

Alec Steep <alec.steep@gmail.com>

FW: 14-265_Genotyping reports

Hans Cheng hcheng@msu.edu>
To: Alec Steep alec.steep@gmail.com

Sun, Dec 28, 2014 at 9:55 PM

Hi Alec.

Good news. Your SNP results have been completed and as expected, all samples passed.

Since the files are large, I will bring them in on a flash drive.

Hans

Hans H. Cheng USDA-ARS Avian Disease and Oncology Laboratory 4279 E. Mount Hope Rd. East Lansing, MI 48823 Tel: (517) 337-6758

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From: Sophie Bernier < sophie.bernier@dnalandmarks.ca>

Date: Sunday, December 28, 2014 at 1:50 PM

To: Hans Cheng < hcheng@msu.edu>

Cc: Tun-Ping Yu < TunPing. Yu@dnalandmarks.ca>

Subject: 14-265 Genotyping reports

Dear Dr. Cheng,

The genotyping reports for 96 samples have been uploaded into your account. You will also find the raw data.

Before producing the genotype report, 2 Qc steps are done.

- 1) The Dish-Qc monitors if the signal intensity is above the background signal. All samples passed this Qc.
- 2) Step 1 genotyping, measure genotype of validated SNPs. Samples with call rate below 97% for these validated SNPs are failed and are not used for the Step 2 genotyping to avoid the introduction of a bias in the clusters. 26 samples failed this Qc. However, we produced a separate report for these 26 samples.

If you have questions or comments, don't hesitate to contact us

Regards

Sophie

Sophie Bernier

Associée de recherche

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