Exploring data quality

In [8]:

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

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

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

In [9]:

```
Y_LIMIT_1 = 0.8 # for group 1a
R2_LIMIT = 0.9 # for S-shape fitting
Y_LOWER_LIMIT  = 0.5 #for group 2a
```

Original data

In [19]:

```
_FOLDER = "C:/Users/junny/GitRepos/DrugProfiles_2/database/"

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[19]:

```
(225384, 28)
```

Group 1: Responses above 1

In [20]:

```
#available functions in a filtering script
print("Available functions in filtering module: ₩n")
for func in content_filtering().keys():
    print(func)
```

```
Available functions in filtering module:

find_high_responses
cut_off_outliers
find_ascending_data
filtering_sigmoid_curves
auc_filtration
filter_good_response
select_group_limits
select_group_1
select_group_1a
select_group_1b
select_group_2
select_group_2a
select_group_2b
```

In [21]:

```
# group 1 - all responses above 1
gr_1 = select_group_1(drug_curves, response_norm)
gr_1.shape
```

Out[21]:

```
(162059, 28)
```

In [22]:

```
gr_1a = select_group_1a(gr_1, response_norm, Y_LIMIT_1)
gr_1a.shape
```

Out[22]:

```
(74115, 28)
```

In [23]:

```
%%time
fit_functions = ["sigmoid_4_param","logistic_4_param"]

gr_1b = select_group_1b(gr_1.loc[list(set(gr_1.index)-set(gr_1a.index))],
                        fit_functions, conc_columns, response_norm,
                        y_limit=Y_LIMIT_1, r2_limit=R2_LIMIT,
                       )
gr_1b.shape
```

```
 sigmoid_4_param

100%|████████████████████████████████████████████████████████████████████████████| 87944/87944 [08:28<00:00, 172.85it/s]

<function sigmoid_4_param at 0x000002864B5791C0>

 logistic_4_param

100%|████████████████████████████████████████████████████████████████████████████| 87944/87944 [07:51<00:00, 186.59it/s]

<function logistic_4_param at 0x000002864B5793A0>
CPU times: total: 16min 23s
Wall time: 16min 20s
```

Out[23]:

```
(41602, 32)
```

In [24]:

```
gr_1b.columns
```

Out[24]:

```
Index(['CELL_LINE_NAME', 'COSMIC_ID', 'DRUG_ID', 'DRUGID_COSMICID',
       'FOLD_DILUTION', 'MAX_CONC', 'fd_num_0', 'fd_num_1', 'fd_num_2',
       'fd_num_3', 'fd_num_4', 'fd_num_5', 'fd_num_6', 'fd_num_7', 'fd_num_8',
       'fd_num_9', 'norm_cells_0', 'norm_cells_1', 'norm_cells_2',
       'norm_cells_3', 'norm_cells_4', 'norm_cells_5', 'norm_cells_6',
       'norm_cells_7', 'norm_cells_8', 'norm_cells_9', 'drug_name', 'CCL_name',
       'sigmoid_4_param_r2', 'sigmoid_4_param', 'logistic_4_param_r2',
       'logistic_4_param'],
      dtype='object')
```

In [25]:

```
gr_1c = gr_1.loc[list(set(gr_1.index)-set(gr_1a.index)-set(gr_1b.index))]
gr_1c.shape
```

Out[25]:

```
(46342, 28)
```

In [26]:

```
assert gr_1.shape[0]==gr_1a.shape[0]+gr_1b.shape[0]+gr_1c.shape[0]
```

In [27]:

```
gr_2 = select_group_2(drug_curves, response_norm)
gr_2.shape
```

Out[27]:

```
(63325, 28)
```

In [28]:

```
gr_2a = select_group_2a(drug_curves, response_norm, Y_LOWER_LIMIT)
gr_2a.shape
```

Out[28]:

```
(26849, 29)
```

In [30]:

```
%%time
fit_functions = ["sigmoid_4_param","logistic_4_param"]

gr_2b = select_group_2b(gr_2.loc[list(set(gr_2.index)-set(gr_2a.index))],
                        fit_functions, conc_columns, response_norm,
                        y_lower_limit =Y_LOWER_LIMIT, r2_limit= R2_LIMIT
                       )
gr_2b.shape
```

```
 sigmoid_4_param

100%|████████████████████████████████████████████████████████████████████████| 3647
6/36476 [03:41<00:00, 164.31it/s]

<function sigmoid_4_param at 0x000002864B5791C0>

 logistic_4_param

100%|████████████████████████████████████████████████████████████████████████| 3647
6/36476 [02:29<00:00, 244.71it/s]

<function logistic_4_param at 0x000002864B5793A0>
CPU times: total: 6min 12s
Wall time: 6min 11s
```

Out[30]:

```
(24026, 32)
```

In [31]:

```
gr_2c = gr_2.loc[list(set(gr_2.index)-set(gr_2a.index)-set(gr_2b.index))]
gr_2c.shape
```

Out[31]:

```
(12450, 28)
```

In [32]:

```
assert gr_2.shape[0]==gr_2a.shape[0]+gr_2b.shape[0]+gr_2c.shape[0]
```

Save figures for the paper

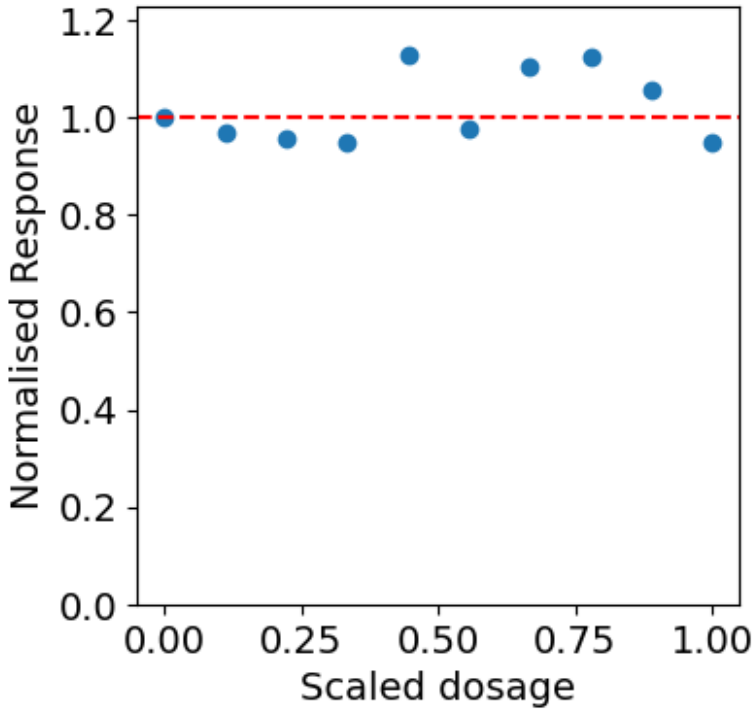
In [46]:

```
def OneFigNoFitting(df, drug_id, ccl_name,
                    x_columns, y_columns, size=8,dpi=300,
                    upper_limit=None, lower_limit=None, save_fig_name=None):

    ind = df[(df["DRUG_ID"]==drug_id)&(df["CELL_LINE_NAME"]==ccl_name)].index
    drug_name = df.loc[ind, "drug_name"].values[0]

    print(f"Drug: {drug_name} ({drug_id}) / CCL: {ccl_name}")# % drug_name +str(drug_id) +" / CCL: "+ s
    x = df.loc[ind, x_columns]
    y = df.loc[ind, y_columns].values[0] #possible problems are here

    plt.figure(figsize=(size, size))
    if max(y)>1:
        max_y= max(y)+0.1
    else:
        max_y = 1.1
    plt.ylim([0, max_y])
    plt.scatter(x,y)

    plt.xlabel("Scaled dosage")
    plt.ylabel("Normalised response")
    if upper_limit:
        plt.axhline(upper_limit,color='red',ls='--')
    if lower_limit:
        plt.axhline(lower_limit, color='black',ls='--')

    plt.tick_params(labelsize=14)
    plt.xlabel("Scaled dosage", fontsize=14)
    plt.ylabel("Normalised Response", fontsize=14)
    if save_fig_name:

        plt.savefig(save_fig_name, bbox_inches='tight', dpi=dpi)
        plt.show();
    else:
        plt.show();
```

In [36]:

```
# group_1a
group = "1a"
drug_id = 205
ccl_name = "ES6"
one_fig_no_fitting(gr_1, drug_id=drug_id, ccl_name=ccl_name, size=4, dpi=500,
                x_columns = conc_columns, y_columns = response_norm,
                upper_limit=1, lower_limit=None,
                save_fig_name=f"figures/gr_{group}_{drug_id}_{ccl_name}.png"
               )
```

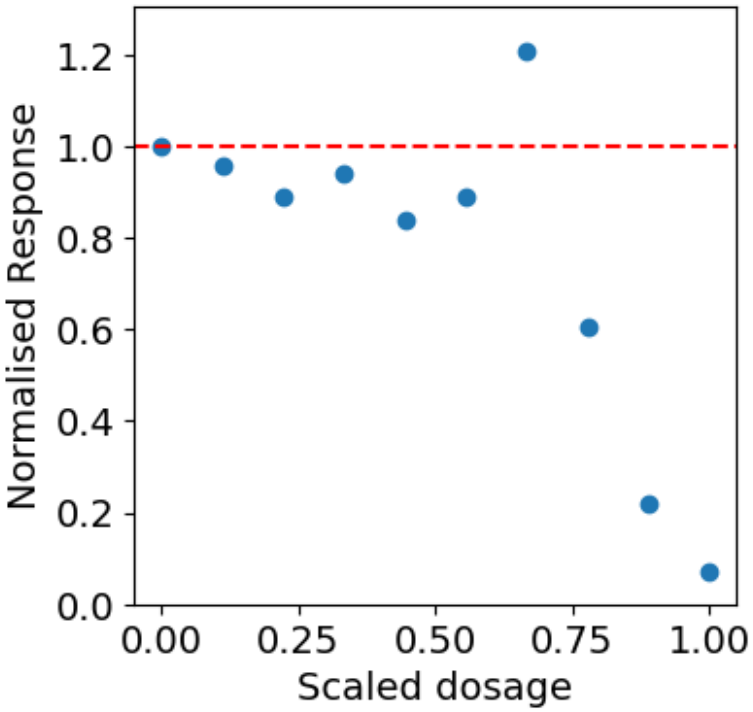
```
Drug: Avagacestat (205) / CCL: ES6
```



In [51]:

```
# group_1b
group = "1b"
drug_id = 245
ccl_name = "HDQ-P1"
OneFigNoFitting(gr_1b, drug_id=drug_id, ccl_name=ccl_name, size=4, dpi=500,
                x_columns = conc_columns, y_columns = response_norm,
                upper_limit=1, lower_limit=None,
                save_fig_name=f"figures/gr_{group}_{drug_id}_{ccl_name}.png"
               )
```

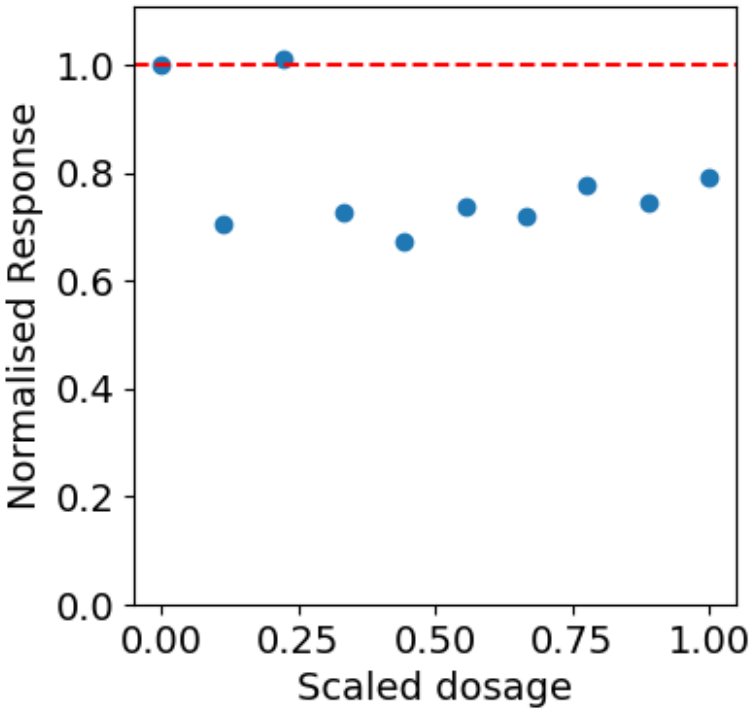
```
Drug: UNC0638 (245) / CCL: HDQ-P1
```



In [50]:

```
# group_1c
group = "1c"
drug_id = 56
ccl_name = "RKO"
OneFigNoFitting(gr_1c, drug_id=drug_id, ccl_name=ccl_name, size=4, dpi=500,
                x_columns = conc_columns, y_columns = response_norm,
                upper_limit=1, lower_limit=None,
                save_fig_name=f"figures/gr_{group}_{drug_id}_{ccl_name}.png"
               )
```

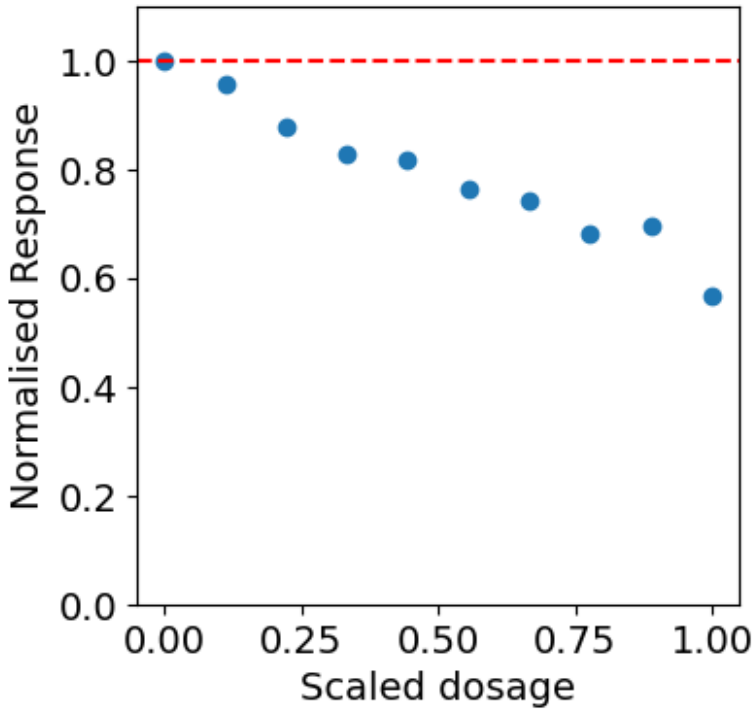
```
Drug: WH-4-023 (56) / CCL: RKO
```



In [49]:

```
# group_2a
group = "2a"
drug_id = 223
ccl_name = "HDQ-P1"
OneFigNoFitting(gr_2a, drug_id=drug_id, ccl_name=ccl_name, size=4, dpi=500,
                x_columns = conc_columns, y_columns = response_norm,
                upper_limit=1, lower_limit=None,
                save_fig_name=f"figures/gr_{group}_{drug_id}_{ccl_name}.png"
               )
```

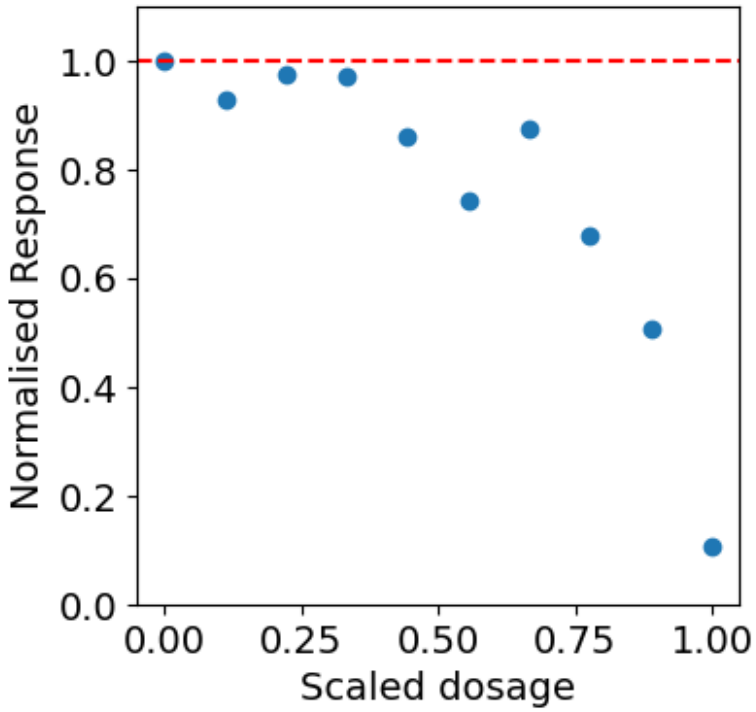
```
Drug: ZSTK474 (223) / CCL: HDQ-P1
```



In [48]:

```
# group_2b
group = "2b"
drug_id = 252
ccl_name = "SK-MEL-30"
OneFigNoFitting(gr_2b, drug_id=drug_id, ccl_name=ccl_name, size=4, dpi=500,
                x_columns = conc_columns, y_columns = response_norm,
                upper_limit=1, lower_limit=None,
                save_fig_name=f"figures/gr_{group}_{drug_id}_{ccl_name}.png"
               )
```

```
Drug: WZ3105 (252) / CCL: SK-MEL-30
```



In [43]:

```
gr_2c.sample(5)
```

Out[43]:

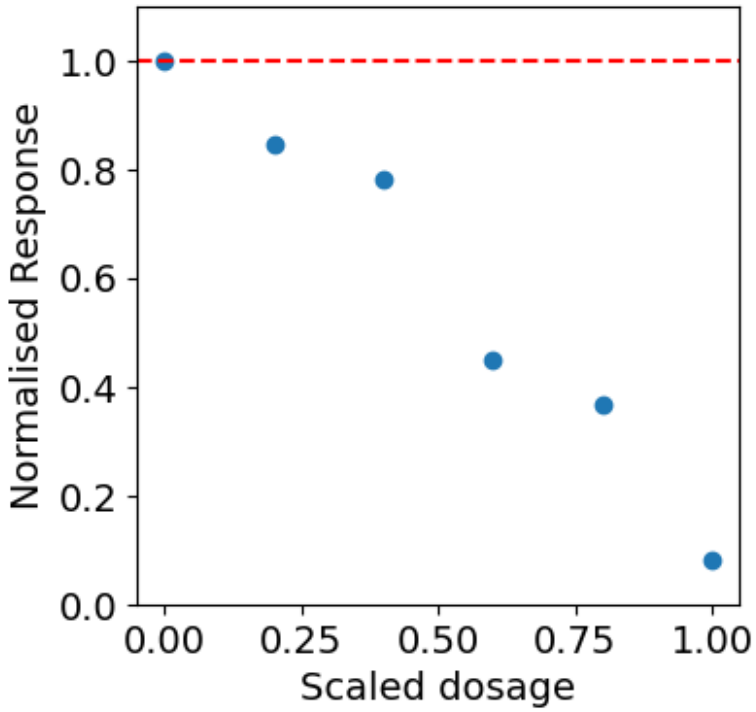
	CELL_LINE_NAME	COSMIC_ID	DRUG_ID	DRUGID_COSMICID	FOLD_DILUTION	MAX_CONC
208137	JHU-028	1298154	1372	1372_1298154	4	1.(
197217	A101D	910921	1219	1219_910921	4	10.(
193023	NB12	949172	1243	1243_949172	4	10.(
216055	ETK-1	906861	1268	1268_906861	4	5.(
164542	ESO51	1503367	1012	1012_1503367	2	10.(

5 rows × 28 columns

In [47]:

```
# group_2c
group = "2c"
drug_id = 1242
ccl_name = "CAL-29"
OneFigNoFitting(gr_2c, drug_id=drug_id, ccl_name=ccl_name, size=4, dpi=500,
                x_columns = conc_columns, y_columns = response_norm,
                upper_limit=1, lower_limit=None,
                save_fig_name=f"figures/gr_{group}_{drug_id}_{ccl_name}.png"
               )
```

```
Drug: (5Z)-7-Oxozeaenol (1242) / CCL: CAL-29
```



In [ ]:

```

```

In [ ]:

```

```

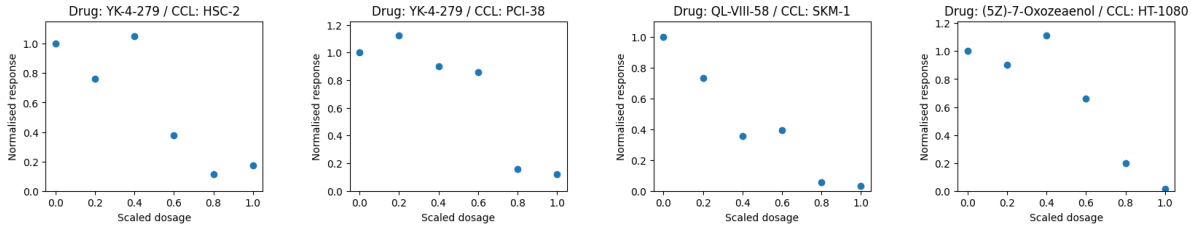
In [63]:

```
import all_functions
```

Ambigous data: Are some points wrong?

In [65]:

```
specific_samples = [("YK-4-279", "HSC-2"),
                    ("YK-4-279", "PCI-38"),
                   ("QL-VIII-58", "SKM-1"),
                    ("(5Z)-7-Oxozeaenol", "HT-1080")
                   ]
show_specific(drug_curves, specific_samples, conc_columns, response_norm)
```



Part 3: Explore curves with normalised responses above 1.0

In [55]:

```
%%time
# Number of responses > 1
drug_curves["high_responses"] = drug_curves[response_norm].apply(lambda row: sum(row>1), axis=1)
drug_curves[["high_responses"]+ response_norm]
```

```
CPU times: total: 16.2 s
Wall time: 16.2 s
```

Out[55]:

	high_responses	norm_cells_0	norm_cells_1	norm_cells_2	norm_cells_3	norm_cells_4	no
0	7	1	1.039343	0.998020	1.005715	1.055723	
1	6	1	0.969418	0.987582	1.052708	1.072808	
2	1	1	0.956127	0.887779	0.941691	0.839059	
3	4	1	1.087946	0.980767	1.118407	1.234735	
4	6	1	1.035268	1.040170	0.972972	1.029729	
...	...	...	...	...	...	...	
225379	3	1	0.970321	0.864856	1.326808	1.100719	
225380	3	1	0.329169	0.284518	1.088894	1.090624	
225381	3	1	0.914628	0.840454	1.116674	1.096159	
225382	2	1	0.884687	1.000038	1.051918	0.790004	
225383	4	1	1.053967	0.831009	1.155885	1.149906	

225384 rows × 11 columns

In [56]:

```
bad_data = drug_curves[drug_curves["high_responses"]>1]
print("Original data:", drug_curves.shape)
print("Ambiguos data:", bad_data.shape)
```

```
Original data: (225384, 29)
Ambiguos data: (127590, 29)
```

Note: Half of the data can be regarded as ambiguous!!!

In [57]:

```
bad_data["high_responses"].value_counts()
```

Out[57]:

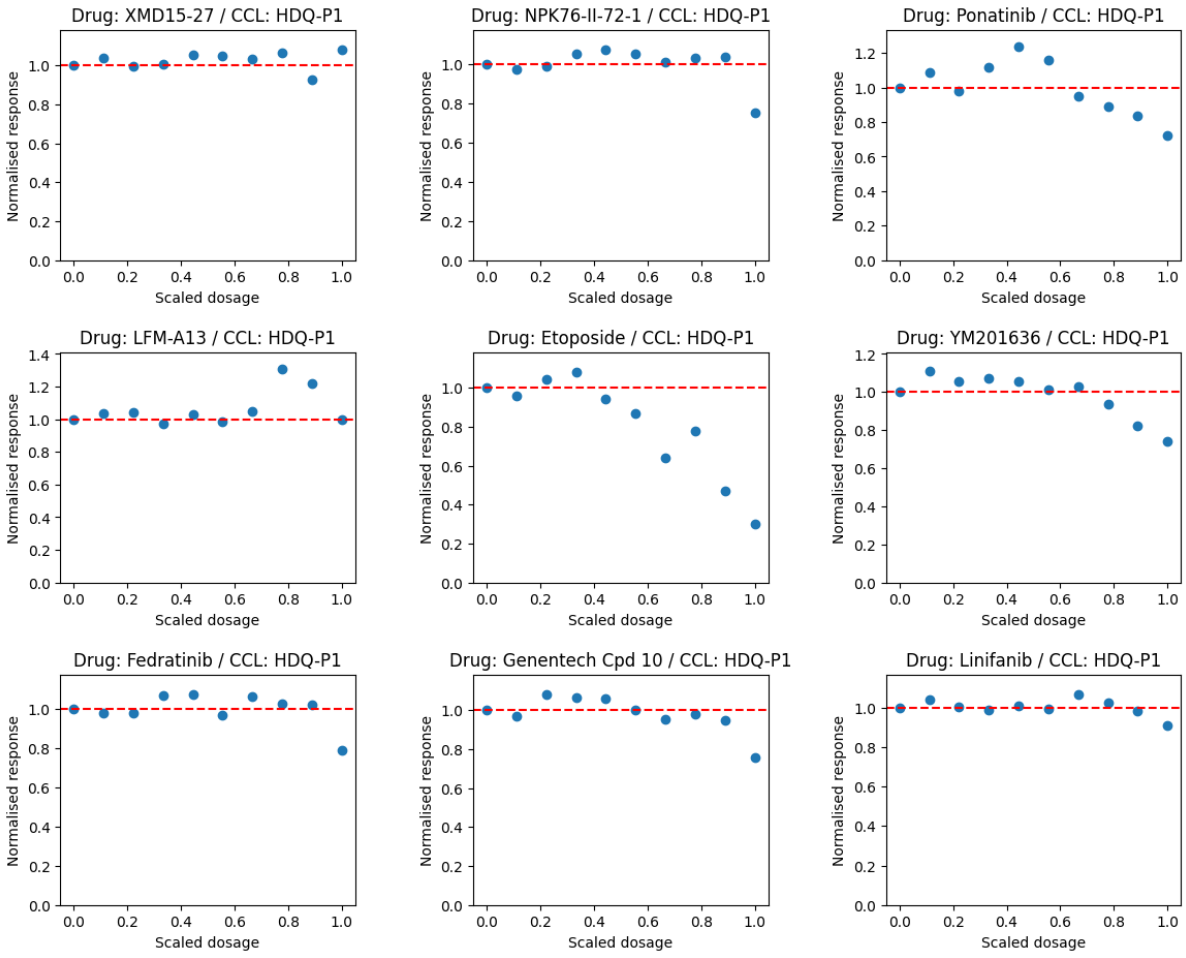
```
2    28485
3    24334
4    20015
5    17201
6    12366
7    10712
8     8487
9     5990
Name: high_responses, dtype: int64
```

Bad data by CCL

Check whether bad data are actually bad

In [66]:

```
df = bad_data
show_response_curves(df, plots_in_row=3, plots_in_column=3, ₩
                     x_columns=conc_columns, y_columns=response_norm, indexes=df.index[:9],
                    drug_dict = drug_names, CCL_dict = CCL_names, upper_limit=1)
```

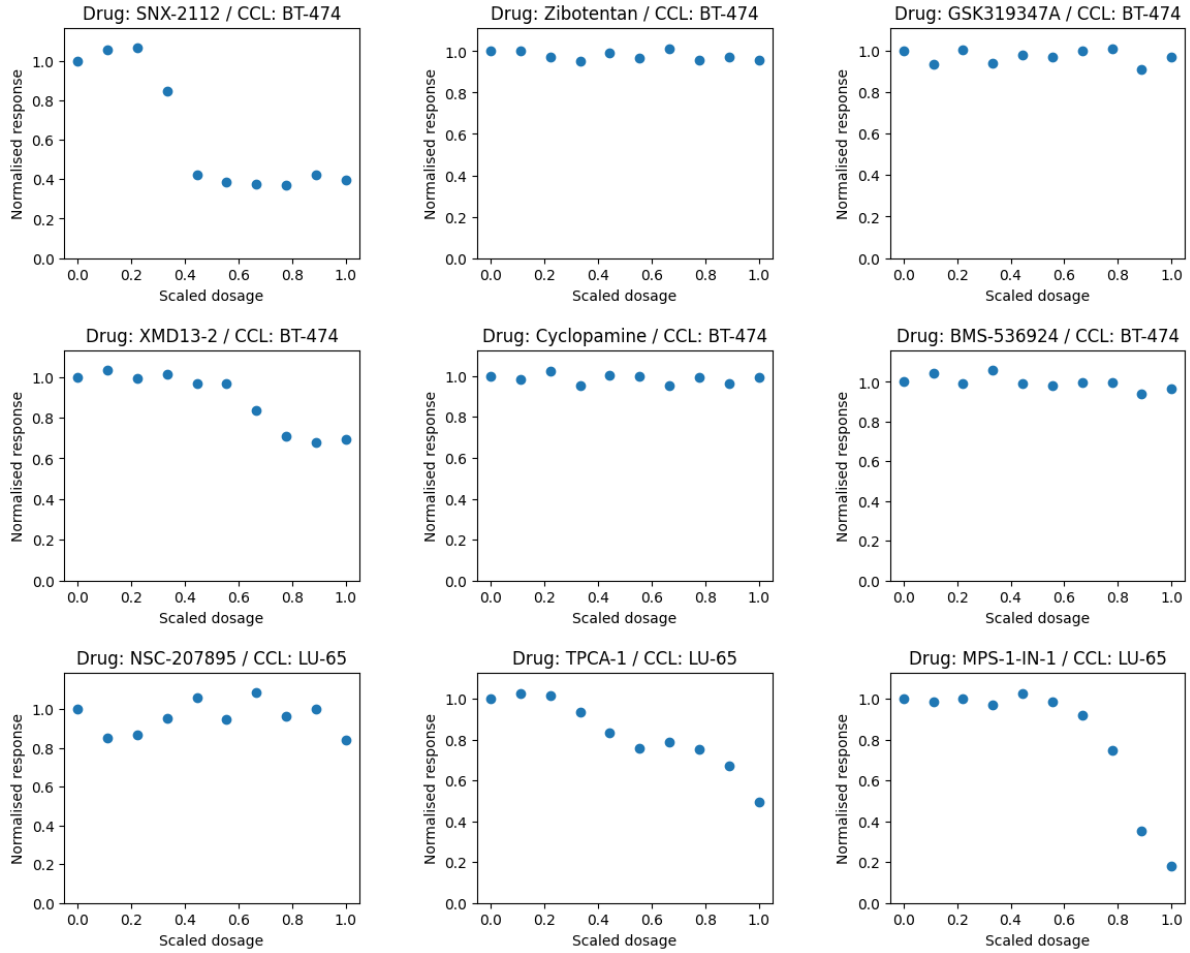


Samples with 2 bad responses

In [67]:

```
N = 2
df = bad_data[bad_data["high_responses"]==N]
print("Number of samples with %d bad responses: %d" % (N, df.shape[0]))

show_response_curves(df, plots_in_row=3, plots_in_column=3, ₩
                     x_columns=conc_columns, y_columns=response_norm, indexes=df.index[20:29],
                    drug_dict = drug_names, CCL_dict = CCL_names)
```

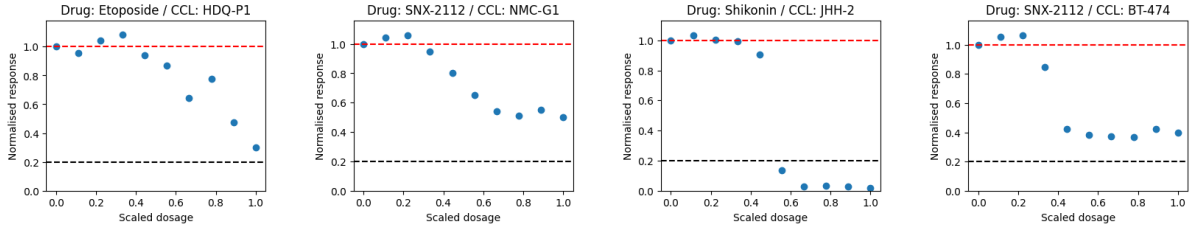
```
Number of samples with 2 bad responses: 28485
```



Among samples with only 2 norm_responses >1 some data are not so bad

In [68]:

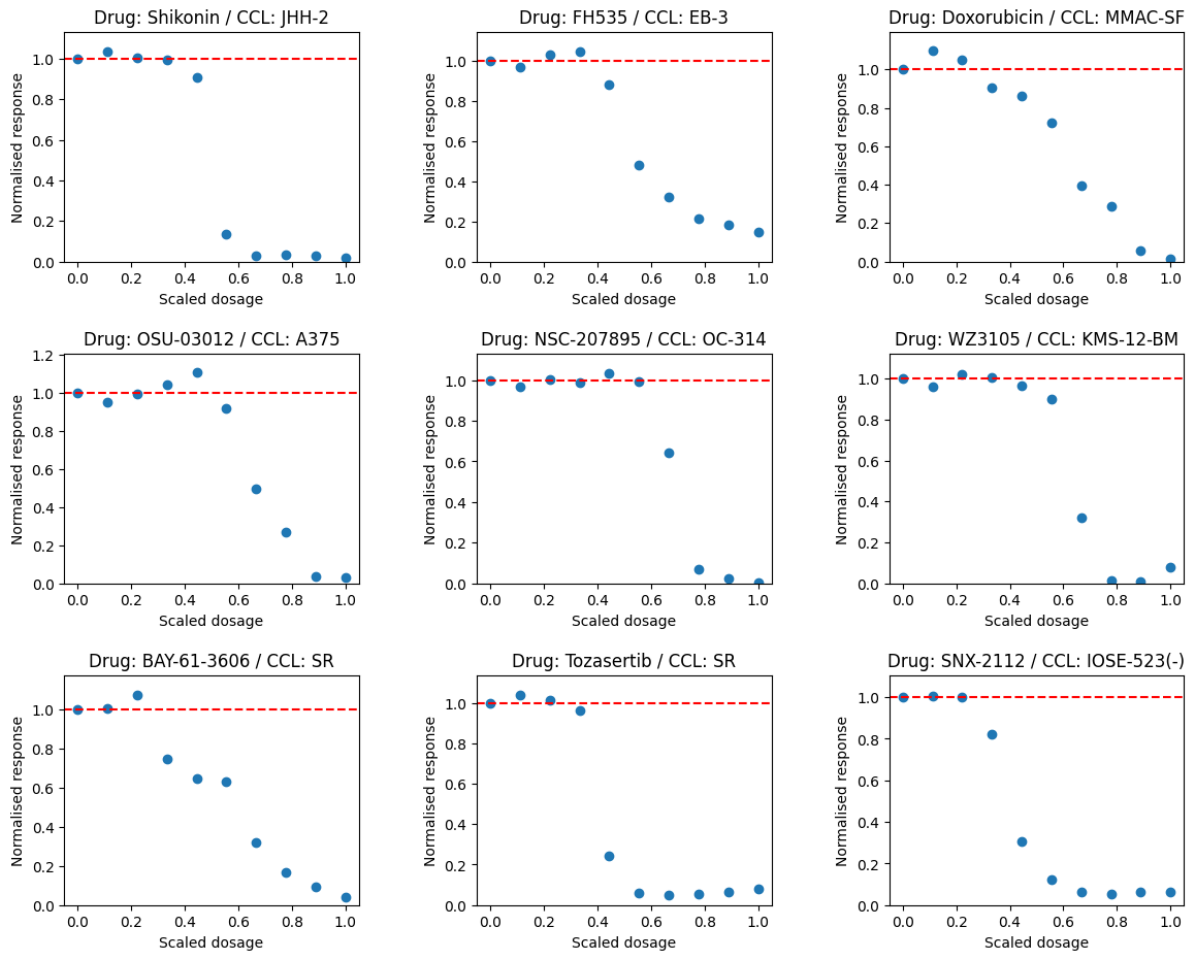
```
specific_samples = [("Etoposide", "HDQ-P1"),
                    ("SNX-2112", "NMC-G1"),
                    ("Shikonin", "JHH-2"),
                    ("SNX-2112", "BT-474")
                   ]
show_specific(bad_data, specific_samples, conc_columns, response_norm, upper_limit=1, lower_limit=0.2)
```



In [69]:

```
N = 2
df = bad_data[(bad_data["high_responses"]==N) & (bad_data["norm_cells_9"]<0.2) & (bad_data["norm_cells_
print("Number of samples with %d bad responses, but with 2 last responses below 0.2: %d" % (N, df.shape

show_response_curves(df, plots_in_row=3, plots_in_column=3, W
                     x_columns=conc_columns, y_columns=response_norm, indexes=df.index[:9],
                    drug_dict = drug_names, CCL_dict = CCL_names, upper_limit=1)
```

```
Number of samples with 2 bad responses, but with 2 last responses below 0.2: 2728
```



Conclusion - we can't delete just samples which with 2 responses>1.0

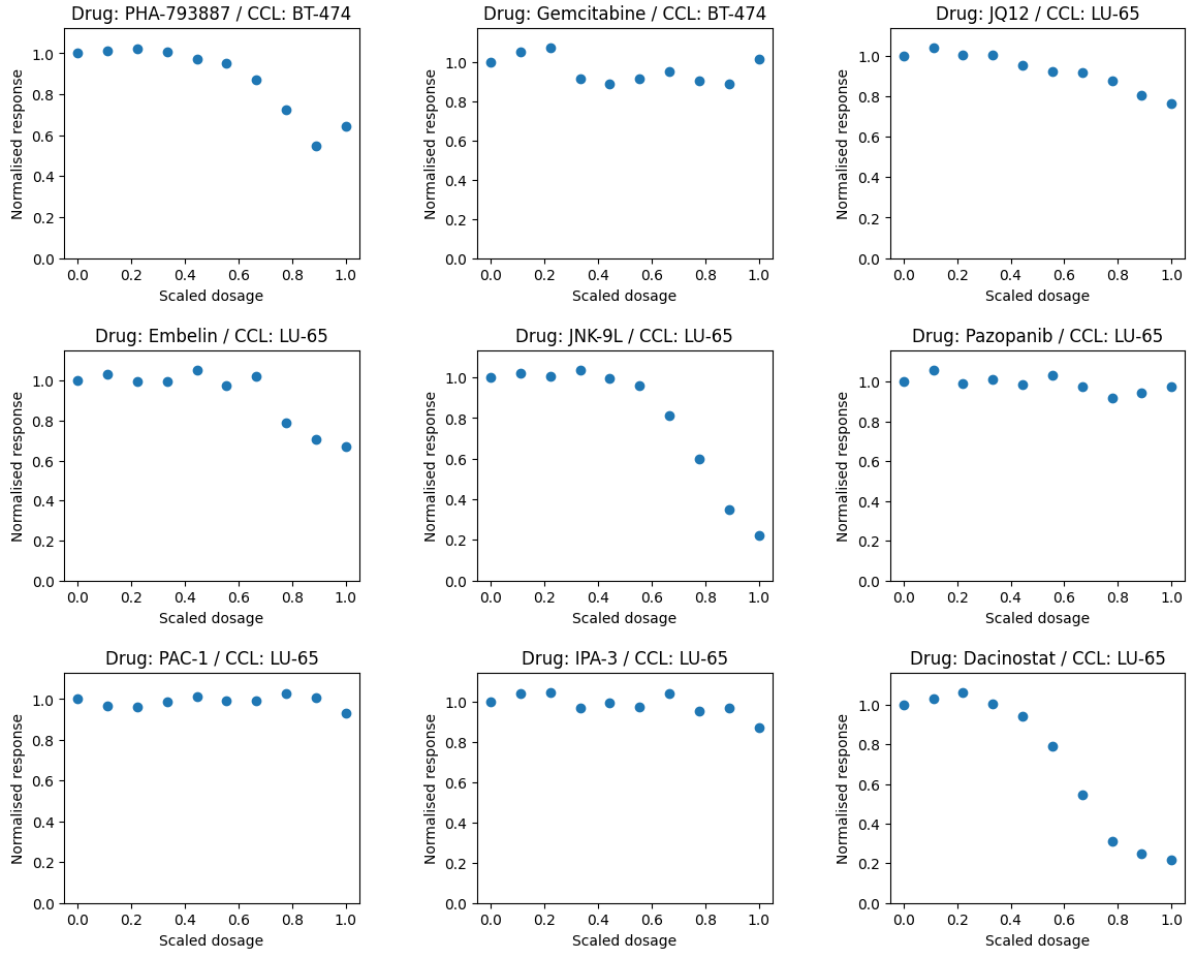
The question: What is the accuracy of measuring responses?
Can we treat samples with responses up to 1.01 as valid ones?

Samples with 3 bad responses

In [70]:

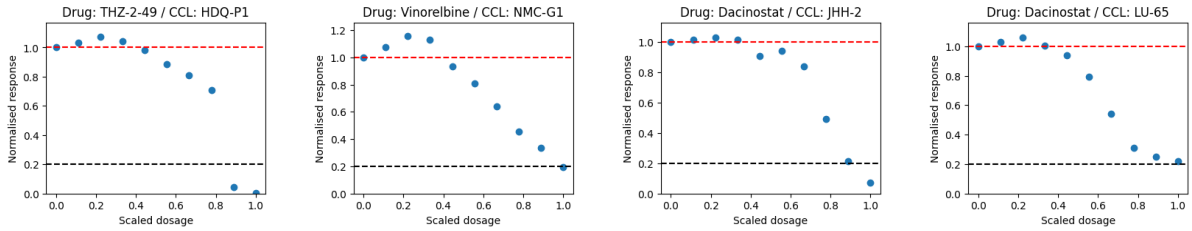
```
N = 3
df = bad_data[bad_data["high_responses"]==N]
print("Number of samples with %d bad responses: %d" % (N, df.shape[0]))

show_response_curves(df, plots_in_row=3, plots_in_column=3, W
                     x_columns=conc_columns, y_columns=response_norm, indexes=df.index[30:39],
                    drug_dict = drug_names, CCL_dict = CCL_names)
```

```
Number of samples with 3 bad responses: 24334
```



In [71]:

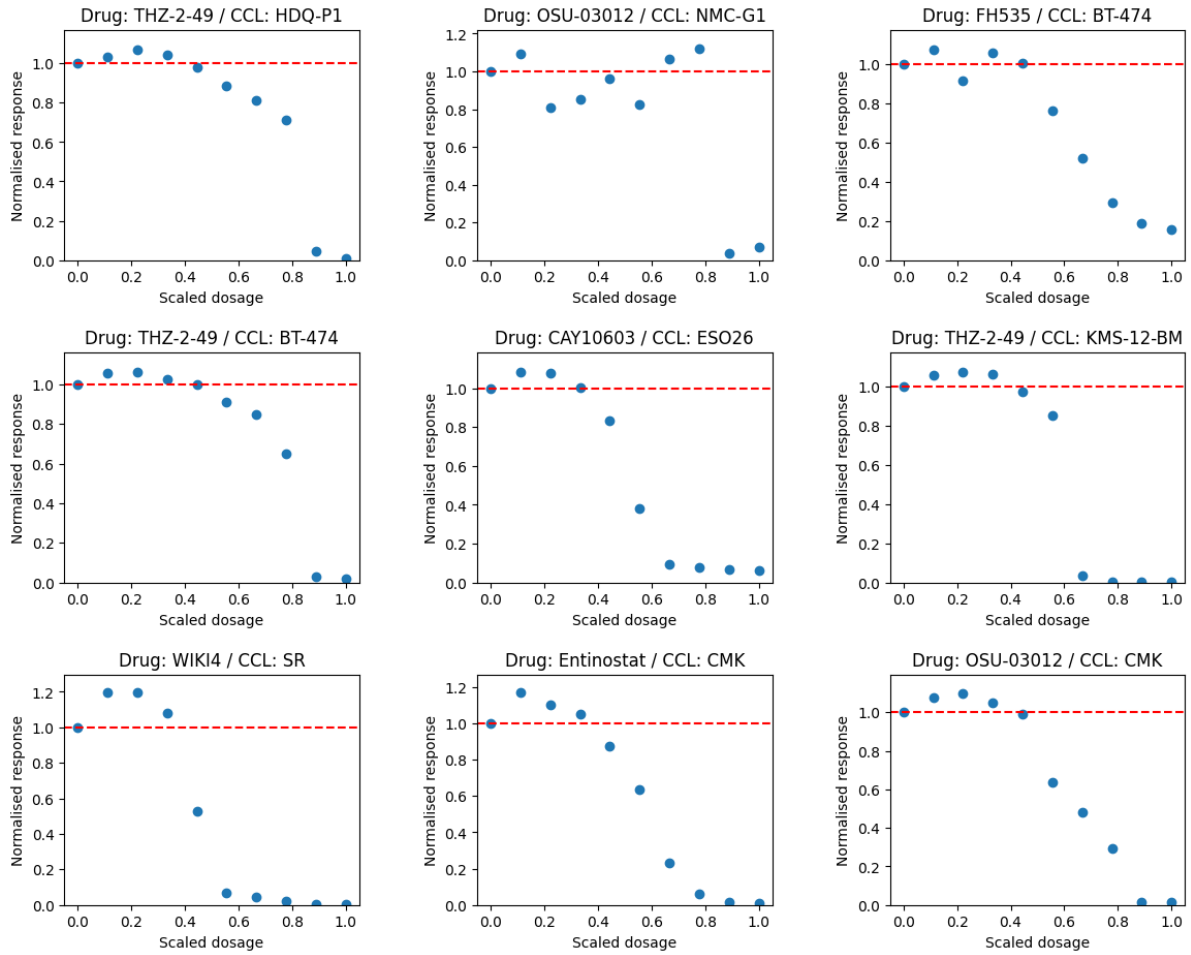
```
specific_samples = [("THZ-2-49", "HDQ-P1"),
                    ("Vinorelbine", "NMC-G1"),
                    ("Dacinostat", "JHH-2"),
                    ("Dacinostat", "LU-65")
                   ]
show_specific(bad_data, specific_samples, conc_columns, response_norm, upper_limit=1, lower_limit=0.2)
```



In [72]:

```
N = 3
df = bad_data[(bad_data["high_responses"]==N) & (bad_data["norm_cells_9"]<0.2) & (bad_data["norm_cells_
print("Number of samples with %d bad responses, but with 2 last responses below 0.2: %d" % (N, df.shape

show_response_curves(df, plots_in_row=3, plots_in_column=3, W
                     x_columns=conc_columns, y_columns=response_norm, indexes=df.index[:9],
                    drug_dict = drug_names, CCL_dict = CCL_names, upper_limit=1)
```

```
Number of samples with 3 bad responses, but with 2 last responses below 0.2: 1780
```

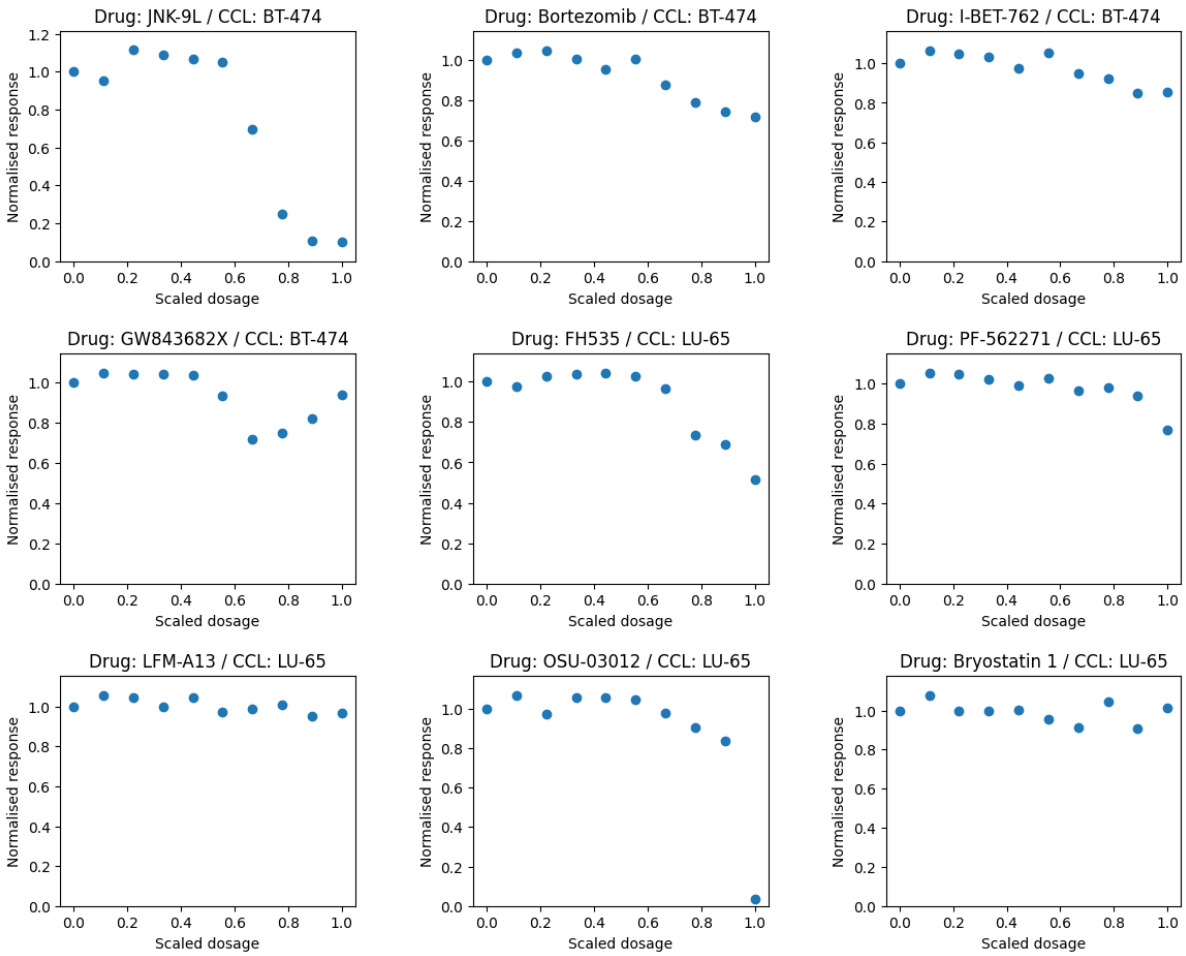


Samples with 4 bad responses

In [73]:

```
N = 4
df = bad_data[bad_data["high_responses"]==N]
print("Number of samples with %d bad responses: %d" % (N, df.shape[0]))

show_response_curves(df, plots_in_row=3, plots_in_column=3, ₩
                     x_columns=conc_columns, y_columns=response_norm, indexes=df.index[20:29],
                    drug_dict = drug_names, CCL_dict = CCL_names)
```

```
Number of samples with 4 bad responses: 20015
```



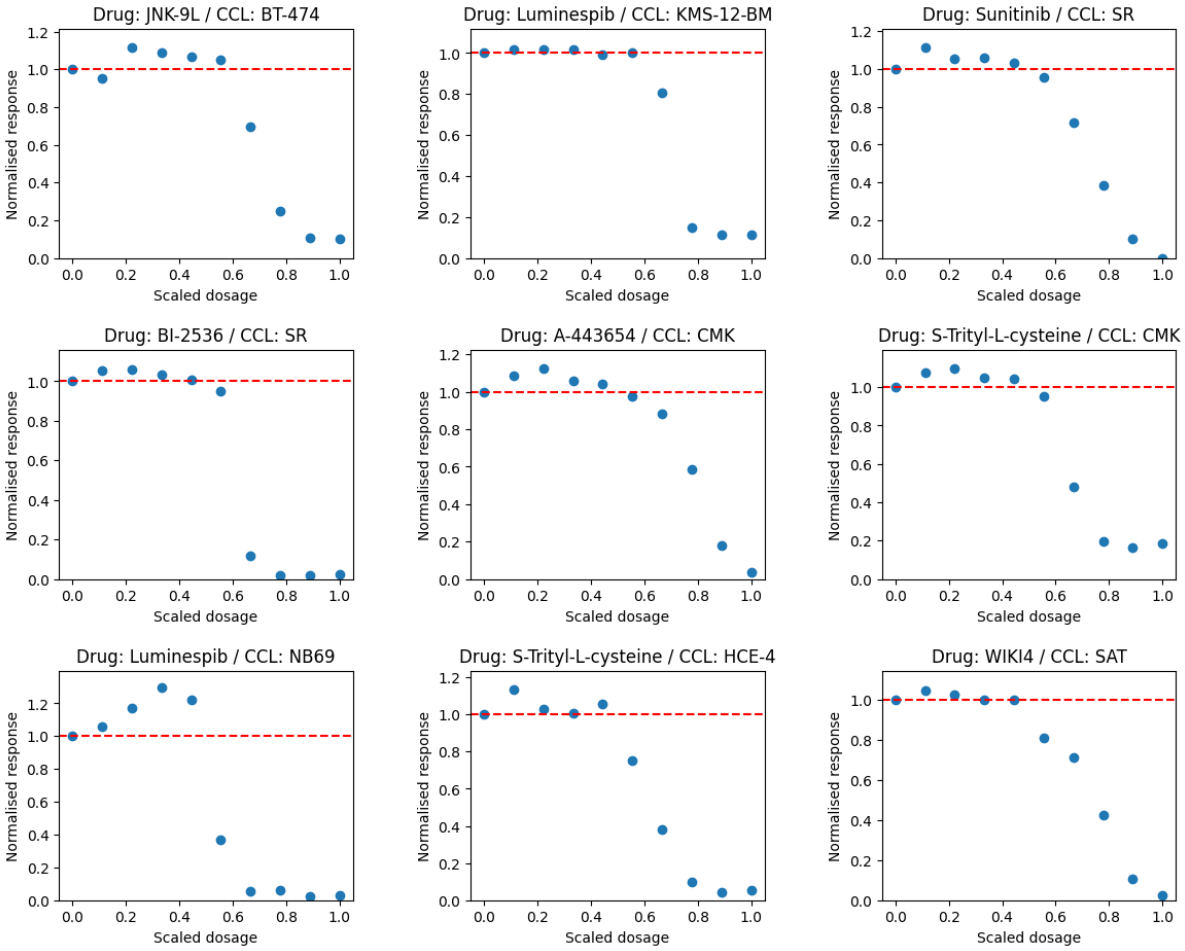
In [ ]:

```
specific_samples = [("THZ-2-49", "HDQ-P1"),
                    ("Cabozantinib", "NMC-G1"),
                    ("Dacinostat", "JHH-2"),
                    ("JNK-9L", "BT-474")
                   ]
show_specific(bad_data, specific_samples, conc_columns, response_norm, upper_limit=1, lower_limit=0.2)
```

In [74]:

```
N = 4
df = bad_data[(bad_data["high_responses"]==N) & (bad_data["norm_cells_9"]<0.2) & (bad_data["norm_cells_
print("Number of samples with %d bad responses, but with 2 last responses below 0.2: %d" % (N, df.shape

show_response_curves(df, plots_in_row=3, plots_in_column=3, ₩
                     x_columns=conc_columns, y_columns=response_norm, indexes=df.index[:9],
                    drug_dict = drug_names, CCL_dict = CCL_names, upper_limit=1)
```

```
Number of samples with 4 bad responses, but with 2 last responses below 0.2: 879
```

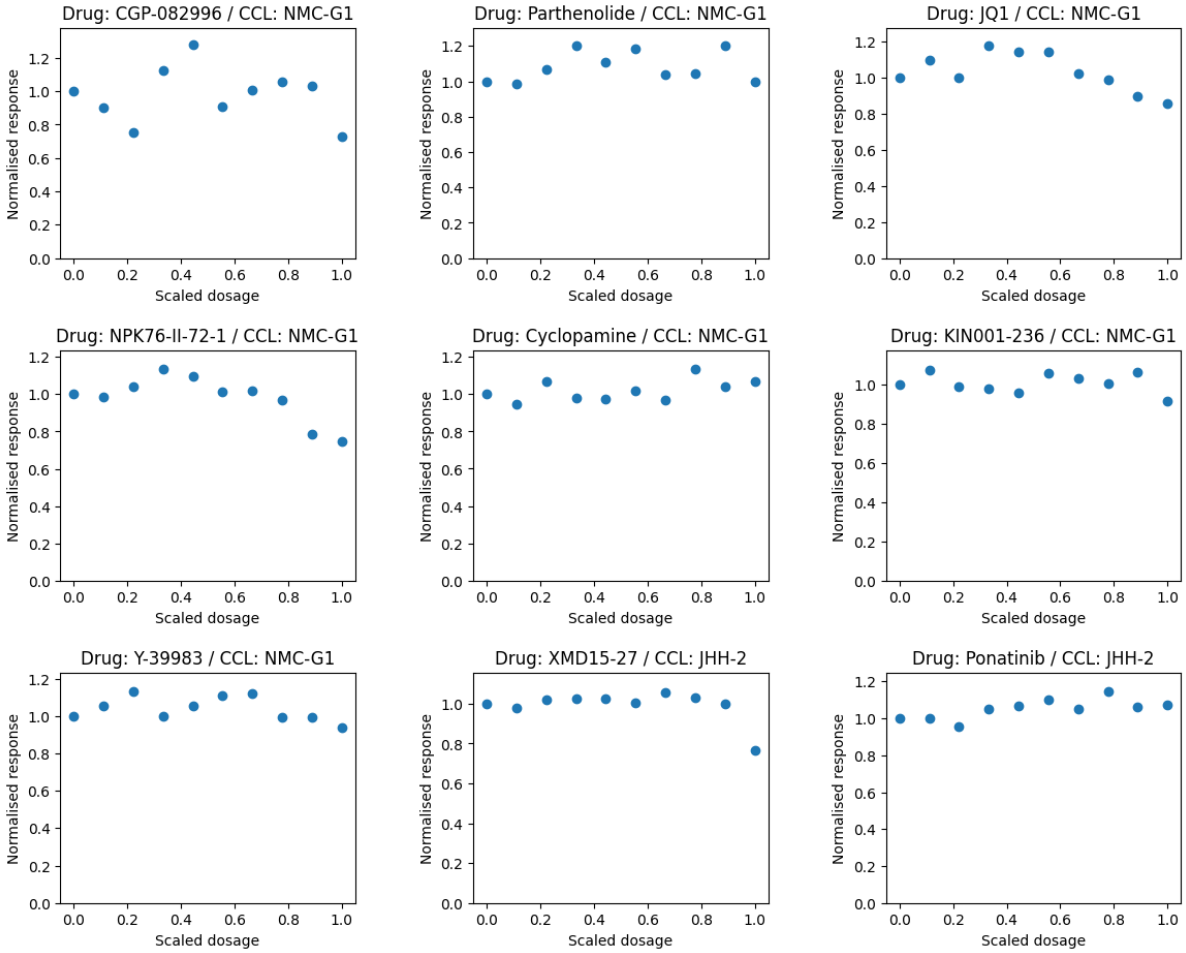


Samples with 5+ bad responses

In [75]:

```
N = 5
df = bad_data[bad_data["high_responses"]>=N]
print("Number of samples with more than %d bad responses: %d" % (N, df.shape[0]))

show_response_curves(df, plots_in_row=3, plots_in_column=3, ₩
                     x_columns=conc_columns, y_columns=response_norm, indexes=df.index[20:29],
                    drug_dict = drug_names, CCL_dict = CCL_names)
```

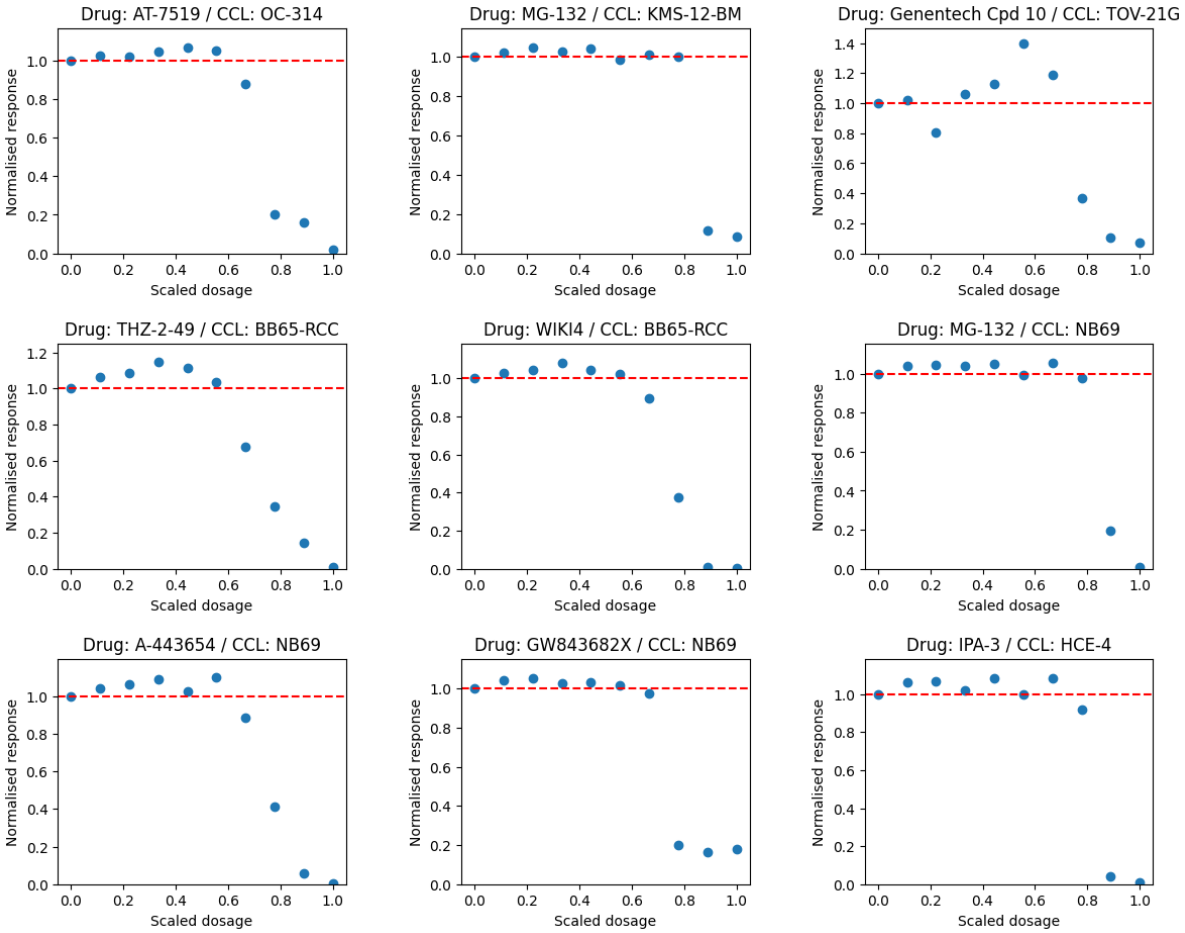
```
Number of samples with more than 5 bad responses: 54756
```



In [76]:

```
N = 5
df = bad_data[(bad_data["high_responses"]==N) & (bad_data["norm_cells_9"]<0.2) & (bad_data["norm_cells_
print("Number of samples with %d bad responses, but with 2 last responses below 0.2: %d" % (N, df.shape

show_response_curves(df, plots_in_row=3, plots_in_column=3, ₩
                     x_columns=conc_columns, y_columns=response_norm, indexes=df.index[:9],
                    drug_dict = drug_names, CCL_dict = CCL_names, upper_limit=1)
```

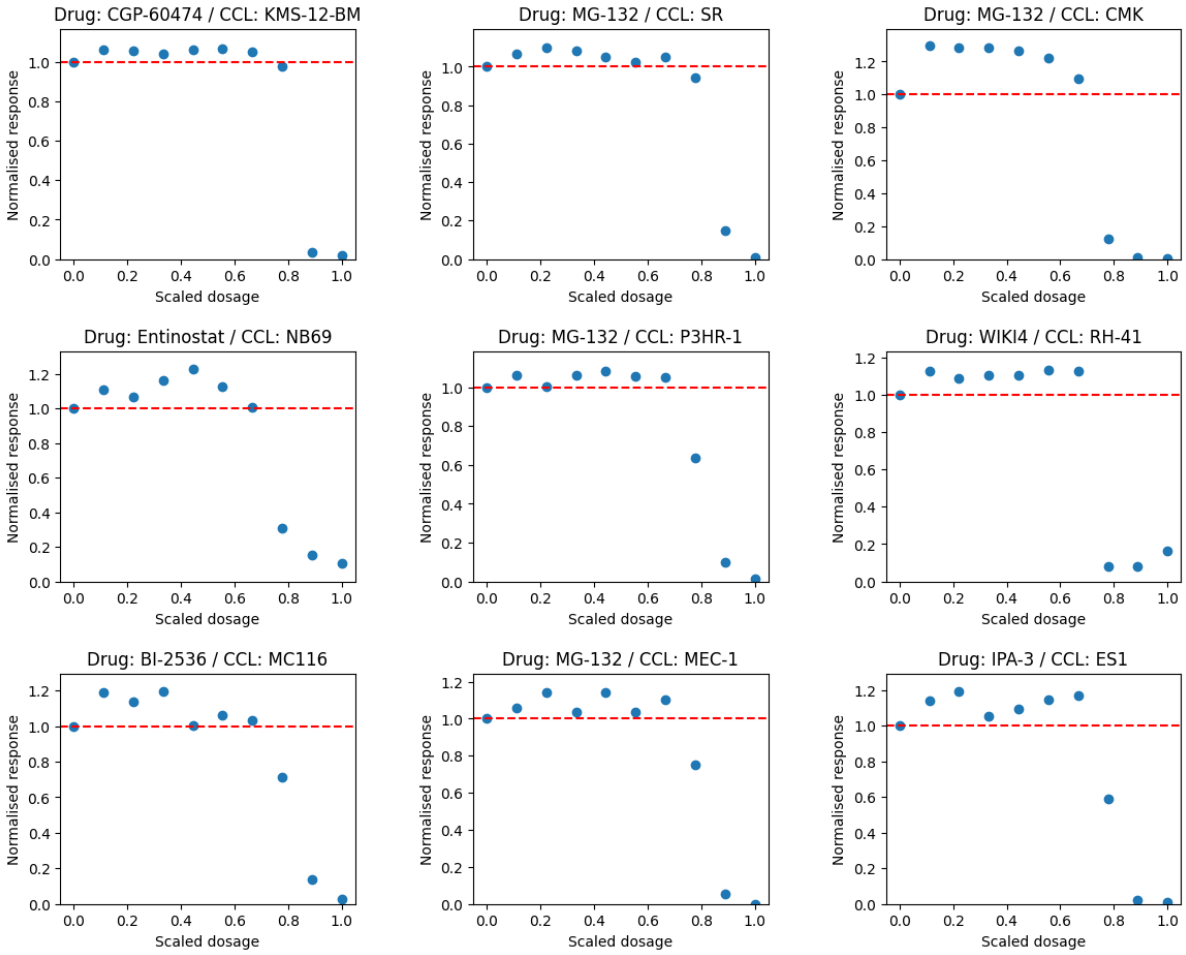
```
Number of samples with 5 bad responses, but with 2 last responses below 0.2: 441
```



In [77]:

```
N = 6
df = bad_data[(bad_data["high_responses"]==N) & (bad_data["norm_cells_9"]<0.2) & (bad_data["norm_cells_
print("Number of samples with %d bad responses, but with 2 last responses below 0.2: %d" % (N, df.shape

show_response_curves(df, plots_in_row=3, plots_in_column=3, ₩
                     x_columns=conc_columns, y_columns=response_norm, indexes=df.index[:9],
                    drug_dict = drug_names, CCL_dict = CCL_names, upper_limit=1)
```

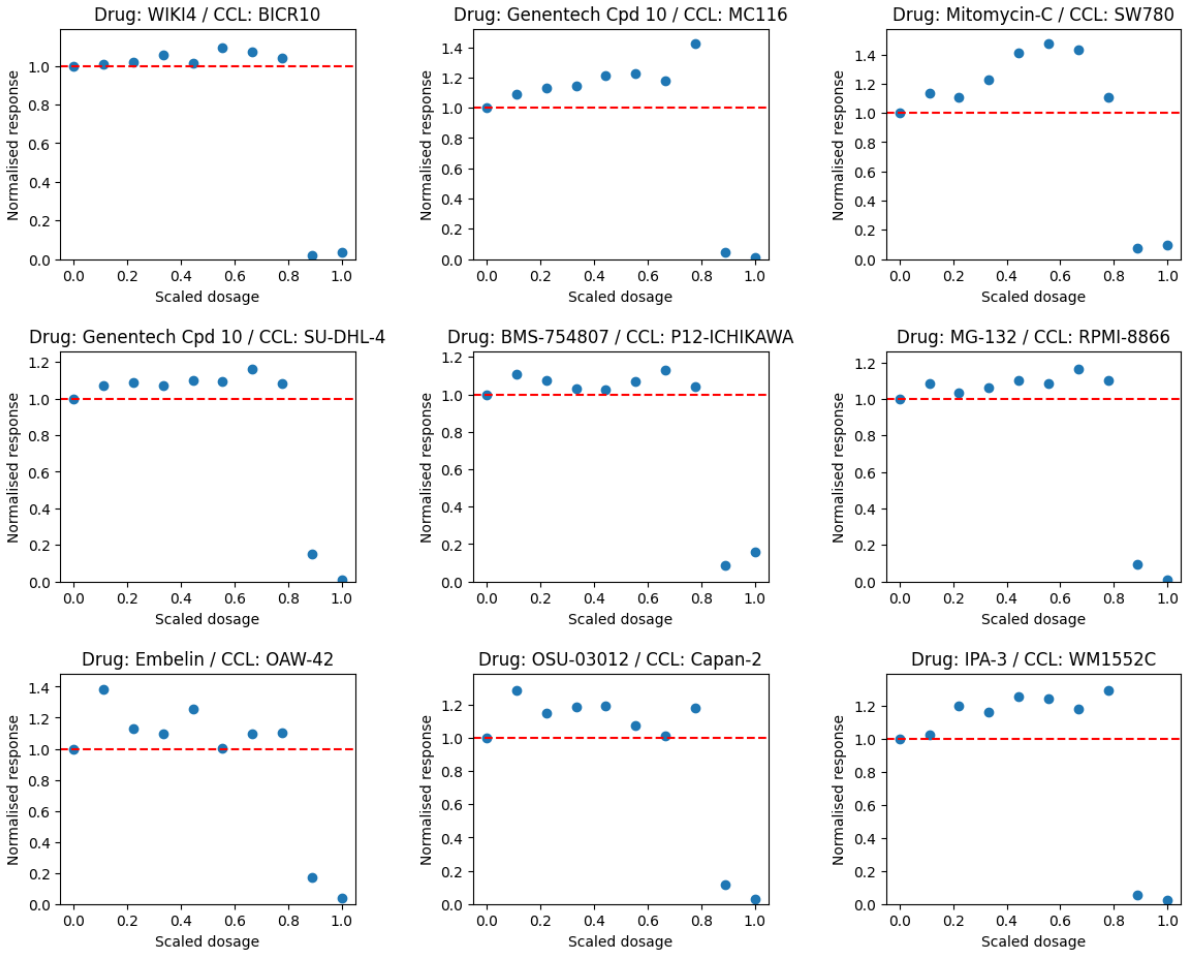
```
Number of samples with 6 bad responses, but with 2 last responses below 0.2: 135
```



In [78]:

```
N = 7
df = bad_data[(bad_data["high_responses"]==N) & (bad_data["norm_cells_9"]<0.2) & (bad_data["norm_cells_
print("Number of samples with %d bad responses, but with 2 last responses below 0.2: %d" % (N, df.shape

show_response_curves(df, plots_in_row=3, plots_in_column=3, W
                     x_columns=conc_columns, y_columns=response_norm, indexes=df.index[:9],
                    drug_dict = drug_names, CCL_dict = CCL_names, upper_limit=1)
```

```
Number of samples with 7 bad responses, but with 2 last responses below 0.2: 18
```



In [79]:

```
N = 8
df = bad_data[(bad_data["high_responses"]==N) & (bad_data["norm_cells_9"]<0.2) & (bad_data["norm_cells_
print("Number of samples with %d bad responses, but with 2 last responses below 0.2: %d" % (N, df.shape

show_response_curves(df, plots_in_row=3, plots_in_column=3, W
                     x_columns=conc_columns, y_columns=response_norm, indexes=df.index[:9],
                    drug_dict = drug_names, CCL_dict = CCL_names, upper_limit=1)
```

```
Number of samples with 8 bad responses, but with 2 last responses below 0.2: 0

<Figure size 1400x1100 with 0 Axes>
```

In [80]:

```
N = 9
df = bad_data[(bad_data["high_responses"]==N) & (bad_data["norm_cells_9"]<0.2) & (bad_data["norm_cells_
print("Number of samples with %d bad responses, but with 2 last responses below 0.2: %d" % (N, df.shape

show_response_curves(df, plots_in_row=3, plots_in_column=3, ₩
                     x_columns=conc_columns, y_columns=response_norm, indexes=df.index[:9],
                    drug_dict = drug_names, CCL_dict = CCL_names, upper_limit=1)
```

```
Number of samples with 9 bad responses, but with 2 last responses below 0.2: 0

<Figure size 1400x1100 with 0 Axes>
```

Conclusion from Part 3: Curves with up to 7 suspiciously high normalised responses look pretty reasonable

Part 4: Explore curves with normalised response above 1 but low final response

In [81]:

```
%%time
drug_curves["low_response_02"] = drug_curves[response_norm].apply(lambda row: sum(row<=0.2), axis=1)
drug_curves["low_response_04"] = drug_curves[response_norm].apply(lambda row: sum(row<=0.4), axis=1)
```

```
CPU times: total: 31.8 s
Wall time: 31.8 s
```

In [82]:

```
not_bad_02 = drug_curves[(drug_curves["high_responses"]>1) & (drug_curves["low_response_02"])]
not_bad_04 = drug_curves[(drug_curves["high_responses"]>1) & (drug_curves["low_response_04"])]
print("Number of all suspicious samples:", bad_data.shape[0])
print("₩nNumber of potentionally good samples among all bad data:")
print("With responses below 0.2:", not_bad_02.shape[0])
print("With responses below 0.4:", not_bad_04.shape[0])
```

```
Number of all suspicious samples: 127590

Number of potentionally good samples among all bad data:
With responses below 0.2: 9892
With responses below 0.4: 16438
```

In [83]:

```
not_bad_02["low_response_02"].value_counts()
```

Out[83]:

```
1    7742
3    1755
5     387
7       8
Name: low_response_02, dtype: int64
```

In [84]:

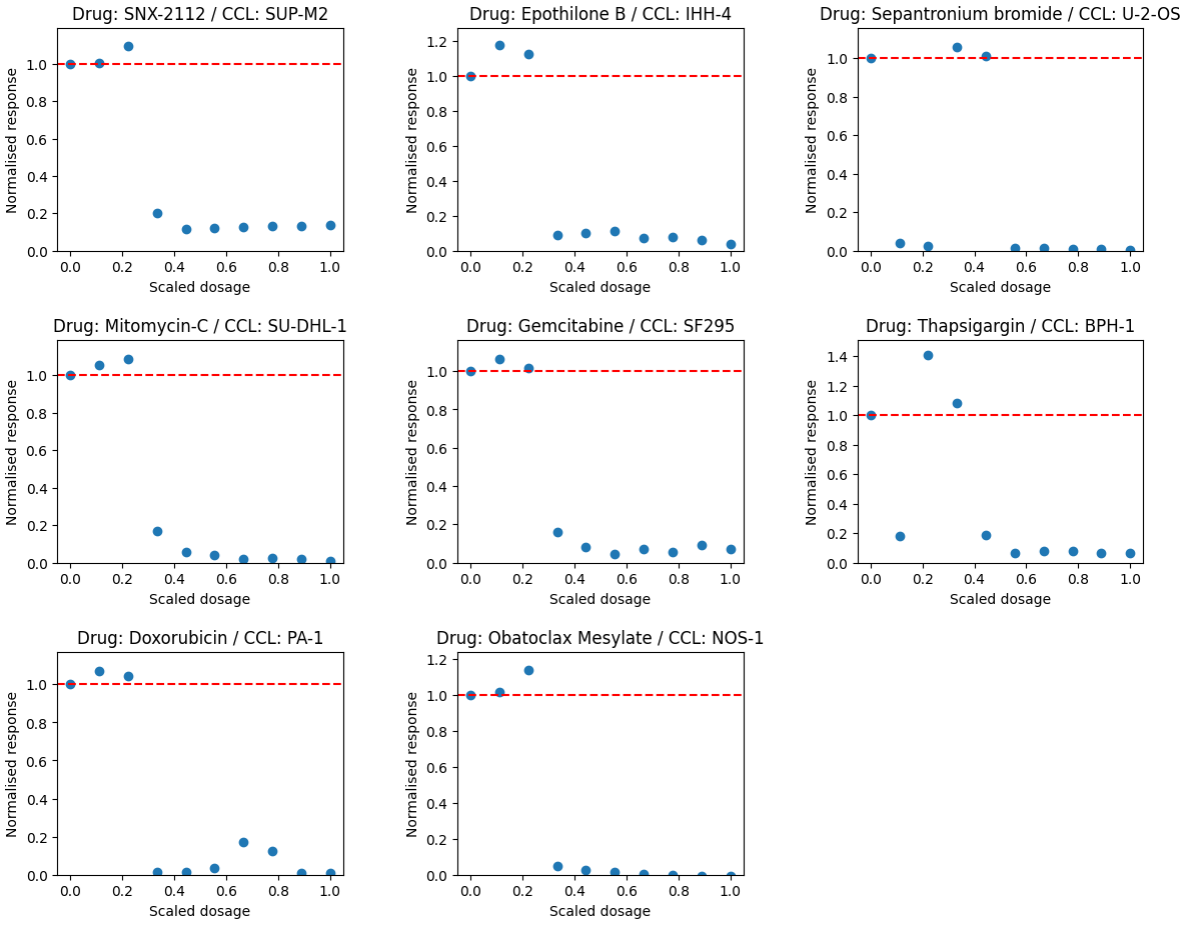
```
not_bad_04["low_response_04"].value_counts()
```

Out[84]:

```
1    12144
3     3301
5      974
7       19
Name: low_response_04, dtype: int64
```

In [85]:

```
df = not_bad_02[not_bad_02["low_response_02"]==7]

show_response_curves(df, plots_in_row=3, plots_in_column=3, W
                     x_columns=conc_columns, y_columns=response_norm, indexes=df.index[:9],
                    drug_dict = drug_names, CCL_dict = CCL_names, upper_limit=1)
```



Part 5: Repeat with an additional constrain

Among all "middle" datapoints a subsequent point should not be higher than antecedent by some limit

In [88]:

```
not_bad_02_2 = cut_off_outliers(drug_curves, middle_points_limit=-0.2, response_columns = response_norm

print("Before filtration: %d, After filtration: %d" % (not_bad_04.shape[0], not_bad_02_2.shape[0]))
not_bad_02_2["low_response_02"].value_counts()
```

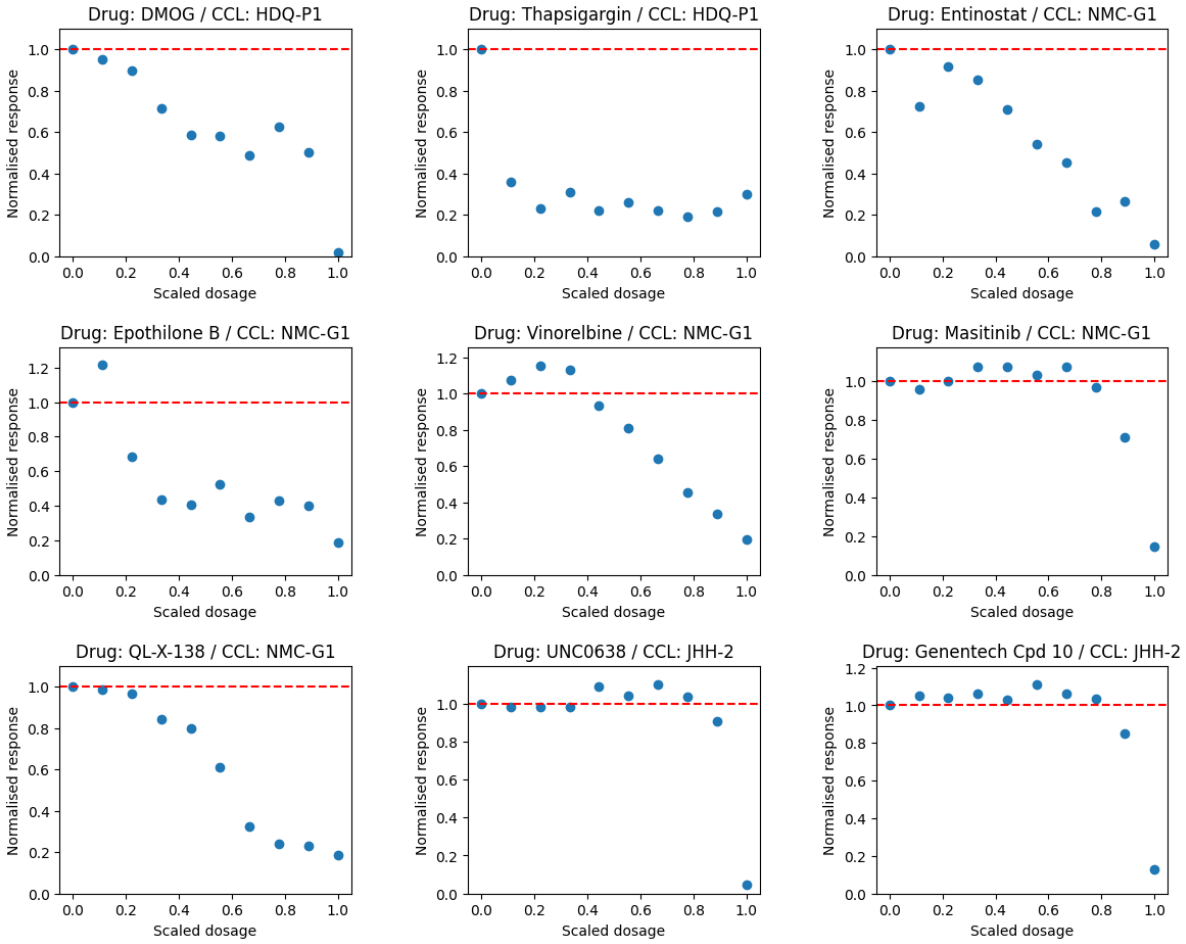
```
Before filtration: 16438, After filtration: 190245
```

Out[88]:

```
0    151335
1     16124
2      7155
3      5384
4      4025
5      2654
6      1551
7       857
9       678
8       482
Name: low_response_02, dtype: int64
```

In [90]:

```
df = not_bad_02_2[not_bad_02_2["low_response_02"]==1]
show_response_curves(df, plots_in_row=3, plots_in_column=3, ₩
                     x_columns=conc_columns, y_columns=response_norm, indexes=df.index[:9],
                    drug_dict = drug_names, CCL_dict = CCL_names, upper_limit=1)
```



In [ ]: