Zimbra   **romain.larive@umontpellier.fr**

AW: Data sharing and collaboration

De : Rambow, Florian <Florian.Rambow@uk-essen.de>   mer., 17 août 2022 09:28

Objet : AW: Data sharing and collaboration

À : Romain Larive <romain.larive@umontpellier.fr>

Les images externes ne seront pas affichées.   <u>Montre les images ci-dessous</u>

Hi Romain,

here the download link for the gene expression data:
https://filesender.belnet.be/?s=download&token=97b9a7b2-6a6a-44d5-a362-1c2a2ff86ba3

it should give you access to 3 files:

GSE65185_CuffnormFPKM (2).txt (12.9 MB) --> Los Angeles

Bolande_MGH_RSEM, BRAFi only, for anyone.txt (7.7 MB) --> Boston

CompleteTEAM5_CS.collapsed_deidentified.xlsx (40.9 MB) --> Sydney

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Von: Romain Larive <romain.larive@umontpellier.fr>
Gesendet: Dienstag, 16. August 2022 16:44:32
An: Rambow, Florian
Betreff: Re: Data sharing and collaboration

Hi Florian,

Thank you for your email, and I'm sorry to hear that your situation has not yet returned to normal. I really hope that you will soon be able to find a calm and functional environment!

Great for these data! We are missing the most important thing for us today: the genomic data (WES). How did you calculate the mutational load?

I'm going to ask Helen Rizos again for her genomic data. I will copy you on the email and explain that we are in touch to collaborate. If she doesn't respond, feel free to weigh-in.

Regarding the gene expression data, yes we are interested. Can you share them through belnet.filesender?

Finally, regarding the PDX data, it's really a big job and I can't imagine the size of their animal house! If their data could be shared, that would be great.

Amicalement,

Romain

De: "Florian Rambow" <florian.rambow@kuleuven.be>
À: "Romain Larive" <romain.larive@umontpellier.fr>
Envoyé: Lundi 15 Août 2022 22:30:54
Objet: Re: Data sharing and collaboration

Hi Romain,
sorry for my late reply. Things are still a bit chaotic here.
Attached you can find a ppt with explanations for the different data sets and related .xls files,
also the supp. table of our paper (mmc2.xls). I hope these files are helpful.
In summary, we never reanalyzed DNA-seq (WES...) from scratch for our paper. We rather