

# USER GUIDE



## GUANIN

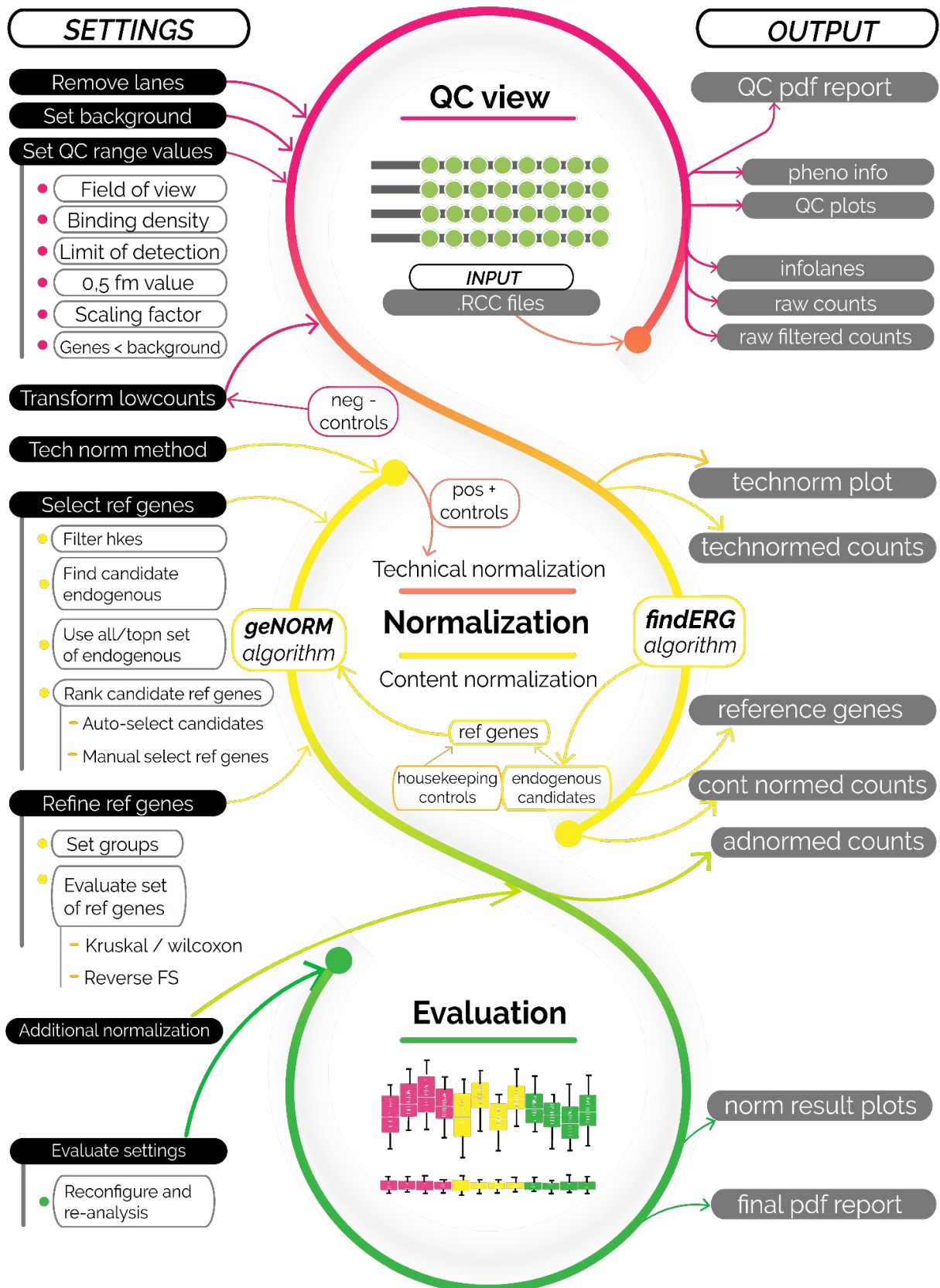
GUI-driven Analysis for Nanostring Interactive Normalization

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Version 0.1: 30/06/2023

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[Tal cual esto lo otro, info de la publicación]



# WORKFLOW DESCRIPTION

## LOADING DATA...

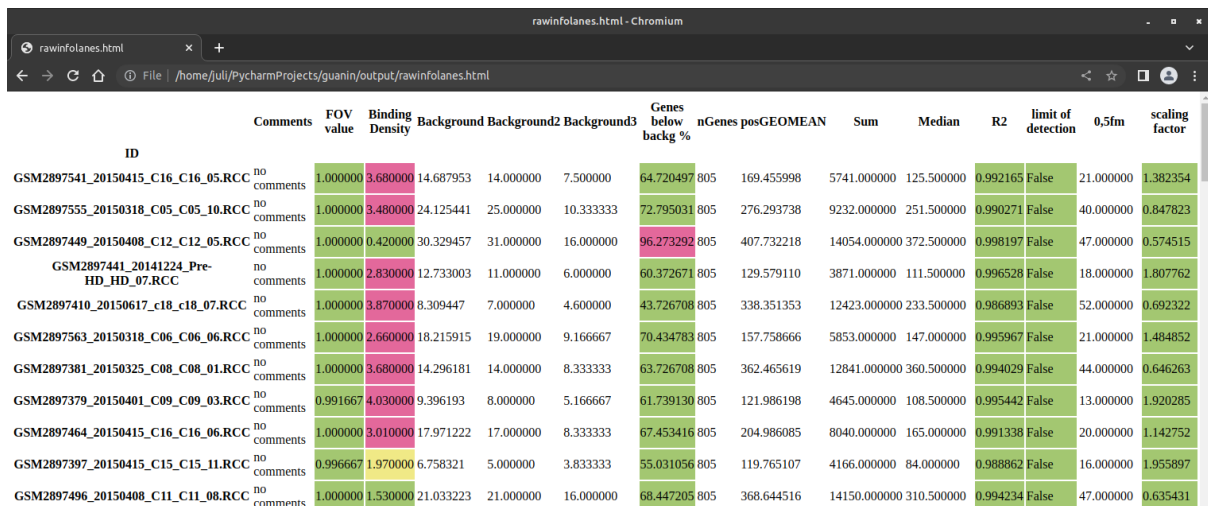
Input for normalization are raw .RCC files. No other Nanostring files need to be provided, neither preprocessing with nSolver or other software is required.

Sample info [condition/group] can be provided to refine content normalization. Although it's recommended, it's not mandatory. This sample info .csv file can be created using a text editor or spreadsheet software such as Excel. It should contain 2 columns: "SAMPLE" (that needs to match sample identification option (sample ID or file name) and "GROUP".

This is intended to represent the phenotype or the condition to study, and should not contain information about batches or replicates.

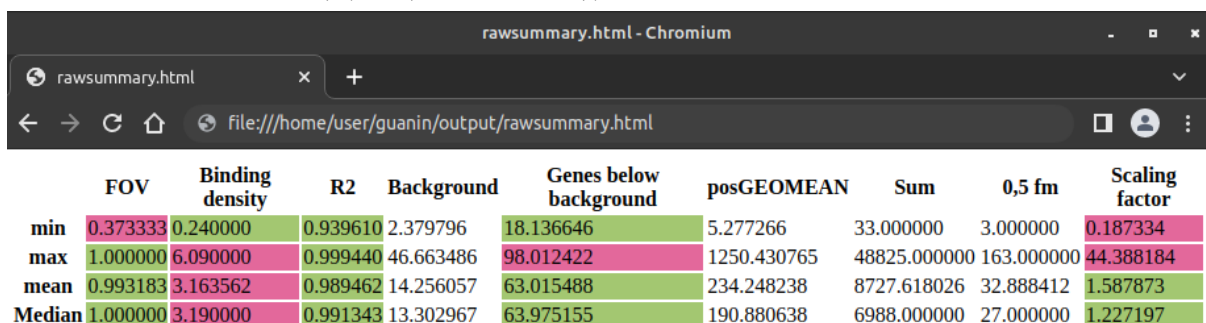
If "sample ID" field in the .RCC files have been declared and you trust this information (no duplicates, etc), "sample ID" is recommended to be used as sample identifier. Else, filename is default parameter as it is foolproof.

→OUTPUT: rawinfofiles.csv (sample information)



ID	Comments	FOV value	Binding Density	Background	Background2	Background3	Genes below backg %	nGenes	posGEOMEAN	Sum	Median	R2	limit of detection	0,5fm	scaling factor
GSM2897541_20150415_C16_C16_05.RCC	no comments	1.000000	3.680000	14.687953	14.000000	7.500000	64.720497	805	169.455998	5741.000000	125.500000	0.992165	False	21.000000	1.382354
GSM2897555_20150318_C05_C05_10.RCC	no comments	1.000000	3.480000	24.125441	25.000000	10.333333	72.795031	805	276.293738	9232.000000	251.500000	0.990271	False	40.000000	0.847823
GSM2897449_20150408_C12_C12_05.RCC	no comments	1.000000	0.420000	30.329457	31.000000	16.000000	96.273292	805	407.732218	14054.000000	372.500000	0.998197	False	47.000000	0.574515
GSM2897441_20141224_Pre-HD_HD_07.RCC	no comments	1.000000	2.830000	12.733003	11.000000	6.000000	60.372671	805	129.579110	3871.000000	111.500000	0.996528	False	18.000000	1.807762
GSM2897410_20150617_c18_c18_07.RCC	no comments	1.000000	3.870000	8.309447	7.000000	4.600000	43.726708	805	338.351353	12423.000000	233.500000	0.986893	False	52.000000	0.692322
GSM2897563_20150318_C06_C06_06.RCC	no comments	1.000000	2.660000	18.215915	19.000000	9.166667	70.434783	805	157.758666	5853.000000	147.000000	0.995967	False	21.000000	1.484852
GSM2897381_20150325_C08_C08_01.RCC	no comments	1.000000	3.680000	14.296181	14.000000	8.333333	63.726708	805	362.465619	12841.000000	360.500000	0.994029	False	44.000000	0.646263
GSM2897379_20150401_C09_C09_03.RCC	no comments	0.991667	4.030000	9.396193	8.000000	5.166667	61.739130	805	121.986198	4645.000000	108.500000	0.995442	False	13.000000	1.920285
GSM2897464_20150415_C16_C16_06.RCC	no comments	1.000000	3.010000	17.971222	17.000000	8.333333	67.453416	805	204.986085	8040.000000	165.000000	0.991338	False	20.000000	1.142752
GSM2897397_20150415_C15_C15_11.RCC	no comments	0.996667	1.970000	6.758321	5.000000	3.833333	55.031056	805	119.765107	4166.000000	84.000000	0.988862	False	16.000000	1.955897
GSM2897496_20150408_C11_C11_08.RCC	no comments	1.000000	1.530000	21.033223	21.000000	16.000000	68.447205	805	368.644516	14150.000000	310.500000	0.994234	False	47.000000	0.635431

→OUTPUT: rawsummary (samples summary).



	FOV	Binding density	R2	Background	Genes below background	posGEOMEAN	Sum	0,5 fm	Scaling factor
min	0.373333	0.240000	0.939610	2.379796	18.136646	5.277266	33.000000	3.000000	0.187334
max	1.000000	6.090000	0.999440	46.663486	98.012422	1250.430765	48825.000000	163.000000	44.388184
mean	0.993183	3.163562	0.989462	14.256057	63.015488	234.248238	8727.618026	32.888412	1.587873
Median	1.000000	3.190000	0.991343	13.302967	63.975155	190.880638	6988.000000	27.000000	1.227197

## PRELIMINARY QC INSPECTION...

### - Background determination:

Negative controls are included in nanostring panels in order to set a threshold of non-expressed genes: the background. It can be more or less restrictive, depending on the characteristics of the experiment.

Default background is calculated as the mean of the negative controls + twice the standard deviation. Max of negative controls or mean of negative controls can be used. Also, Guanin implements a new method of selection alternative negative controls, useful in the case there is a problem with predefined negative controls (i.e: they are expressed). In this case, an alternative background is calculated from low-expressed genes among the endogenous. Additionally, background can be set manually.

### - Background correction:

Once background is set, there are several options to handle values below background (low counts):

- a Assimilate to background: Sets all values < background as equal to background.
- b Subtract background: Sets all values as value - background, assigning 0 value to genes expressed equally or lower than background level. (default)
- c Skip: Ignores background correction by not performing any correction.

### - Sample inspection:

Samples with QC abnormalities can be a) flagged or b) removed from the analysis. QC flag values can be set:

- a % of genes below background: A big amount of genes being expressed below background can relate problems with the sample. By default, Guanin flags samples that have more than 80% of their genes less expressed than the background. Lower % values can refine more strictly.

Samples with FOV, BD, linearity or scaling factor values below or above recommended levels can be related with errors:

- b Field of view: Default values: [0.75 - 1]
- c Binding density: Default values: [0.1 - 1.8]
- d Linearity: Default values: [0.75 - 1]
- e Scaling factor: Default values: [0.3 - 3]

Additionally, samples can be manually selected to remove from the analysis. SampleIDs or filenameIDs should not contain spaces, and files manually selected to remove are input separated by spaces ("sample1 sample2 sample3").

Default values for preliminary QC inspection need to be set for plotting and calculations. Then, parameters can be modified in order to re-run QC and refine QC thresholds.

→OUTPUT\_files:

rawcounts.csv (raw matrix counts of endogenous genes)

rawfcounts.csv (raw matrix counts of filtered samples, endogenous genes)

dfhkecounts.csv (raw matrix counts of housekeeping genes)

posnegcounts.csv (raw matrix counts of positive and negative controls)

→OUTPUT\_reports: QC inspection pdf in output/reports (ejemplo adjunto)

Summary infolanes (filtered lanes info)

QCflags.txt (info about what samples have been flagged/discarded and why)

## TECHNICAL NORMALIZATION

In order to perform technical normalization replicates with known concentration are used.

These positive controls are used to calculate a lane-specific scaling factor that can be derived from:

- a posgeomean of positive controls (default)
- b summation of positive controls
- c median of positive controls

Note: \*Although Nanostring nCounter performs first background correction and after that technical normalization, other tools that throw better normalization results apply background correction over technically normalized data, Guanin has shown to obtain better normalization results with this procedure too. For this reason, although for the user this is a conceptually posterior process, QC inspection and technical normalization are performed together.

[esto no lo explica ninguna otra herramienta... tampoco tenemos "datos" para justificarlo (los demás tampoco lo justifican...) igual sobra esta info?]

→OUTPUT\_files:

tnormcounts.csv (matrix counts after technical normalization)

## CONTENT NORMALIZATION

Choosing appropriate housekeeping genes is crucial for normalization. That's why content normalization can be performed using:

- a Default panel housekeeping genes (filtered or not)
- b Default housekeeping + best endogenous candidate reference genes
- c All endogenous genes
- d Manual selection of genes

As housekeeping genes are supposed to have stable high expression on every sample, it is recommended to discard any of them if it is lowly expressed at any sample. Default value for exclusion is set as 50, but higher values are encouraged.

Including most promising endogenous genes that can be used as housekeeping is a Guanin unique feature, that uses findERG (ERgene) algorithm. It finds among endogenous genes the most stably and high expressed among all lanes.

As a standard panel includes 12 housekeeping genes, a number of endogenous candidates is encouraged to be included between 4 and 12 (default 6). This endogenous candidates enter with housekeeping in a evaluation pool and, depending on the results of the final reference genes selection, can be reasonable to re-run including more or less (if housekeeping are bad and all endogenous are chosen over them, for example, more endogenous could be included).

For this evaluation of candidate reference genes, geNorm algorithm is used, retrieving a ranked list of best candidate reference genes, and calculating the optimal number to use. Indeed, a brand new content normalization approach is provided, using ponderated weights of every reference gene based on its ranking geNorm value.

In this way, several combination of parametrizations can be used and refined:

- a What genes to include in the pool as candidate ref genes?
  - a.i Housekeeping only
  - a.ii Housekeeping + n best endogenous (default)
- b Wich genes from the pool will be selected?
  - b.i geNorm n and gene names intelligent selection (default)
  - b.ii genorm n and gene names intelligent ponderated selection (best genes contribute more to normalization that bad genes) [exclusife feature]
  - b.iii Top n best from genorm ranking
- c Avoid geNorm calculations, use...
  - c.i All endogenous genes (useful when default housekeeping genes are bad)

- c.ii Top n most expressed genes (useful when default housekeeping genes are bad)
- c.iii Manual selection of reference genes

Once reference genes are chosen, Guanin allows to perform an [exclusive feature] additional filtering in order to ensure they are not differentially expressed between groups.

If groups are set, they can be flagged or filtered if Kruskal-Wallis or Wilcoxon's tests reveal that they are significantly differentially expressed among groups. In the case of Wilcoxon's tests, Guanin performs every pair of group comparisons (if groups > 2).

Additionally, a (only informative) reverse feature selection ranking can be shown in order to dilucidate what reference genes are more significantly (and how much) revealing a relation with group predicting. Can be interesting to interpret wich genes are the ones the machine learning algorithm considers the most representative and discards them the last, and with what accuracy the algorithm can predict to wich groups belongs a sample from one or a group of reference genes. This accuracy should be close to  $1/j$ , where  $j$  is the number of groups declared in our experiment, and approximately could be warning that something wrong is happening if accuracy is closer to  $2*(1/j)$  than to  $1/j$ .

In case of individual genes, this predictive ability will be spotted by Kruskal or Wilcoxon filtering, so no relevant results should be thrown. But it is in case of additive effect of a combination of genes that results in predictive vinculating effects with the output group when we can spot problems with our reference genes selection.

[Esto es un poco liada conceptualmente, creo que es un buen punto pero no sé yo si estoy sabiendo expresarlo bien pa que se entienda de una sin enrollarme mucho]

OUTPUT\_files: refgenes.csv (count matrix of chosen reference genes)  
rnormcounts.csv (content-normalized count matrix)

OUTPUT\_reports: ranking\_kruskal\_wilcox.csv (p values of association of reference gene expression with groups. Values > 0.05 for all association are encouraged)

Kruskal p-value wilcox: Moderate/Severe wilcox: Moderate/Mild wilcox: Moderate/Control wilcox: Severe/Mild wilcox: Severe/Control wilcox: Mild/Control							
Genes							
S100A9	0.001021	0.271899	0.044164	0.005616	0.004906	0.000636	0.420113
IFITM1	0.001500	0.498962	0.956622	0.000978	0.662956	0.000906	0.003559
GAPDH	0.001685	0.204894	0.141940	0.001551	0.043311	0.001791	0.072097
EEF1G	0.009353	0.017960	0.586491	0.644392	0.004906	0.000636	0.852404
ABCF1	0.014935	0.108319	0.114705	0.391337	0.010013	0.283051	0.009195
RPL19	0.018095	0.014248	0.785650	0.692379	0.007939	0.003415	0.420113
ALAS1	0.025680	0.612090	0.355133	0.012223	0.165518	0.008415	0.106864
TUBB	0.058973	0.176296	0.744154	0.029559	0.284719	0.625585	0.013113
PPIA	0.071057	0.062979	0.663459	0.597843	0.029318	0.008415	0.619796
HPRT1	0.071141	0.128190	0.785650	0.004578	0.191040	0.922258	0.153753
G6PD	0.078426	0.108319	0.586491	0.644392	0.019405	0.011170	0.756495
SDHA	0.095822	0.310494	0.663459	0.113532	0.191040	0.494525	0.013113
POLR1B	0.104936	0.204894	0.462764	0.210270	0.062574	0.625585	0.034980
IL32	0.135682	0.062979	0.446359	0.029559	0.284719	0.922258	0.321062
GUSB	0.182524	0.672604	0.586491	0.040946	0.781511	0.171857	0.094038
HLA-A	0.182960	0.498962	0.624463	0.086457	0.250547	0.063709	0.214847
TBP	0.194641	0.075927	0.703389	0.509651	0.062574	0.171857	0.352236
HLA-B	0.252409	0.176296	0.703389	0.509651	0.074592	0.118420	0.321062
CTSS	0.272561	0.090969	0.384145	0.428794	0.191040	0.118420	0.950549
POLR2A	0.356808	0.398025	0.956622	0.468257	0.165518	0.063709	0.456750
B2M	0.479580	0.398025	0.956622	0.428794	0.250547	0.845252	0.136641
FCGR3A/B	0.536637	0.310494	0.624463	1.000000	0.191040	0.241567	0.576738
OAZ1	0.549882	0.932647	0.210922	0.644392	0.219348	0.558185	0.576738
PTPRC_all	0.775771	0.554113	1.000000	0.428794	0.552297	0.845252	0.385261

metrics\_reverse\_feature\_selection.csv (predictability of groups by association of several reference genes. Values similar to 1/groups are encouraged. High accuracy prediction with few combination of genes may indicate bad combination of reference genes)

	feature_idx	cv_scores	avg_score	feature_names	ci_bound	std_dev	std_err
17	(0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16)	[0.36904762 0.36666667]	0.367857	('G6PD', 'GUSB', 'PPIA', 'POLR1B', 'TUBB', 'HPRT1', 'POLR2A', 'TBP', 'OAZ1', 'SDHA', 'IL32', 'B2M', 'FCGR3A/B', 'CTSS', 'HLA-B', 'PTPRC_all', 'HLA-A')	0.005122	0.001190	0.001190
16	(0, 1, 2, 3, 4, 5, 6, 7, 9, 10, 11, 12, 13, 14, 15, 16)	[0.44047619 0.36666667]	0.403571	('G6PD', 'GUSB', 'PPIA', 'POLR1B', 'TUBB', 'HPRT1', 'POLR2A', 'TBP', 'SDHA', 'IL32', 'B2M', 'FCGR3A/B', 'CTSS', 'HLA-B', 'PTPRC_all', 'HLA-A')	0.158788	0.036905	0.036905
15	(0, 1, 2, 3, 4, 5, 6, 7, 9, 10, 11, 12, 13, 14, 15)	[0.44047619 0.36666667]	0.403571	('G6PD', 'GUSB', 'PPIA', 'POLR1B', 'TUBB', 'HPRT1', 'POLR2A', 'TBP', 'SDHA', 'IL32', 'B2M', 'FCGR3A/B', 'CTSS', 'HLA-B', 'PTPRC_all')	0.158788	0.036905	0.036905
14	(0, 1, 2, 3, 4, 5, 6, 7, 9, 10, 11, 12, 13, 14)	[0.44047619 0.36666667]	0.403571	('G6PD', 'GUSB', 'PPIA', 'POLR1B', 'TUBB', 'HPRT1', 'POLR2A', 'TBP', 'SDHA', 'IL32', 'B2M', 'FCGR3A/B', 'CTSS', 'HLA-B')	0.158788	0.036905	0.036905
13	(0, 1, 2, 3, 4, 5, 6, 7, 9, 10, 11, 12, 13)	[0.44047619 0.36666667]	0.403571	('G6PD', 'GUSB', 'PPIA', 'POLR1B', 'TUBB', 'HPRT1', 'POLR2A', 'TBP', 'SDHA', 'IL32', 'B2M', 'FCGR3A/B', 'CTSS')	0.158788	0.036905	0.036905
12	(0, 1, 2, 3, 4, 5, 6, 7, 10, 11, 12, 13)	[0.44047619 0.36666667]	0.403571	('G6PD', 'GUSB', 'PPIA', 'POLR1B', 'TUBB', 'HPRT1', 'POLR2A', 'TBP', 'IL32', 'B2M', 'FCGR3A/B', 'CTSS')	0.158788	0.036905	0.036905
11	(0, 1, 2, 3, 4, 5, 6, 10, 11, 12, 13)	[0.44047619 0.36666667]	0.403571	('G6PD', 'GUSB', 'PPIA', 'POLR1B', 'TUBB', 'HPRT1', 'POLR2A', 'IL32', 'B2M', 'FCGR3A/B', 'CTSS')	0.158788	0.036905	0.036905
10	(0, 1, 2, 3, 4, 5, 10, 11, 12, 13)	[0.44047619 0.36666667]	0.403571	('G6PD', 'GUSB', 'PPIA', 'POLR1B', 'TUBB', 'HPRT1', 'IL32', 'B2M', 'FCGR3A/B', 'CTSS')	0.158788	0.036905	0.036905
9	(0, 1, 2, 3, 4, 10, 11, 12, 13)	[0.44047619 0.36666667]	0.403571	('G6PD', 'GUSB', 'PPIA', 'POLR1B', 'TUBB', 'IL32', 'B2M', 'FCGR3A/B', 'CTSS')	0.158788	0.036905	0.036905
8	(0, 1, 2, 3, 10, 11, 12, 13)	[0.44047619 0.36666667]	0.403571	('G6PD', 'GUSB', 'PPIA', 'POLR1B', 'IL32', 'B2M', 'FCGR3A/B', 'CTSS')	0.158788	0.036905	0.036905
7	(0, 1, 2, 10, 11, 12, 13)	[0.44047619 0.36666667]	0.403571	('G6PD', 'GUSB', 'PPIA', 'IL32', 'B2M', 'FCGR3A/B', 'CTSS')	0.158788	0.036905	0.036905
6	(0, 1, 10, 11, 12, 13)	[0.44047619 0.36666667]	0.403571	('G6PD', 'GUSB', 'IL32', 'B2M', 'FCGR3A/B', 'CTSS')	0.158788	0.036905	0.036905
5	(0, 10, 11, 12, 13)	[0.44047619 0.36666667]	0.403571	('G6PD', 'IL32', 'B2M', 'FCGR3A/B', 'CTSS')	0.158788	0.036905	0.036905
4	(10, 11, 12, 13)	[0.44047619 0.36666667]	0.403571	('IL32', 'B2M', 'FCGR3A/B', 'CTSS')	0.158788	0.036905	0.036905
3	(10, 11, 13)	[0.31071429 0.4375 ]	0.374107	('IL32', 'B2M', 'CTSS')	0.272757	0.063393	0.063393
2	(11, 13)	[0.36666667 0.28333333]	0.325000	('B2M', 'CTSS')	0.179277	0.041667	0.041667
1	(11,)	[0.33333333 0.325 ]	0.329167	('B2M,')	0.017928	0.004167	0.004167



## ADDITIONAL NORMALIZATION...

Additional normalization can be useful in the case we need our data in an specific format, such as in a range to 0-1, etc. For that, it can be implemented:

- quantile normalization
- standarization

OUTPUT\_files: adnormcounts.csv (count matrix of additionaly normalized data)

## EVALUATION OF NORMALIZATION

In order to assess if normalization is offering reasonable results, two measures can be used that make use of relative log expression.

Relative log expression are useful for visualizing unwanted variation.

- RLE plots, comparing pre-normalization and post-normalization. Narrow boxplots mean less unknown expression differences.
- IQR, that can be used to numerically compare different normalization parametrizations that could suit our experiment.

OUTPUT\_reports: norm\_report.pdf (showing genorm results for reference genes chosen, RLE plots and IQR).

<https://i.imgur.com/TBTcTnm.png>

GUANIN: Nanostring Interactive Normalization

**- Loading data -**

Select RCC files: Select folder containing RCC

Selected folder: /home/juli/PycharmProjects/guanin/data

Select groups file: Select csv file

Selected groups file: groups\_s5.csv

Sample identifier: Filename

Pop up infolanes and rawQC report ☐ Run load RCCs

**- Technical normalization parameters -**

Method for technical normalization: Use posgeomean

Run technical normalization

**- Content normalization parameters -**

Filter housekeeping panel genes by min counts: 50

Include best endogenous as reference candidates: ☒

How many best endogenous genes to include: 6

What reference genes selection to use? Genorm auto selection (default)

If n genes to be set from last option: 6

If manual selection is chosen, input genes:

How to filter/flag reference genes: Kruskal-Wallis filtering

Perform additional normalization? No

Format export results: Normalized count matrix

Pop out info about ref genes: ☒ Run content normalization

**- Quality Control parameters -**

Choose background: Alternative background (Filtered neg ctrls)

Set manual background: 0

Background correction (low counts): Subtract background value

% of low counts for lane remove: 80

Min fov: 0.75 Max fov: 1.00

Min binding density: 0.10 Max binding density: 1.80

Min linearity: 0.75 Max linearity: 1.00

Min scaling factor: 0.30 Max scaling factor: 3.00

Remove bad samples? Remove auto-QC flagged

Manual input lanes to remove:

Pop out new infolanes and QC report ☐ Run QC filtering

Flagged lanes: 6 badlanes detected, check output/reports/QCFlags.txt

**- Normalization evaluation -**

Run RLE plot, IQR: 32.48584779658899

Normalized RLE plot, IQR: 29.507975000912857

Run evaluation

**Genes**

Genes	Kruskal p-value	wilcox g0/g1	wilcox g0/g2	wilcox g0/g3
S100A9	0.001021	0.271899	0.000636	0.0049
IFITM1	0.001500	0.498962	0.000906	0.6629
GAPDH	0.001685	0.204894	0.001791	0.0433
EEF1G	0.009333	0.017968	0.000636	0.0049
ABCF1	0.012531	0.176296	0.204539	0.0062
RPL19	0.018095	0.014248	0.003415	0.0079
ALAS1	0.026424	0.612099	0.008415	0.1655
POLR1B	0.041524	0.128319	0.283051	0.0156
HPRT1	0.050176	0.108319	0.922258	0.1655
TUBB	0.051763	0.176296	0.625585	0.2505
PPIA	0.052740	0.042522	0.008415	0.0239
SDHA	0.082832	0.310494	0.494525	0.1655
G6PD	0.094397	0.108319	0.014697	0.0194
IL32	0.135682	0.062979	0.922258	0.2847
GUSB	0.140948	0.735317	0.241567	0.8429
TBP	0.149148	0.062979	0.118420	0.0433
HLA-A	0.182960	0.498962	0.063709	0.2305
HLA-B	0.252409	0.176296	0.118420	0.0745
CTSS	0.272561	0.090969	0.118420	0.1910
POLR2A	0.361733	0.399025	0.063709	0.1910
B2M	0.479580	0.399025	0.845252	0.2305
FCGR3A/B	0.536637	0.310494	0.241567	0.1910
OAZ1	0.549882	0.932647	0.550185	0.2193
PTPRC_all	0.775773	0.554113	0.845252	0.5522

Evaluation and data export ready, check "output" folder

Performing additional normalization. Elapsed 94.61888121231079 seconds

Exporting normalization results. Elapsed 94.60184612358464 seconds

Evaluating and plotting normalization results. Elapsed 94.18920832623291 seconds

Plotting raw RLE plot...

Plotting normalized RLE plot...

Finished. Elapsed 94.801139345169867 seconds



## EXAMPLE DATASETS:

D1: GSE183071 – Blood study of gene expression profiling on the nasal epithelium in COVID-19 severity.

This dataset consists on 54 samples including controls, mild, moderate and severe severity.

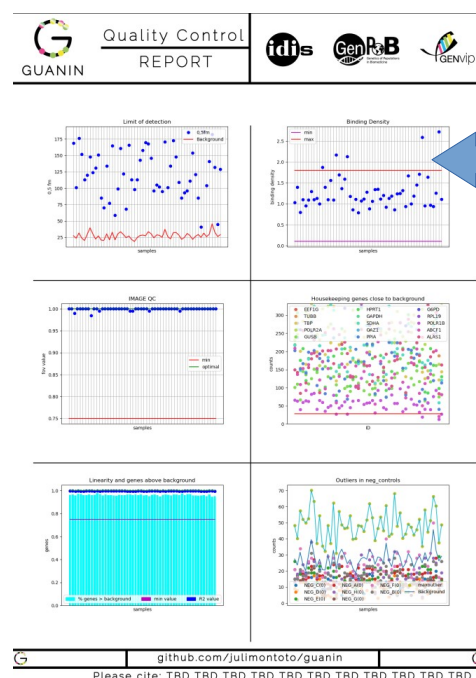
Raw data inspection may suggest there is a problem with binding density, while the rest of the samples are QC-ok.

	FOV	Binding density	R2	Background	Genes below background	posGEOMEAN	Sum	0,5 fm	Scaling factor
min	0.984536	0.790000	0.994647	18.754359	13.980263	458.621941	13395.000000	41.000000	0.667838
max	1.000000	2.720000	0.999137	45.756282	32.565789	1726.146285	60421.000000	186.000000	2.513586
mean	0.999045	1.282963	0.996747	27.727611	22.947125	1152.785765	40192.481481	122.944444	1.087117
Median	1.000000	1.155000	0.997049	27.624700	23.273026	1165.965936	41032.500000	121.500000	0.988744

We can see that 5 samples (B0513, B0318, B0319, B0369, B0343) have high binding density value. We can choose to alter or not max binding density values to exclude this samples, as default option will be to discard them.

Rest of settings run by default, after QC filtering we can see after discarding 5 lanes all values are QC-ok.

At this point, we can view QC inspection plots and info about flagged/discarded lanes in the selected output folder:



After running default technical normalization, content normalization can be performed with few restrictions and no suggested endogenous reference genes.

We can see GUANIN filters POLR1B for having less than 50 counts (housekeeping genes are supposed to be expressed), but continues the analysis with the rest of the 14 genes, and after applying geNorm selection of the n reference genes, GUANIN has used 13 to perform content normalization.

Ref. genes selected (auto): ['EEF1G', 'OAZ1', 'POLR2A', 'G6PD', 'GAPDH', 'ALAS1', 'GUSB', 'TUBB', 'SDHA', 'ABCF1', 'HPRT1', 'TBP', 'PPIA']

As we see, if we apply Wilcoxon filtering genes that can be associated to any of the conditions, only three valid housekeeping genes remain ['SDHA', 'TBP', 'ABCF10']. This is usually not enough for proper normalization, or even for genorm preprocess.

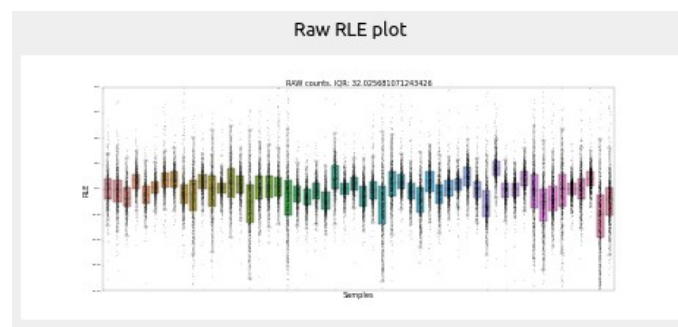
We can fix that selecting kruskal-wallis filter, which is less sensitive, but that could skew our results in the way of the related to a condition but selected anyways as reference genes.

In order to assess this common problematic, we can use ERgene to find best endogenous and include them in the pool that are validated by kruskal/wilcox and into genorm algorithm. Changing that parameters in guanin, including 6 most promising endogenous and wilcoxon filtering, we get a subselection of 5 genes, both endogenous and housekeeping, that can be used for content normalization: ['B2M', 'CTSS', 'PTPRC\_all', 'SDHA', 'TBP'].

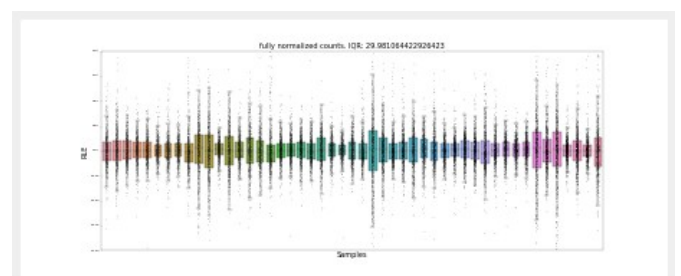
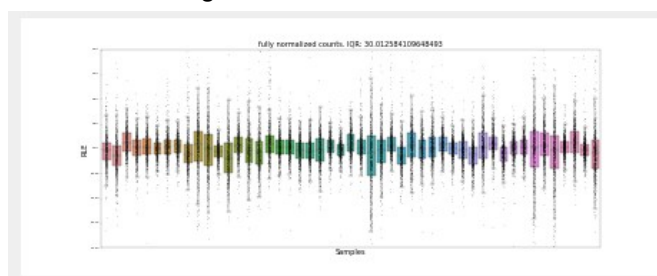
As we see, 2 out of 3 preselected housekeeping are included too, but GUANIN has found better company for them as reference genes for three endogenous genes.

When running evaluation, we expect to see narrower bars with means closer to the center. Nevertheless, this can also mean loss of biological variability (we want the experimental variability out, but not the biological one). So RLE plots are useful to have an idea of how the normalization behaves on different processes.

Note: for some methods that intend to remove all unwanted variation possible, RLE plots can be even narrower because of removing as variability as possible, with risk of removing biological variability. On the other hand, methods intended to target remove technical and biological variation preserve more general variation and have less cute RLE plots. So RLE plots are informative, but not definitive. Indeed, using all genes to cont norm is a method that is almost only used when others fail, as you can be losing significance on the results of the experiment, and usually, this method reports narrower RLE plots, because of removing "too much" variability.



Reference genes



selected content normalization vs all genes normalization RLE plots

## EXAMPLE DATASETS:

D2: GSE160208 – Gene expression in the brain of sporadic Creutzfeldt-Jakob disease patients (CJD), and normal controls (CT).

This dataset contains 47 samples from 2 groups disease and control.

For this dataset we see all samples are QC-ok, so we proceed with technical normalization.

Results on evaluation of reference genes (panel housekeeping and best endogenous), results in only 2 genes suitable to be reference genes for content normalization. As it is minimum required 3 genes, we may have several options:

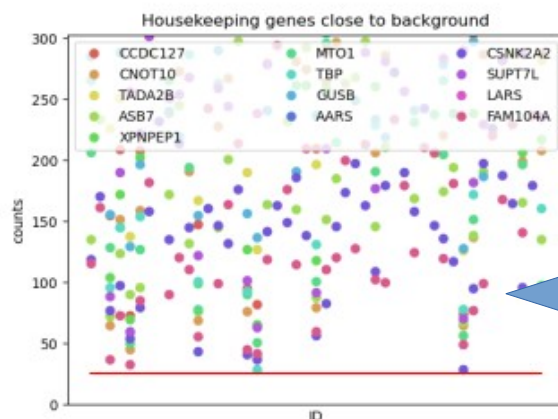
- Lower the threshold of min counts for housekeeping, in case there is any low but stably expressed that can be rescued.
- Include more best endogenous as candidates (
- Introduce a selection of best bad genes (not very good idea as kruskal values of bad genes are very low)

Using first approach, from info in the QC report:

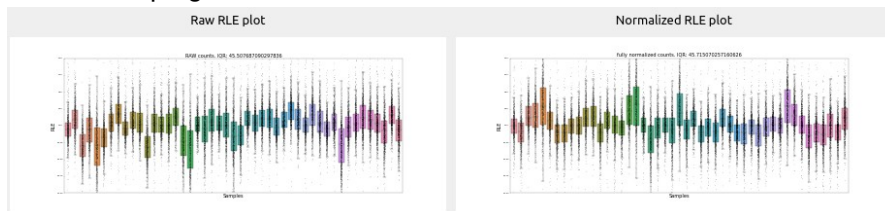
We can see there are a few genes behind 50 counts but above the background, so a threshold between 50 and the background should be a reasonable choice.

In the other hand, we can include 25 of the best endogenous genes instead of 6.

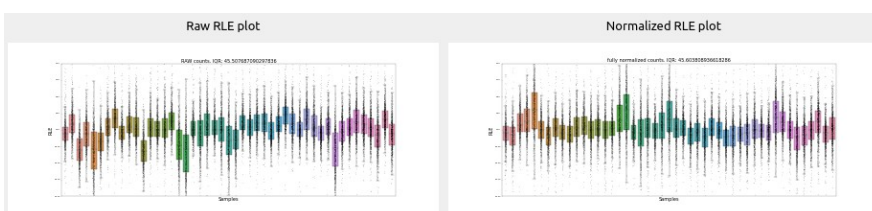
From this we get 1 more gene. We can decide to perform normalization with these 3 suitable genes, or proceed with alternative approaches like all expressed endogenous genes.



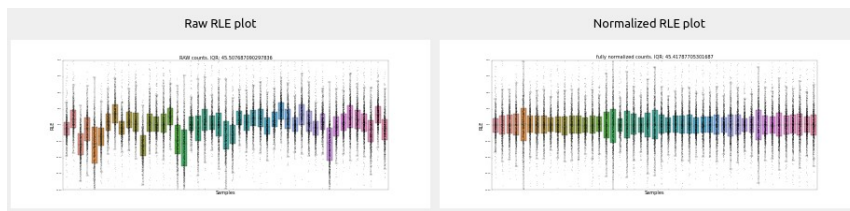
- Housekeeping normalization:



- Filtered and refined reference genes selected from housekeeping+ endogenous (3 genes) normalization:



- All endogenous genes normalization:



The scientist can choose which normalization method better suits the experiment.

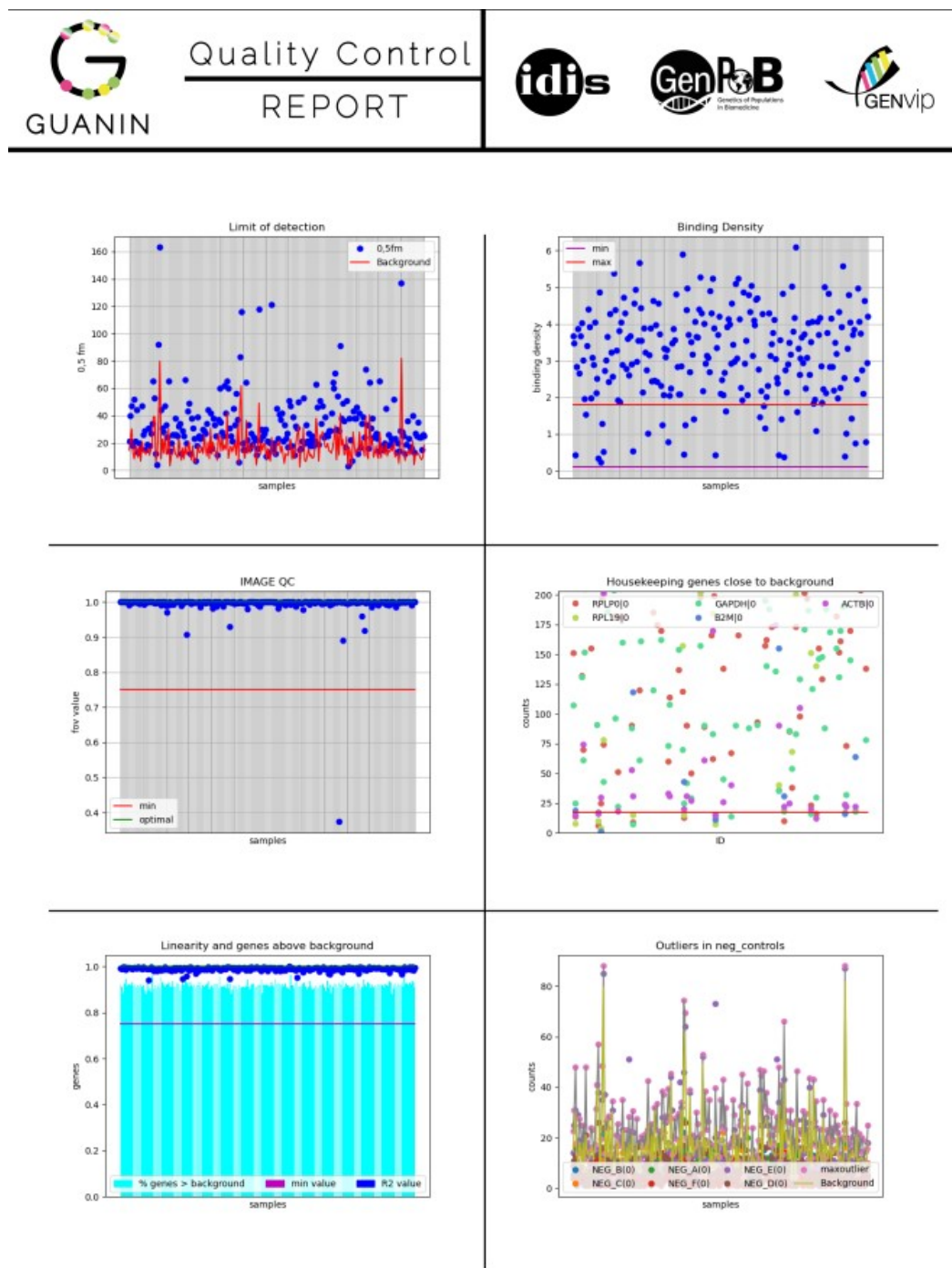
## EXAMPLE DATASETS:

D3: GSE160208 – Gene expression in the brain of sporadic Creutzfeldt-Jakob disease patients (CJD), and normal controls (CT).

This dataset contains 233 samples from 2 groups disease and control.

This dataset, as many others found in databases, has a lot of QC problems that would be more difficult to address with other normalization tools.

We can see in QC report that a lot of samples are above max binding density, some of them below limit of detection, one has very low fov value, there are several housekeeping genes close to background and there also are a lot of outliers in negative controls.





Discarding and repeating the experiment could be a reasonable choice. But if we would continue with the analysis we can tweak QC settings in order to allow some more than 14 out of the 233 to pass QC.

Probably the safest choice would be to set to 3 maximum binding density, as it is the biggest problem, hoping we get a good number of samples for both groups.

We also detect that around 200 samples have more than 50% of their genes with values below background, which may reveal a technical problem with the experiment.

Anyways as a “bad data” example, we can tweak:

- Alternative background (as there are outliers in negative controls).
- 90% of low counts to remove (maybe there is very little expression in the panel, for some biological reason).
- 3 max fov.

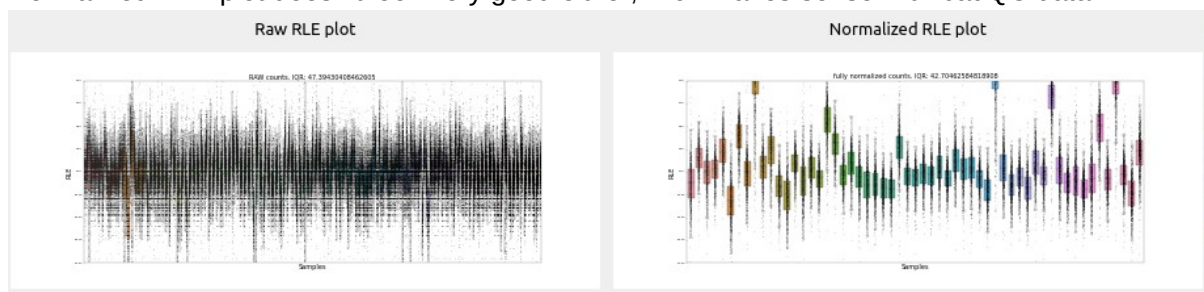
With this, we have 57 samples Qc-“ok” in the analysis.

As some of housekeeping genes are not expressed, we will refine them with a selection of the most suitable endogenous (12 in this case, for example).

We can see only 5 housekeeping genes are suitable to be used as reference genes.

Kruskal-wallis test discard none of the 17 preselected genes for being associated with the condition, so we let geNorm algorithm to choose how many and which genes are most suitable for the analysis. From these 17 preselected genes, it selects 13 as reference genes: 4 of the 5 housekeeping valid and 9 endogenous suitable to be used as reference genes.

Normalized RLE plot doesn't look very good either, which makes sense with badQC data.



Note: Although modification of parameters and re-running blocks for interactive normalization should work, the combination of possibilities is untestable, so when you find the best normalization settings for your experiment we recommend a complete re-run of the full process.



## CLI COMMANDS HELP:

- Argument: '-f', '--folder', *type=*str, *default=* pathlib.Path.cwd() / 'examples/d1\_COV\_GSE183071', *help=*'relative folder where RCC set is located.'
- Argument: '-minf', '--minfov', *type=*float, *default=*0.75, *help=*'set manually min fov for QC'
- Argument: '-maxf', '--maxfov', *type=*float, *default=*1, *help=*'set manually max fov for QC'
- Argument: '-minbd', '--minbd', *type=*float, *default=*0.1, *help=*'set manually min binding density for QC'
- Argument: '-maxbd', '--maxbd', *type=*float, *default=*1.8, *help=*'set manually max binding density for QC'
- Argument: '-minlin', '--minlin', *type=*float, *default=*0.75, *help=*'set manually min linearity for QC'
- Argument: '-maxlin', '--maxlin', *type=*float, *default=*1, *help=*'set manually max linearity for QC'
- Argument: '-minscf', '--minscalingfactor', *type=*float, *default=*0.3, *help=*'set manually min scaling factor for QC'
- Argument: '-maxscf', '--maxscalingfactor', *type=*float, *default=*3, *help=*'set manually max scaling factor for QC'
- Argument: '-swbrrq', '--showbrowserrawqc', *type=*bool, *default=*False, *help=*'pops up infolanes and qc summary'
- Argument: '-swbrq', '--showbrowserqc', *type=*bool, *default=*False, *help=*'pops up infolanes and qc summary')
- Argument: '-swbrcn', '--showbrowsercnorm', *type=*bool, *default=*False, *help=*'pops up infolanes and qc summary')
- Argument: '-lc', '--lowcounts', *type=*str, *default=*'sustract', *choices=*['skip', 'asim', 'sustract'], *help=*'what to do with counts below background?')
- Argument: '-mi', '--modeid', *type=*str, *default=*'filename', *choices=*['sampleID', 'filename', 'id+filename'], *help=*'choose sample identifier. sampleID: optimal if assigned in rccs. filenames: easier to be unique. id+filename: care with group assignment coherence')
- Argument: '-mv', '--modeview', *type=*str, *default=*'view', *choices=*['justrun', 'view'], *help=*'choose if plot graphs or just run calculations')
- Argument: '-tnm', '--tecnormeth', *type=*str, *default=*'posgeomean', *choices=*['posgeomean', 'Sum', 'Median', 'regression'], *help=*'choose method for technical normalization')
- Argument: '-reg', '--refendgenes', *type=*str, *default=*'endhkes', *choices=*['hkes', 'endhkes'], *help=*'choose refgenes, housekeeping, or hkes and endogenous')
- Argument: '-re', '--remove', *type=*str, *nargs=*'+', *default=*None, *help=*'lanes to be removed from the analysis')
- Argument: '-bg', '--background', *type=*str, *default=*'Background', *choices=*['Background', 'Background2', 'Background3', 'Backgroundalt'], *help=*'choose background: b1=meancneg+(2\*std), b2=maxcneg, b3=meancneg, balt=')
- Argument: '-pbb', '--pbelowbackground', *type=*int, *default=*85, *help=*'if more than %bb genes are below background, sample gets removed from analysis')
- Argument: '-mbg', '--manualbackground', *type=*float, *default=*None, *help=*'set manually background')
- Argument: '-crg', '--chooserefgenes', *type=*str, *nargs=*'+', *default=*None, *help=*'list of strings like. choose manually reference genes to use over decided-by-program ones')
- Argument: '-fgv', '--filtergroupvariation', *type=*str, *default=*'filterkrus', *choices=*['filterkrus', 'filterwilcox', 'flagkrus', 'flagwilcox', 'nofilter'], *help=*'filter or flag preselected ref genes by significant group-driven differences? needs groups to be declared')
- Argument: '-fsn', '--featureselectionneighbors', *type=*float, *default=*4, *help=*'number of neighbors for feature selection analysis of refgenes. Recommended 3-6')
- Argument: '-g', '--groups', *type=*str, *default=*'yes', *choices=*['yes', 'no'], *help=*'defining groups for kruskal/wilcox/fs analysis?')
- Argument: '-ne', '--numend', *type=*int, *default=*6, *help=*'number of endogenous to find by ERgene to include in analysis to check viability as refgenes')
- Argument: '-ar', '--autorename', *type=*str, *default=*'off', *choices=*['on', 'off'], *help=*'turn on when sample IDs are not unique, be careful on sample identification detail')
- Argument: '-cn', '--contnorm', *type=*str, *default=*'refgenes', *choices=*['ponderaterefgenes', 'refgenes', 'all', 'topn'])
- Argument: '-an', '--adnormalization', *type=*str, *default=*'no', *choices=*['no', 'standardization'],

'quantile'], *help*='perform additional normalization? standarization and quantile normalization available')

- Argument: '-tn', '--topngenestocontnorm', *type*=int, *default*=100, *help*='set n genes to compute for calculating norm factor from top n expressed endogenous genes')
- Argument: '-mch', '--mincounthkes', *type*=int, *default*=80, *help*='set n min counts to filter hkes candidate as refgenes')
- Argument: '-nrg', '--nrefgenes', *type*=int, *default*=None, *help*='set n refgenes to use, overwriting geNorm calculation')
- Argument: '-lr', '--laneremover', *type*=str, *default*='yes', *choices*=['yes', 'no'], *help*='option to perform analysis with all lanes if set to no')
- Argument: '-grn', '--groupsinnormgenes', *type*=str, *default*='no', *choices*=['yes', 'no'], *help*='want groups to be specified in last column of rnormgenes dataframe?')
- Argument: '-lo', '--logarizedoutput', *type*=str, *default*='10', *choices*=['2', '10', 'no'], *help*='want normed output to be logarized? in what logbase?')
- Argument: '-le', '--logarizeforeval', *type*=str, *default*='10', *choices*=['2', '10', 'no'], *help*='logarithm base for RLE calculations')
- Argument: '-gf', '--groupsfile', *type*=str, *default*='examples/groups\_d1\_COV\_GSE183071.csv', *help*='enter file name where groups are defined')
- Argument: '-st', '--start\_time', *type*=float, *default* = time.time())
- Argument: '-cs', '--current\_state', *type*=str, *default*='Ready')
- Argument: '-ftl', '--firsttransformlowcounts', *type*=bool, *default*=True)
- Argument: '-of', '--outputfolder', *type*=str, *default*= tempfile.gettempdir() + '/guanin\_output')
- Argument: '-sll', '--showlastlog', *type*=bool, *default* = False)