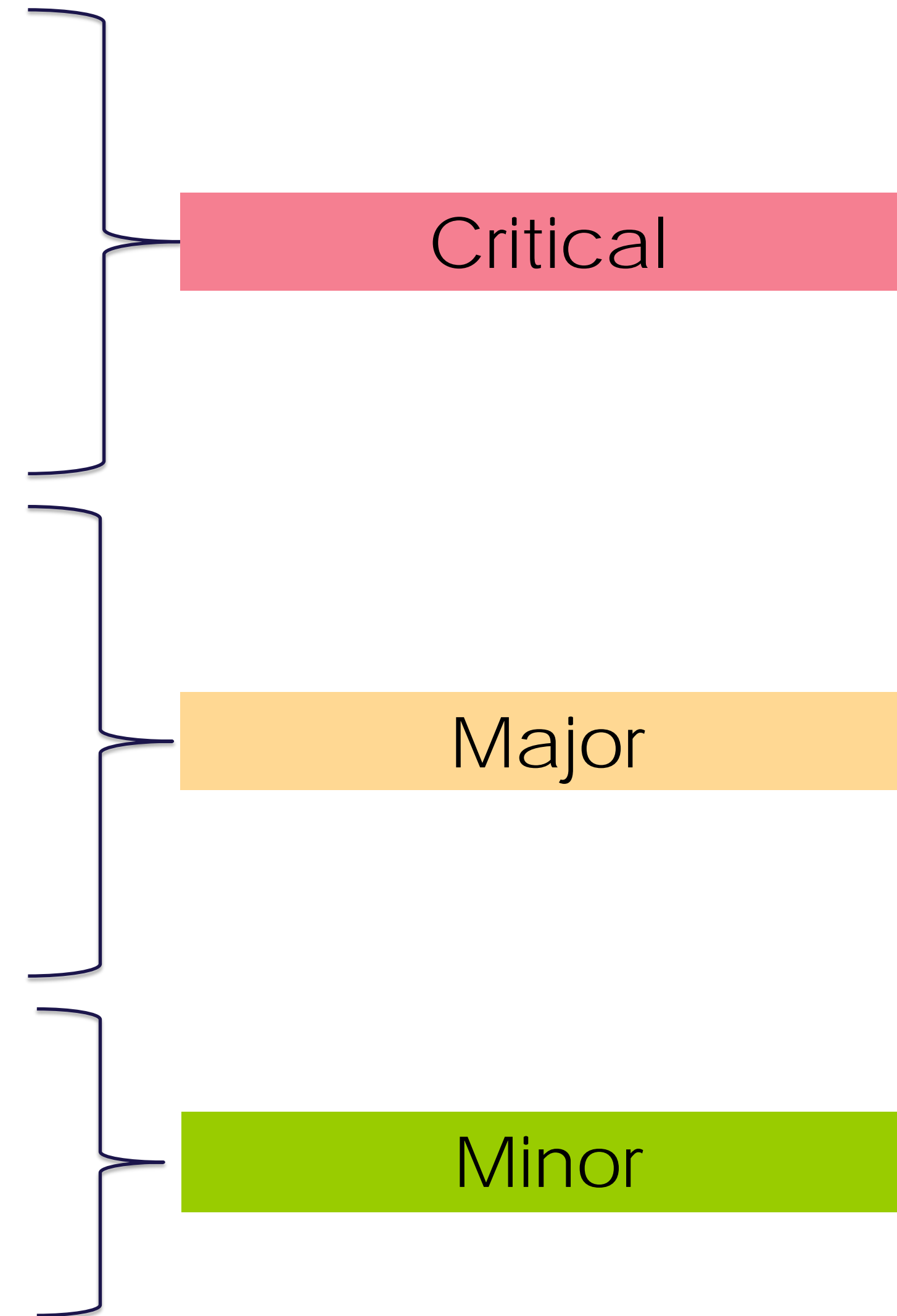


# Purpose of QC Audit Review

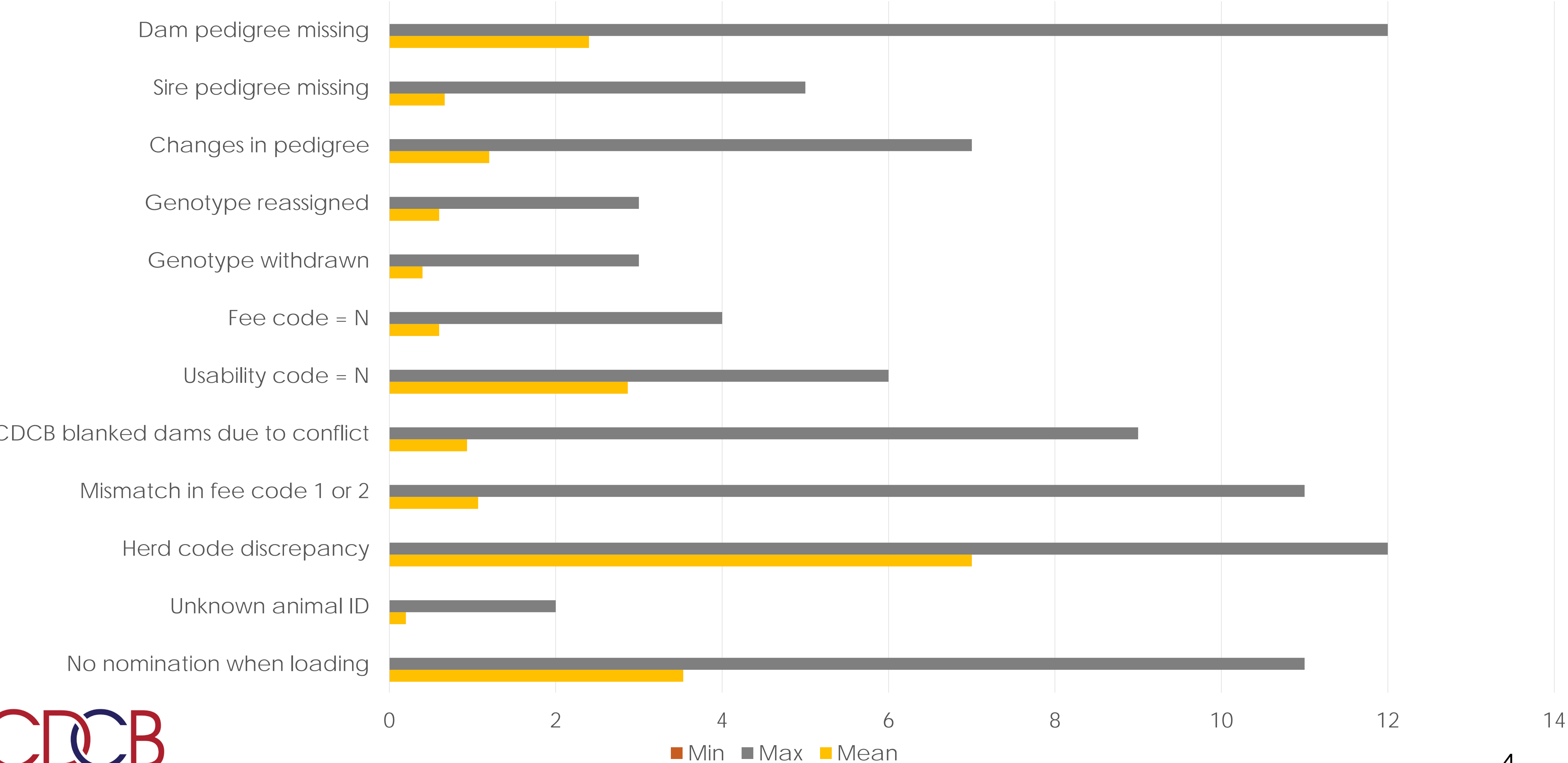
- To monitor certified nominator's performance regularly to ensure quality of data that nominators provide to CDCB
- To advise on or to find solutions for issues/concerns that nominators are facing, in order to help improve nominator's performance
- For CDCB to know the needs or issues that CDCB can work on to facilitate nominator's work flow
- To provide an opportunity to exchange information or have communication between CDCB and nominators to keep each other informed
- Punishing nominators **IS NOT** the purpose of this review

# QC Metrics and Threshold

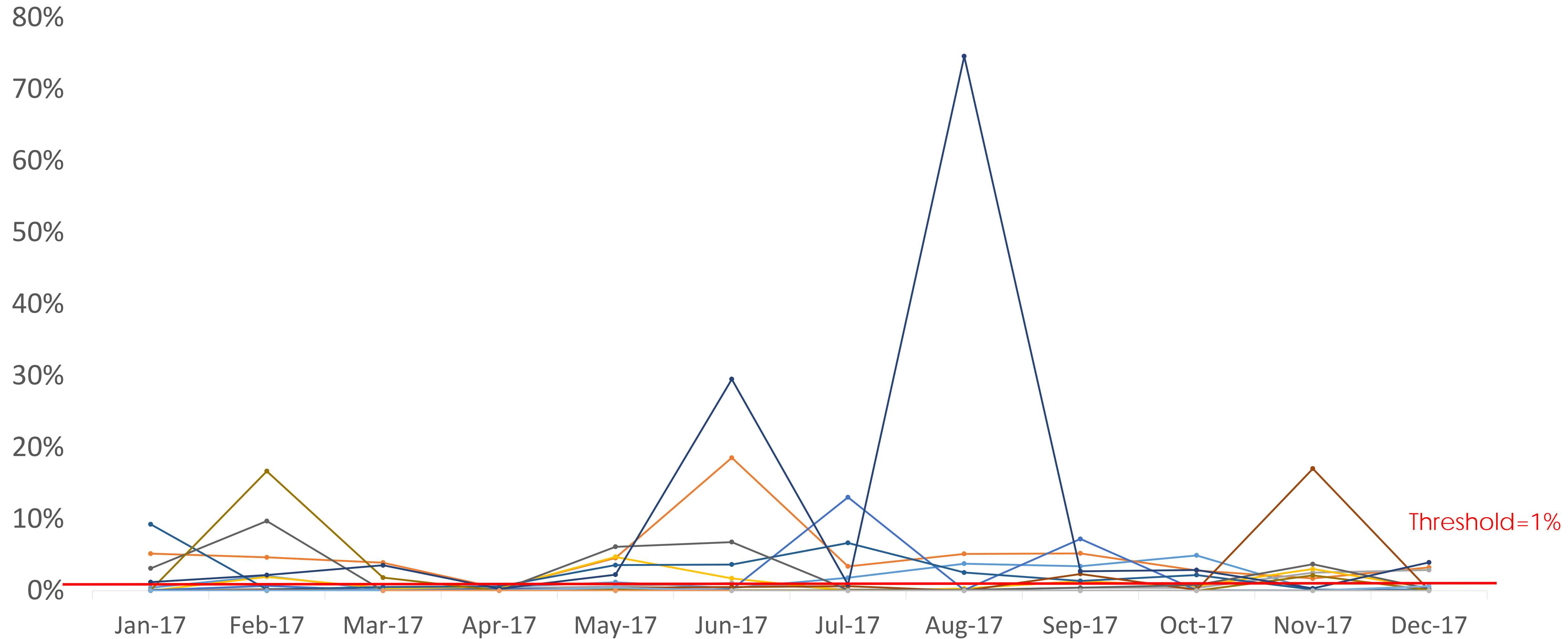
- **No nomination when loading** Threshold: 1%
- **Unknown animal ID** Threshold: 1%
- **IDs with 573/574** Threshold: 1%
- **Herd code discrepancy** Threshold: 1%
- **Mismatch in fee code 1 or 2** Threshold: 2%
- **CDCB blanked dams due to conflict** Threshold: 2%
- **Usability code = N** Threshold: 5%
- **Fee code = N** Threshold: 1%
- **Genotype withdrawn** Threshold: 1%
- **Genotype reassigned** Threshold: 1%
- **Changes in pedigree** Threshold: 25%
- **Sire pedigree missing** Threshold: 1%
- **Dam pedigree missing** Threshold: 10%



# # of Month that Exceeded QC Threshold in 2017



% No Nomination When Loading by Nominator in 2017



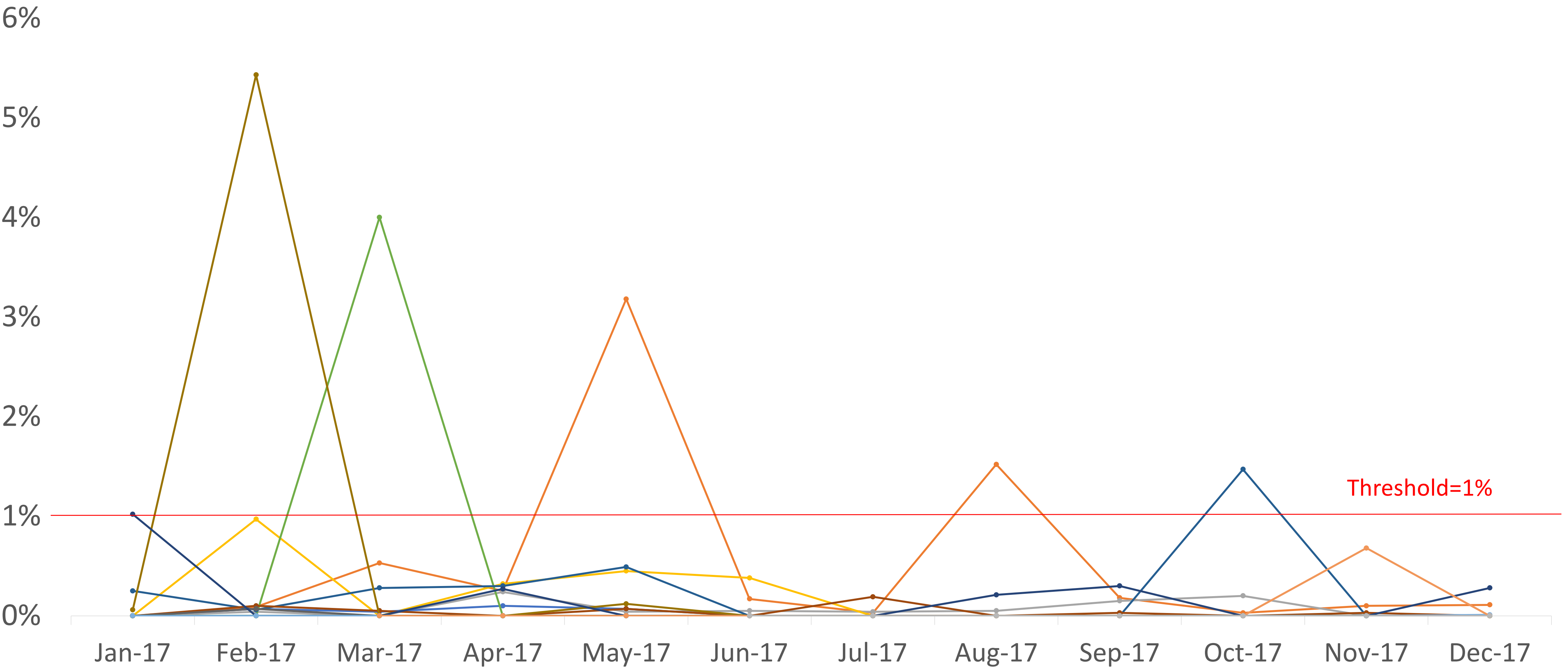
# No Nomination when loading

	# Month No Nom when Loading
Mean	3.53
Min	0
Max	11

## ***Main Explanations:***

1. Change in roles or procedures within the organization
2. Miscommunication between the lab and nominator
3. Insufficient system to detect missing/incomplete nomination
4. Personal issue/event
5. Problems at CDCB (FTP down time, too long fmt1G processing time)

% Unknown Animal ID Provided by Nominator in 2017



# Unknown Animal ID

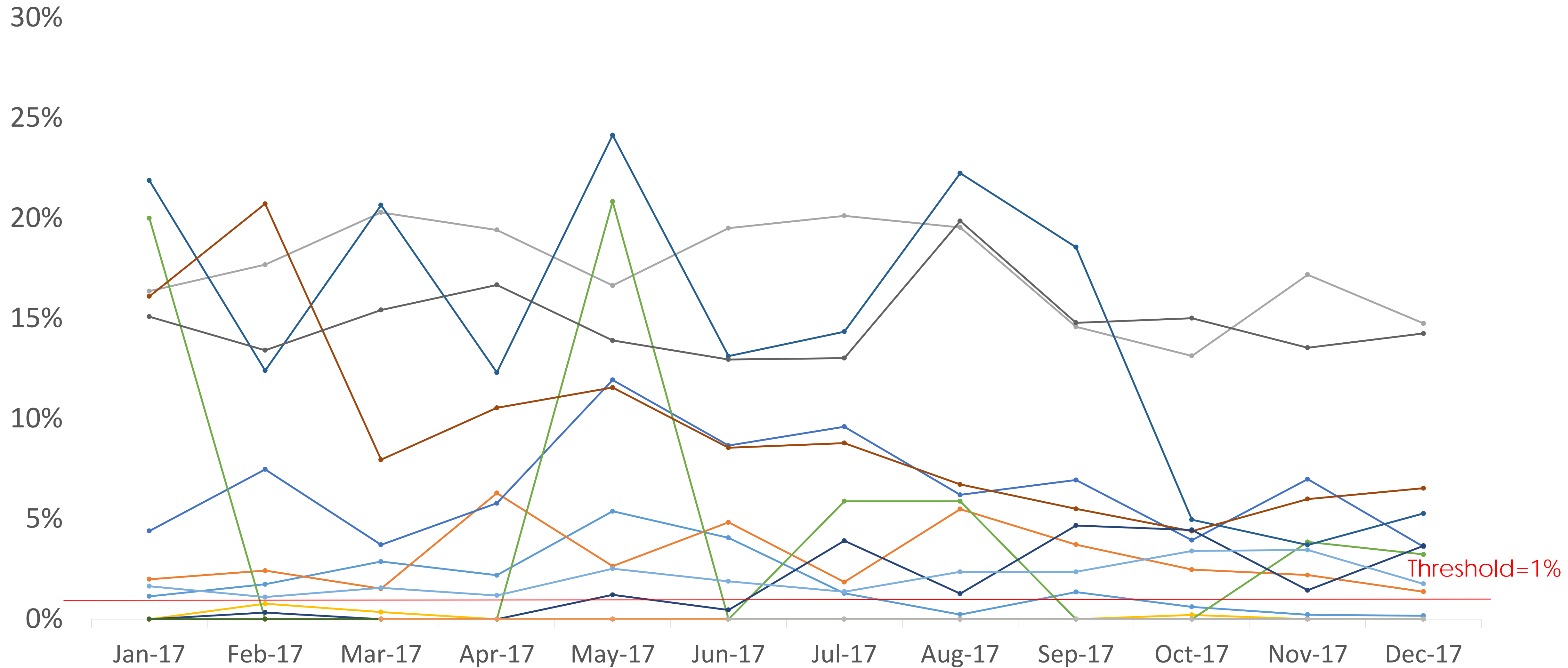
	Unknown Animal ID
Mean	0.20
Min	0
Max	2

## *Main Explanations:*

There were only 3 occurrences in total and not so critical, but this is related to missing nomination, as unknown animal ID can be caused by missing nomination. Unknown animal ID was counted if that was not fixed by **monthly cutoff** – same explanation as for missing nomination could apply



% Herd Code Discrepancy Reported by Nominator in 2017



# Herd code discrepancy

Ref.165

	Herd code Discrepancy
Mean	7.00
Min	0
Max	12

Herd code difference reason code	
Code	Description
P	purchased
M	owner has multiple herds
N	not participating in calf program and flushed dam, not in milk or dam not yet tested following calving

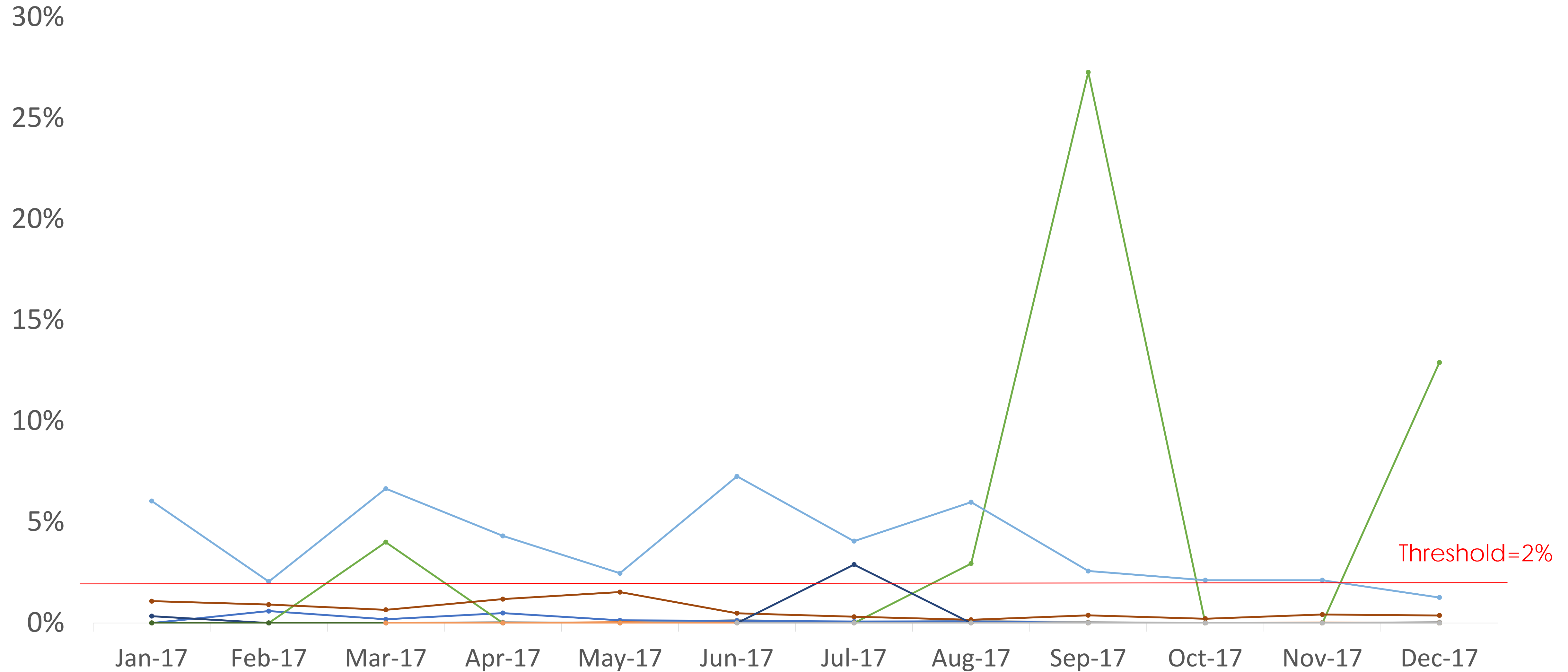
Byte Position(s)	Num Bytes	Field Format	Data Type	Ref Note(s)	Field Description
140	1	A	CH	165	Herd code difference reason code (G record-type only)

## Main Explanations:

1. The animal is not in the herd of the dam
2. The herd code of the animal has not yet been reported to CDCB
3. CDCB web tool was not used or herd codes reported by customers were used

\*\*CDCB is working on adding a function in nomination query that allows nominators to assign herd reason code

% Mismatch in Fee Code 1 or 2 Reported by Nominator in 2017



# Mismatch in Fee Code 1 or 2

	Mismatch in fee=1 or 2
Mean	1.07
Min	0
Max	11

## ***Main Explanations:***

1. CDCB web tool was not used or herd codes reported by customers were used
2. Frequent animal relocation, which results in discrepancy in fee code

# CDCB Blanked dams due to conflict

	Blanked dams
Mean	0.93
Min	0
Max	9

***Main Explanations:***  
1. Difficulty getting accurate ET reporting (MBC, birthdate)

# Usability=N

	Usability Code=N
Mean	2.87
Min	0
Max	6

## *Main Explanations:*

1. Changes and actions are taken based on the owner of the animal, therefore delay in genomic corrections can happen, depending on how fast/late the nominator gets response from the owner
2. All available tools(files) from CDCB were not utilized, in order to facilitate genomic conflict corrections

# Fee Code= N

	Fee Code=N
Mean	0.60
Min	0
Max	4

## ***Main Explanations:***

1. Fee code=N was assigned because of specific program or project where fee code=N is most appropriate (CAN, chip validation etc)

# Genotype Withdrawn

	GT withdrawn
Mean	0.4
Min	0
Max	3

## ***Main Explanations:***

1. Withdrawal policy was unclear, so sample might have been withdrawn for invalid reasons



# Genotype Reassigned

	GT reassigned
Mean	0.6
Min	0
Max	3

## *Main Explanations:*

1. There was a sample-mixed up at the lab/farm

# Changes in Pedigree

	Change in Pedigree
Mean	1.20
Min	0
Max	7

## ***Main Explanations:***

1. Some customers do not send correct (accurate) information at the time of nomination
2. Do not require complete pedigree information from customers

# Sire and Dam Pedigree Missing

	Sire pedigree missing
Mean	0.67
Min	0
Max	5

## *Main Explanations:*

1. Some customers do not send complete pedigree information (esp. dam's pedigree of commercial and international animals )

# Summary

- The very first QC audit was successful and CDCB harvested very good information from nominators.
- It was a very good opportunity for CDCB to know nominator's needs for us to improve CDCB system
- Most of nominators are very responsible and willing to improve their performance
- Final QC audit report should have been sent to each nominator