

Filtering

In [10]:

```
import pandas as pd
import numpy as np
import os
import gc
import matplotlib.pyplot as plt
import time

from functions.filtering import *
from functions.plotting import *
from functions.fitting import *

_FOLDER = "database/"
_FOLDER_2 = "figures/"
_FOLDER_3 = "results/"
SAVE_FIGURES = False

R2_limit = 0.99
```

Original data

In [11]:

```
drug_curves = pd.read_csv(_FOLDER+"normalised_dose_response_data.csv")

if "Unnamed: 0" in drug_curves:
    drug_curves.drop("Unnamed: 0", axis=1, inplace=True)

col_to_drop = ["per_slope_change_"+str(i) for i in range(8)] + W
              ["slope_" + str(i) for i in range(9)]
drug_curves.drop(col_to_drop, axis=1, inplace=True)

conc_columns= ["fd_num_"+str(i) for i in range(10)]
response_norm = ['norm_cells_'+str(i) for i in range(10)]
CCL_names = dict(zip(drug_curves["COSMIC_ID"], drug_curves["CELL_LINE_NAME"]))
df= pd.read_csv(_FOLDER+'Drug_Features.csv')
drug_names = dict(zip(df["Drug ID"].values, df["Drug Name"].values))
del df
drug_curves["drug_name"] = drug_curves["DRUG_ID"].map(drug_names)
drug_curves["CCL_name"] = drug_curves["COSMIC_ID"].map(CCL_names)
drug_curves.shape
```

Out[11]:

(225384, 28)

Filtering 1: 4 stage filtering

```
# Description of filtering_sigmoid_curves:
"""
    filtering_scenario = [1,2,3,4]
```

0.2
|| || ||

```
%%time
# difference between middle points 0.2
df_filt_1234 = filtering_sigmoid_curves(drug_curves, filtering_scenario=[1,2,3,4], W
                                         response_columns = response_norm, W
                                         first_points_lower_limit = 0.8, last_points_upper_limit = 0.2,
                                         middle_points_limit = -0.2)
df_filt_1234.to_csv(_FOLDER_3+"filt_1234_02.csv", index=False)
```

In [13]:

```
100%|███████████████████████████████████████████████████████████|  
█ | 2108/2108 [00:03<00:00, 633.77it/s]
```

localhost:8888/notebooks/1_4_Filtering_Fitting.ipynb

```
# description of auc_filtration
"""
    1. Remove all the curves where the normalised response value is greater than one at zero
dosage.
    2. Leave only those curves with an Area Under the Curve (AUC) >0.7.
    3. Compute the Spearman correlation coefficient between the normalised response
and the scaled dosage (so the x-axis and the y-axis).
    4. Further remove the curves for which the Spearman correlation coefficient is zero or
positive.
    5. Cut off samples with last response above 0.2
"""
```

```
%time
df_filt_auc = pd.read_csv(_FOLDER_3+"filt_auc_02.csv")
df = df_filt_auc.copy()
fitting_function = "sigmoid_4_param"

r2, fit_param = fitting_column(df, df.index, x_columns=conc_columns, y_columns= response_norm,
                               fitting_function = fitting_function, default_param=True)
df[fitting_function+"_r2"] = r2
df[fitting_function] = fit_param
df = df[df[fitting_function+"_r2"]>R2_limit]
print(df_filt_auc.shape, df.shape)
df.to_csv(_FOLDER_3+"fit_auc_02.csv", index=False)
```

```
<function sigmoid_4_param at 0x0000024E37FCC900>
(14084, 31) (3062, 33)
CPU times: total: 1min 53s
Wall time: 1min 52s
```

```
functions = [
    "fsigmoid",
    "sigmoid_2_param",
    "sigmoid_3_param",
    "sigmoid_4_param",
    "logistic_4_param",
    "ll4_4_param",
    "ll4R_4_param",
    "logLogist_3_param"]
```

```
%%time
df_no_filt = compare_fitting_functions(drug_curves, functions, conc_columns, response_norm,
                                       save_file_name = _FOLDER_3 + "fit_no_filt.csv")
```

In []:

