Exploring data quality

```
Content:
    Part 1: Duplicates
    Part 2: Missing data
    Part 3: Curves with normalised responses above 1.0
    Part 4: Curves with normalised responses above 1.0 but low final responses
    Part 5: Cut off outliers inside drug response curves
```

Main findings

1. Original data - 225384 samples
2. Among all 250 drugs, 15 drugs have 2 different drug_id:
   'AKT inhibitor VIII': [228, 171], 'AZD6482': [156, 1066], 'Afatinib': [1032, 1377], 'Avagacestat': [205, 1072], 'BMS-536924': [62, 1091], 'Bicalutamide': [150, 1502], 'CHIR-99021': [154, 1241], 'GSK269962A': [127, 1192], 'JQ1': [163, 1218], 'Olaparib': [1017, 1495], 'PLX-4720': [1036, 1371], 'Pictilisib': [1058, 1527], 'Refametinib': [1014, 1526], 'Selumetinib': [1062, 1498], 'UNC0638': [245, 1236]
3. For all the pairs drug+CCL with one concentraion and two records, one of the records is reduced, i.e has missing values
4. There are 33740 profiles with missing points. And among them only 9120 have dublicates/alternatives
5. Curves with up to 7 suspiciously high normalised responses can look pretty reasonable

Main question - what drug response curves are valid for further analysis

In [1]:

```
import pandas as pd
import numpy as np
import gc
import matplotlib.pyplot as plt
import os, sys
sys.path.insert(1, os.path.relpath("../functions"))
from filtering import *
from plotting import *

_FOLDER = "../data/"
_FOLDER_2 = "../figures/"
_FOLDER_3 = "../results/"
SAVE_FIGURES = False
```

Original data

In [2]:

```
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[2]:

```
(225384, 28)
```

In [3]:

```
drug_curves["MAX_CONC"].value_counts()
```

Out[3]:

```
20.0000       29693
10.2400       29275
10.0000       28841
2.0000        15984
5.1200        15672
5.0000        15154
16.0000       11652
2.5600         8985
4.0000         8315
1.0240         8032
1.0000         5838
8.0000         5415
0.1000         4150
32.0000        3771
0.1280         2903
0.5120         2814
0.5000         2733
0.2000         2681
2.5000         2295
0.2560         2212
4000.0000      1916
1.2800         1791
0.2500         1712
5.2400          980
40.0000         975
50.0000         973
0.0500          969
6.6000          967
30.0000         945
0.0640          941
0.0080          932
64.0000         932
0.0320          932
65.8000         911
0.0125          894
2000.0000       893
1.2000          427
0.0200          427
0.1024          427
6.0000           25
Name: MAX_CONC, dtype: int64
```

In [4]:

```
drug_curves["FOLD_DILUTION"].value_counts()
```

Out[4]:

```
2    191644
4     33740
Name: FOLD_DILUTION, dtype: int64
```

Part 1: Duplicates

Some drugs have several Drug_Id

In [5]:

```
print("All drugs:", drug_curves["DRUG_ID"].nunique())
print("Unique drug names:", drug_curves["drug_name"].nunique())
gr = drug_curves.groupby("drug_name").agg(n_ids = ("DRUG_ID", "nunique"))
gr["n_ids"].value_counts()
```

```
All drugs: 265
Unique drug names: 250
```

Out[5]:

```
1    235
2     15
Name: n_ids, dtype: int64
```

In [6]:

```
print("Drugs with several drug ids:")
multiple_ids = list(gr[gr["n_ids"]>1].index)
drugs_with_id = {}
for drug_name in multiple_ids:
    ids = drug_curves[drug_curves["drug_name"]== drug_name]["DRUG_ID"].unique()
    drugs_with_id[drug_name] = list(ids)
print(drugs_with_id)
```

```
Drugs with several drug ids:
{'AKT inhibitor VIII': [228, 171], 'AZD6482': [156, 1066], 'Afatinib': [1032, 137
7], 'Avagacestat': [205, 1072], 'BMS-536924': [62, 1091], 'Bicalutamide': [150, 1
502], 'CHIR-99021': [154, 1241], 'GSK269962A': [127, 1192], 'JQ1': [163, 1218],
'Olaparib': [1017, 1495], 'PLX-4720': [1036, 1371], 'Pictilisib': [1058, 1527],
'Refametinib': [1014, 1526], 'Selumetinib': [1062, 1498], 'UNC0638': [245, 1236]}
```

Several MAX_CONC for a pair drug+CCL

In [7]:

```
drug_curves["count_missing"] = drug_curves[response_norm].isnull().sum(axis=1)
conc_gr = drug_curves.groupby(["drug_name", "CCL_name"]).agg(n_conc = ("MAX_CONC", "nunique"),
                                                             n_samples = ("MAX_CONC", "count"),
                                                             sum_missing = ("count_missing", "sum"
conc_gr.shape
```

Out[7]:

```
(213603, 3)
```

In [8]:

```
df_multi = conc_gr[(conc_gr["n_conc"]>1) | (conc_gr["n_samples"]>1)].copy()
df_multi["compare"] = df_multi["n_conc"] - df_multi["n_samples"]
df_multi["compare"].value_counts()
```

Out[8]:

```
 0    8573
-1    3208
Name: compare, dtype: int64
```

In [9]:

```
df_multi[df_multi["compare"] == 0]["n_conc"].value_counts()
```

Out[9]:

```
2    8573
Name: n_conc, dtype: int64
```

In [10]:

```
df_multi["n_conc"].value_counts()
```

Out[10]:

```
2    8573
1    3208
Name: n_conc, dtype: int64
```

In [11]:

```
conc_multi = df_multi[df_multi["n_conc"]>1]
conc_multi
```

Out[11]:

		n_conc	n_samples	sum_missing	compare
drug_name	**CCL_name**				
	201T	2	2	0	0
	22RV1	2	2	0	0
AKT inhibitor VIII	**23132-87**	2	2	0	0
	42-MG-BA	2	2	0	0
	451Lu	2	2	0	0
...	**...**	...	...	...	...
	YKG-1	2	2	4	0
	YT	2	2	4	0
UNC0638	**huH-1**	2	2	4	0
	no-10	2	2	4	0
	no-11	2	2	4	0

8573 rows × 4 columns

In [12]:

```
conc_multi["sum_missing"].value_counts()
```

Out[12]:

```
4    5912
0    2661
Name: sum_missing, dtype: int64
```

In [13]:

```
conc_multi[conc_multi["sum_missing"]==0]
```

Out[13]:

		n_conc	n_samples	sum_missing	compare
drug_name	CCL_name				
	201T	2	2	0	0
	22RV1	2	2	0	0
AKT inhibitor VIII	**23132-87**	2	2	0	0
	42-MG-BA	2	2	0	0
	451Lu	2	2	0	0
...	**...**	...	...	...	...
	YKG-1	2	2	0	0
	YT	2	2	0	0
Avagacestat	**huH-1**	2	2	0	0
	no-10	2	2	0	0
	no-11	2	2	0	0

2661 rows × 4 columns

In [14]:

```
multi_pairs = df_multi[(df_multi["compare"]==0)
                       & (df_multi["n_conc"]==2)
                      & (df_multi["sum_missing"]==0)].index.unique()
len(multi_pairs)
```

Out[14]:

```
2661
```

In [15]:

```
multi_pairs[1000]
```

Out[15]:

```
('AZD6482', 'CAL-54')
```

In [16]:

```
drug_curves[(drug_curves["drug_name"]=="AKT inhibitor VIII") & (drug_curves["CCL_name"]=="201T")
```

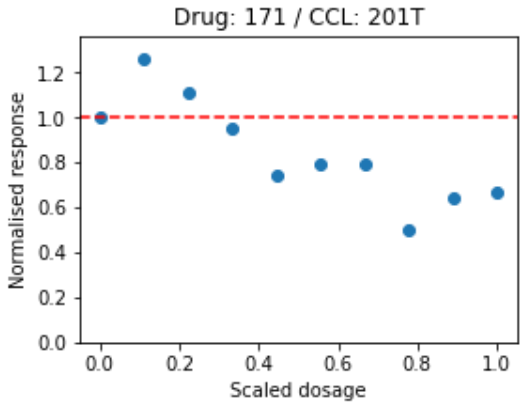
Out[16]:

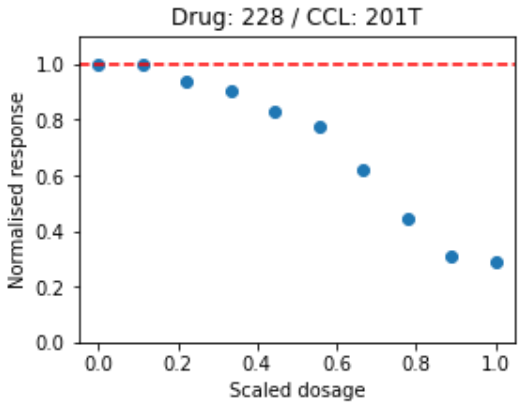
	CELL_LINE_NAME	COSMIC_ID	DRUG_ID	DRUGID_COSMICID	FOLD_DILUTION	MA
120529	201T	1287381	228	228_1287381	2	
126556	201T	1287381	171	171_1287381	2	

2 rows × 29 columns

In [17]:

```
specific_samples = [(171, "201T"), #lower concentration
                    (228, "201T"),
                   ]
show_specific(drug_curves, specific_samples, conc_columns, response_norm,
              drug_col ="DRUG_ID",  upper_limit =1)
```





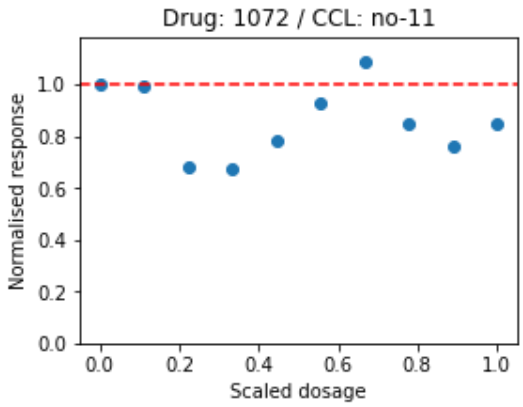
Conclusion: Low concentration didn't work well (but effect was recognisable), so they increased the concentration 4 times (case for drug_id=228) ???

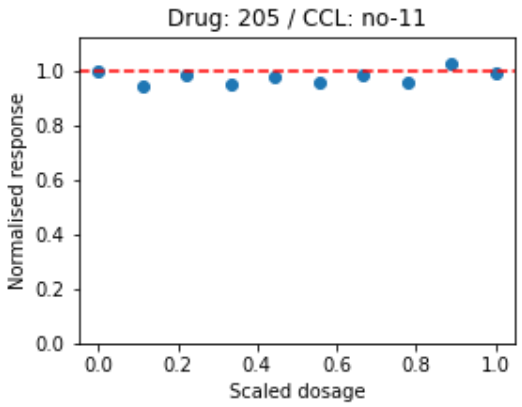
In [18]:

```
display(drug_curves[(drug_curves["drug_name"]=="Avagacestat") & (drug_curves["CCL_name"]=="no-11

specific_samples = [(1072, "no-11"), #lower concentration
                    (205, "no-11"),
                   ]
show_specific(drug_curves, specific_samples, conc_columns, response_norm,
              drug_col ="DRUG_ID",  upper_limit =1)
```

	CELL_LINE_NAME	COSMIC_ID	DRUG_ID	DRUGID_COSMICID	FOLD_DILUTION	MA
109714	no-11	908450	205	205_908450	2	
161336	no-11	908450	1072	1072_908450	2	

2 rows × 29 columns





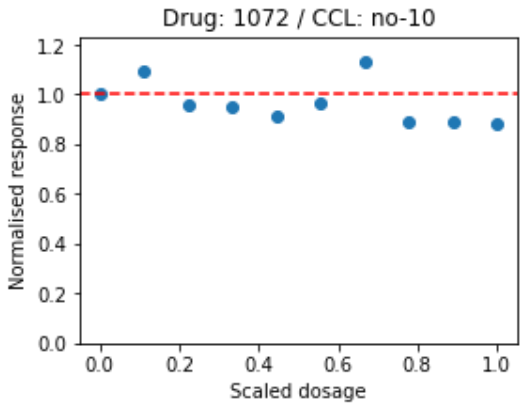
Need for explanation: Some effect for low concentration and no effect for higher concentration???

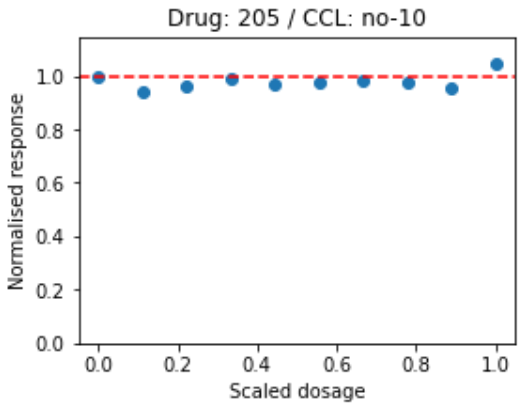
In [19]:

```
display(drug_curves[(drug_curves["drug_name"]=="Avagacestat") & (drug_curves["CCL_name"]=="no-10

specific_samples = [(1072, "no-10"), #lower concentration
                    (205, "no-10"),
                   ]
show_specific(drug_curves, specific_samples, conc_columns, response_norm,
              drug_col ="DRUG_ID",  upper_limit =1)
```

	CELL_LINE_NAME	COSMIC_ID	DRUG_ID	DRUGID_COSMICID	FOLD_DILUTION	MA
122793	no-10	908452	205	205_908452	2	
167111	no-10	908452	1072	1072_908452	2	

2 rows × 29 columns



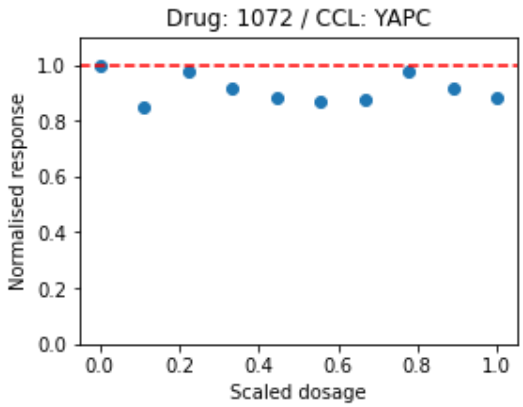


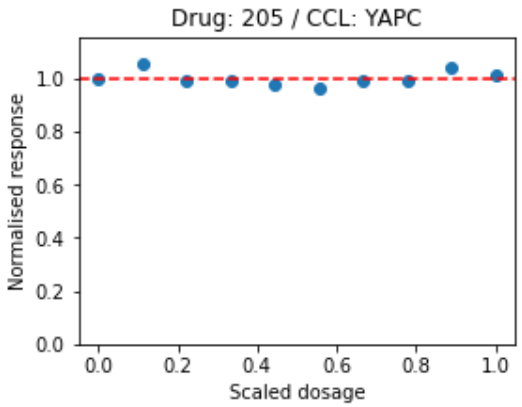
In [20]:

```
display(drug_curves[(drug_curves["drug_name"]=="Avagacestat") & (drug_curves["CCL_name"]=="YAPC"

specific_samples = [(1072, "YAPC"), #lower concentration
                    (205, "YAPC"),
                   ]
show_specific(drug_curves, specific_samples, conc_columns, response_norm,
              drug_col ="DRUG_ID",  upper_limit =1)
```

	CELL_LINE_NAME	COSMIC_ID	DRUG_ID	DRUGID_COSMICID	FOLD_DILUTION	MA
84299	YAPC	909904	205	205_909904	2	
173538	YAPC	909904	1072	1072_909904	2	

2 rows × 29 columns





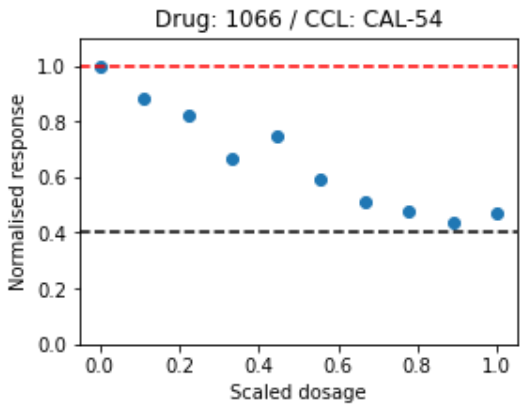
Conclusion: Strange case for Avagacestat

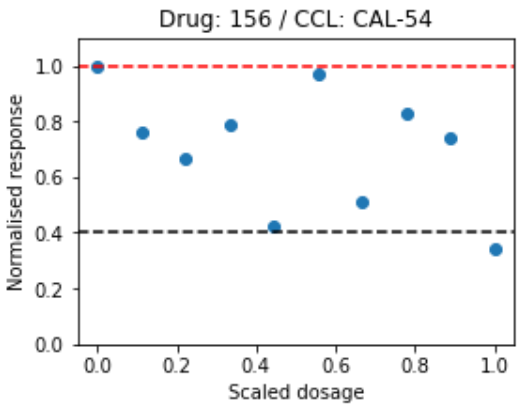
In [21]:

```
display(drug_curves[(drug_curves["drug_name"]=="AZD6482") & (drug_curves["CCL_name"]=="CAL-54")]

specific_samples = [(1066, "CAL-54"), #lower concentration
                    (156, "CAL-54"),
                   ]
show_specific(drug_curves, specific_samples, conc_columns, response_norm,
              drug_col ="DRUG_ID",  upper_limit =1, lower_limit=0.4)

# Almost the same concentrations!!!
```

	CELL_LINE_NAME	COSMIC_ID	DRUG_ID	DRUGID_COSMICID	FOLD_DILUTION	MA
30665	CAL-54	910952	156	156_910952	2	
151706	CAL-54	910952	1066	1066_910952	2	

2 rows × 29 columns



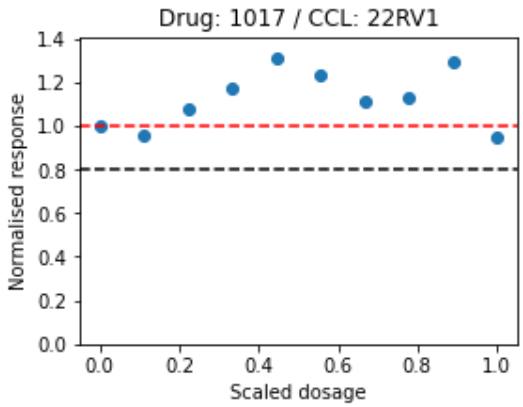


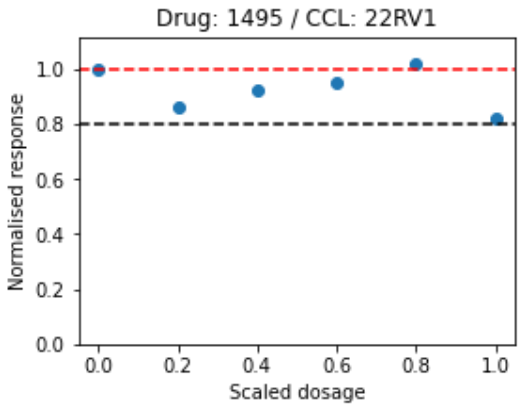
In [22]:

```
display(drug_curves[(drug_curves["drug_name"]=="Olaparib") & (drug_curves["CCL_name"]=="22RV1")]

specific_samples = [(1017, "22RV1"), #lower concentration
                    (1495, "22RV1"),
                   ]
show_specific(drug_curves, specific_samples, conc_columns, response_norm,
              drug_col ="DRUG_ID",  upper_limit =1, lower_limit=0.8)
```

	CELL_LINE_NAME	COSMIC_ID	DRUG_ID	DRUGID_COSMICID	FOLD_DILUTION	MA
175276	22RV1	924100	1017	1017_924100	2	
210290	22RV1	924100	1495	1495_924100	4	

2 rows × 29 columns





Pairs with one concentration and two records

In [23]:

```
df_multi[df_multi["compare"] == -1]["n_conc"].value_counts()
```

Out[23]:

```
1    3208
Name: n_conc, dtype: int64
```

In [24]:

```
df_multi[(df_multi["compare"]==-1)]
```

Out[24]:

		n_conc	n_samples	sum_missing	compare
drug_name	CCL_name				
	22RV1	1	2	4	-1
	23132-87	1	2	4	-1
PLX-4720	**42-MG-BA**	1	2	4	-1
	451Lu	1	2	4	-1
	5637	1	2	4	-1
...	**...**	...	...	...	...
	YKG-1	1	2	4	-1
	YT	1	2	4	-1
Selumetinib	**ZR-75-30**	1	2	4	-1
	huH-1	1	2	4	-1
	no-11	1	2	4	-1

3208 rows × 4 columns

In [25]:

```
multi_pairs = list(df_multi[(df_multi["compare"]==-1)].index.unique())
len(multi_pairs)
```

Out[25]:

3208

In [26]:

```
[multi_pairs[i] for i in [10, 1000, 2000, 3000]]
```

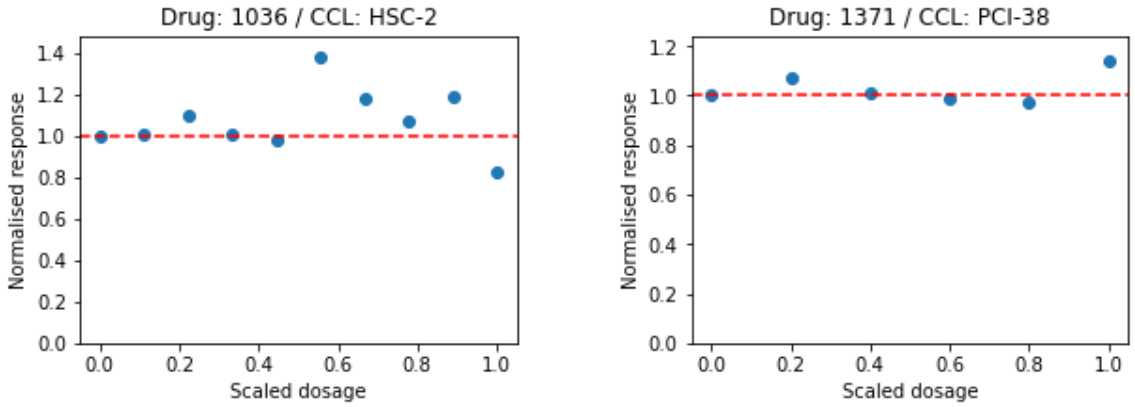
Out[26]:

```
[('PLX-4720', '8305C'),
 ('Pictilisib', 'EN'),
 ('Refametinib', 'LS-411N'),
 ('Selumetinib', 'OVKATE')]
```

One concentration and 2 records for each pair

In [27]:

```
drug_curves[(drug_curves["drug_name"]=="PLX-4720")& (drug_curves["CCL_name"]=="22RV1")]

specific_samples = [(1036, "HSC-2"),
                    (1371, "PCI-38"),
                   ]
show_specific(drug_curves, specific_samples, conc_columns, response_norm, drug_col ="DRUG_ID",
              upper_limit =1)
```



Hypothesis: for the pairs drug+CCL with one concentraion and two records, one of the records is reduced, i.e has missing values

In [28]:

```
nul_samples = df_multi[(df_multi["compare"]==-1) & (df_multi["sum_missing"]>0)].index.unique()

print("Total number of multiples:", len(multi_pairs))
print("Number of pairs with missing data:", len(nul_samples))
```

```
Total number of multiples: 3208
Number of pairs with missing data: 3208
```

Conclusions: for all the pairs drug+CCL with one concentraion and two records, one of the records is reduced, i.e has missing values

Part 2: Missing values

In [29]:

```
drug_curves["count_missing"] = drug_curves[response_norm].isnull().sum(axis=1)
drug_curves["count_missing"].value_counts()
```

Out[29]:

```
0      191644
4       33740
Name: count_missing, dtype: int64
```

In [30]:

```
df = drug_curves[drug_curves["count_missing"]!=0]
df[["drug_name", "CCL_name"] + conc_columns + response_norm].head()
```

Out[30]:

	drug_name	CCL_name	fd_num_0	fd_num_1	fd_num_2	fd_num_3	fd_num_4	fd_n
191644	IOX2	HDQ-P1	0	0.2	0.4	0.6	0.8	
191645	UNC0638	HDQ-P1	0	0.2	0.4	0.6	0.8	
191646	UNC1215	HDQ-P1	0	0.2	0.4	0.6	0.8	
191647	Tamoxifen	HDQ-P1	0	0.2	0.4	0.6	0.8	
191648	(5Z)-7-Oxozeaenol	HDQ-P1	0	0.2	0.4	0.6	0.8	

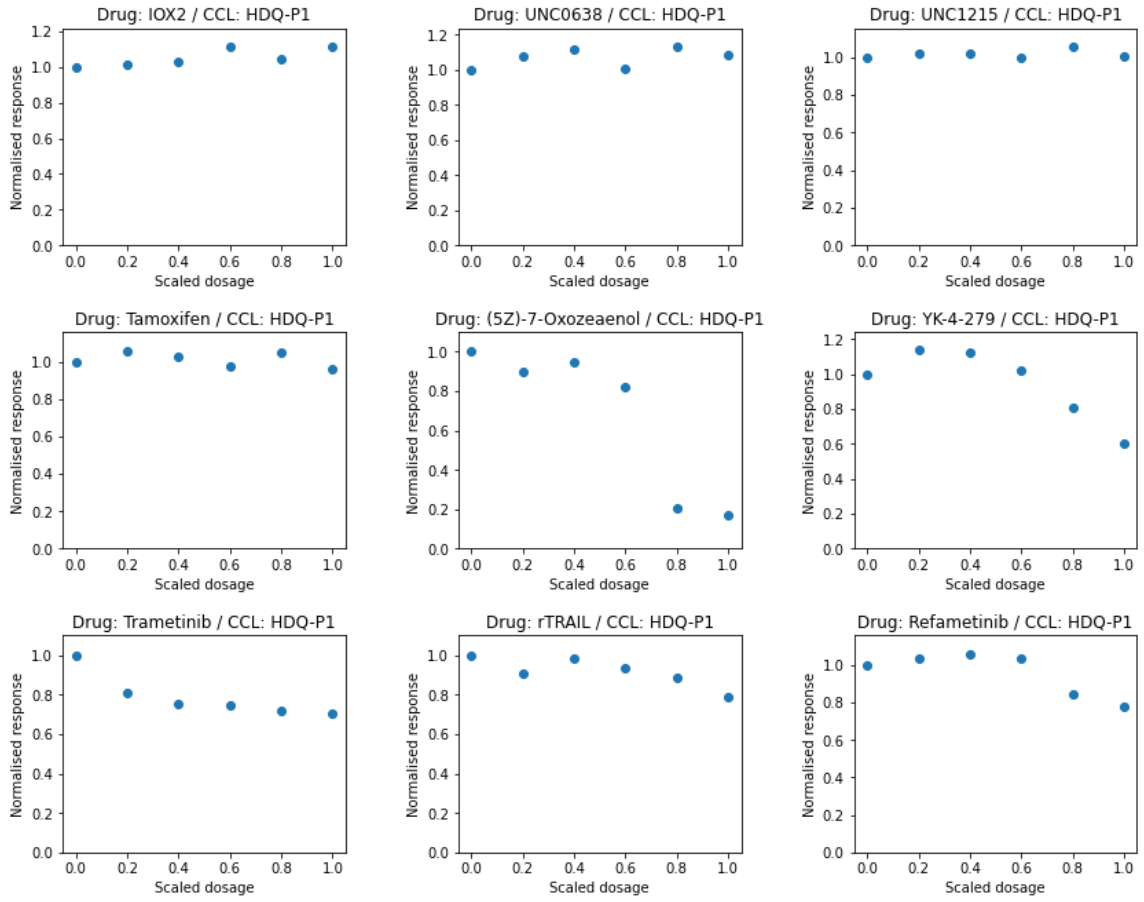
5 rows × 22 columns

Conclusion: 33740 profiles have only 6 points (instead of usual 10)

In [31]:

```
df = drug_curves[drug_curves["count_missing"]!=0]
print("Number of samples with missing data", 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[:9],
                    drug_dict = drug_names, CCL_dict = CCL_names)
```

```
Number of samples with missing data 33740
```



Hypothesis: for all the records with missing data there is a "dublicate" with the whole range

In [32]:

```
drug_curves["count_missing"] = drug_curves[response_norm].isnull().sum(axis=1)
conc_gr = drug_curves.groupby(["drug_name", "CCL_name"]).agg(n_conc = ("MAX_CONC", "nunique"),
                                                             n_samples = ("MAX_CONC", "count"),
                                                             sum_missing = ("count_missing", "sum"


conc_gr.groupby(["sum_missing", "n_samples"]).agg(count = ("n_conc", "count"))
```

Out[32]:

		count
sum_missing	**n_samples**	
0	**1**	177202
	2	2661
4	**1**	24620
	2	9120

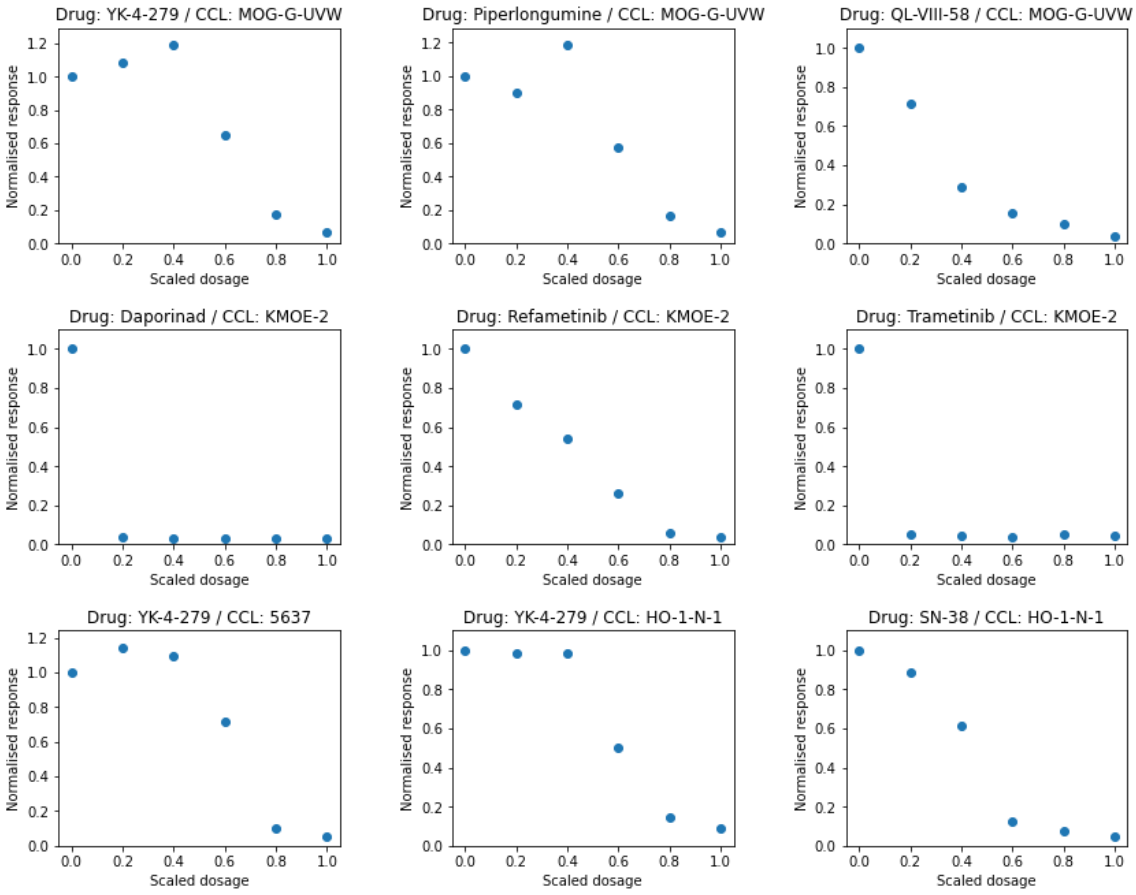
Conclusion: Among 33740 profiles with missing points, only 9120 have dublicates/alternatives

Some of the profiles with missing data are not so bad

In [33]:

```
df = drug_curves[(drug_curves["count_missing"]!=0 )
                 & (drug_curves["norm_cells_4"]<0.2)
                 & (drug_curves["norm_cells_5"]<0.2)
                ]

print("Number of not bad data:", 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[60:69],
                    drug_dict = drug_names, CCL_dict = CCL_names)
```

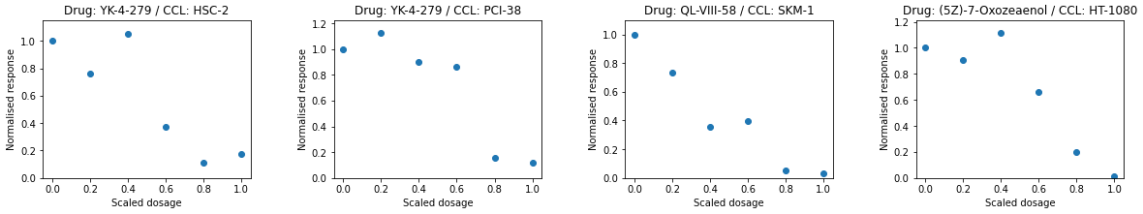
```
Number of not bad data: 1389
```



Ambigous data: Are some points wrong?

In [34]:

```
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 [35]:

```
%%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: user 44.3 s, sys: 385 ms, total: 44.6 s
Wall time: 46.1 s
```

Out[35]:

	high_responses	norm_cells_0	norm_cells_1	norm_cells_2	norm_cells_3	norm_cells
0	7	1	1.039343	0.998020	1.005715	1.055
1	6	1	0.969418	0.987582	1.052708	1.072
2	1	1	0.956127	0.887779	0.941691	0.839
3	4	1	1.087946	0.980767	1.118407	1.234
4	6	1	1.035268	1.040170	0.972972	1.029
...	...	...	...	...	...	
225379	3	1	0.970321	0.864856	1.326808	1.100
225380	3	1	0.329169	0.284518	1.088894	1.090
225381	3	1	0.914628	0.840454	1.116674	1.096
225382	2	1	0.884687	1.000038	1.051918	0.790
225383	4	1	1.053967	0.831009	1.155885	1.149

225384 rows × 11 columns

In [36]:

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

```
Original data: (225384, 30)
Ambiguos data: (127590, 30)
```

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

In [37]:

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

Out[37]:

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

Bad data by drug

In [38]:

```
%%time
dr1 = drug_curves.groupby(["DRUG_ID"], as_index=False).agg(curves_count_all = ("COSMIC_ID", "cou

dr2 = bad_data.groupby(["DRUG_ID"], as_index=False).agg(curves_count_bad = ("COSMIC_ID", "count"
                                                        min_bad_responses = ("high_responses", "mi
                                                         max_bad_response = ("high_responses", "ma
                                                         avg_bad_responses = ("high_responses", "m
                                                        )

dr2["avg_bad_responses"] = round(dr2["avg_bad_responses"], 2)

dr = pd.merge(right = dr1, left =dr2, on="DRUG_ID", how="left")
dr["drug_name"] = dr["DRUG_ID"].map(drug_names)
dr["percent_bad"] = round(dr["curves_count_bad"]/dr["curves_count_all"], 3)

show_columns = ['DRUG_ID', 'drug_name', 'percent_bad', 'curves_count_all','curves_count_bad',
                'min_bad_responses', 'max_bad_response','avg_bad_responses']
dr = dr[show_columns].copy()
```

```
CPU times: user 63.5 ms, sys: 9.51 ms, total: 73 ms
Wall time: 88.2 ms
```

In [39]:

```
dr.sort_values("percent_bad", ascending = False, inplace=True)
dr.head(10)
```

Out[39]:

	DRUG_ID	drug_name	percent_bad	curves_count_all	curves_count_bad	min_bad_resp
190	1025	SB216763	0.954	786	750	
197	1033	Vismodegib	0.950	893	848	
47	150	Bicalutamide	0.947	932	883	
161	332	XMD15-27	0.947	980	928	
183	1018	Veliparib	0.919	894	822	
178	1013	Nilotinib	0.915	844	772	
182	1017	Olaparib	0.908	894	812	
185	1020	Lenalidomide	0.908	894	812	
232	1170	CCT-018159	0.901	945	851	
163	341	Selisistat	0.899	975	877	

Bad data by CCL

In [40]:

```
%%time
cl1 = drug_curves.groupby(["COSMIC_ID"], as_index=False).agg(curves_count_all = ("DRUG_ID", "cou

cl2 = bad_data.groupby(["COSMIC_ID"], as_index=False).agg(curves_count_bad = ("DRUG_ID", "count"
                                                          min_bad_responses = ("high_responses", "mi
                                                           max_bad_response = ("high_responses", "ma
                                                           avg_bad_responses = ("high_responses", "m
                                                          )

cl2["avg_bad_responses"] = round(cl2["avg_bad_responses"], 2)

cl = pd.merge(right = cl1, left =cl2, on="COSMIC_ID", how="left")
cl["CCL_name"] = cl["COSMIC_ID"].map(CCL_names)
cl["percent_bad"] = round(cl["curves_count_bad"]/cl["curves_count_all"], 3)

show_columns = ['COSMIC_ID', 'CCL_name', 'percent_bad', 'curves_count_all','curves_count_bad',
                'min_bad_responses', 'max_bad_response','avg_bad_responses']
cl = cl[show_columns].copy()
```

```
CPU times: user 54.8 ms, sys: 8.12 ms, total: 62.9 ms
Wall time: 67.3 ms
```

In [41]:

```
cl.sort_values("percent_bad", ascending = False, inplace=True)
cl.head(10)
```

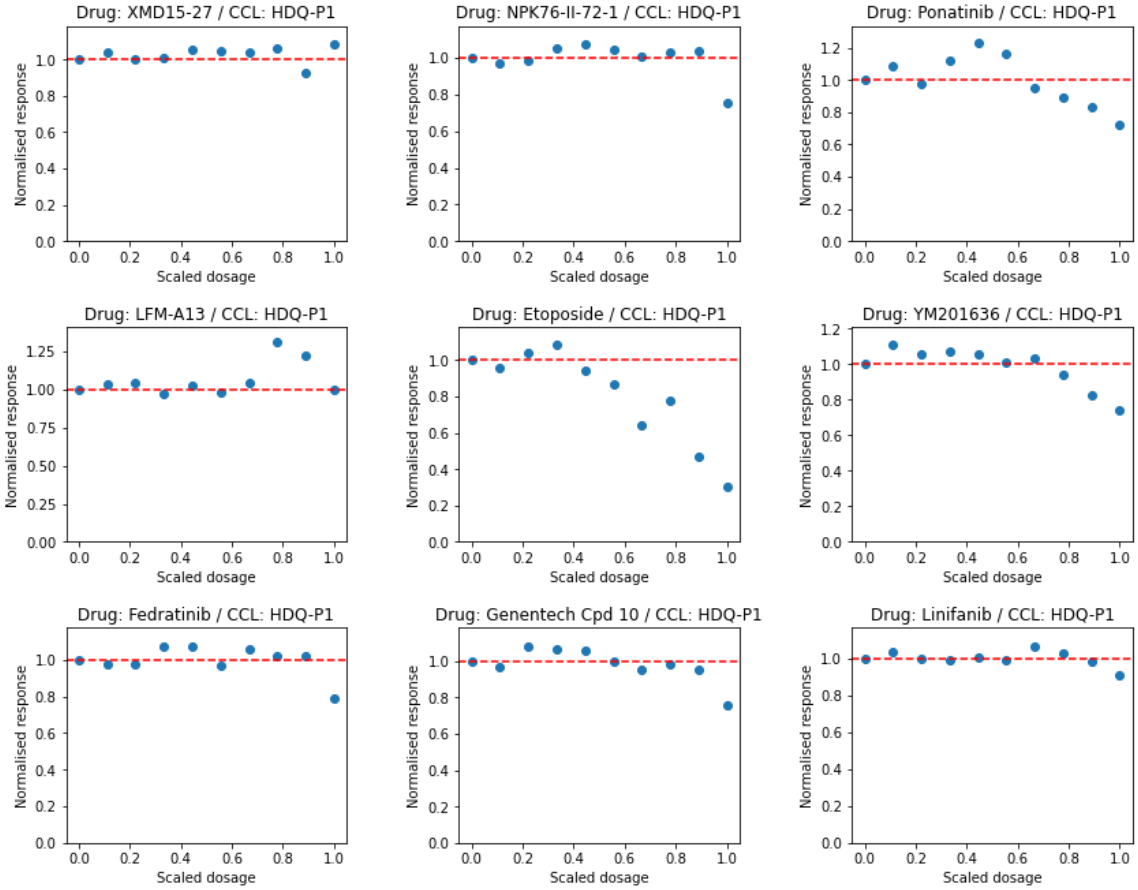
Out[41]:

	COSMIC_ID	CCL_name	percent_bad	curves_count_all	curves_count_bad	min_bad_res
62	688022	NCI-H378	1.000	2	2	
670	924241	NCI-H250	1.000	1	1	
985	1330969	NCI-H1404	0.837	43	36	
75	713880	SBC-5	0.816	217	177	
564	909907	ZR-75-30	0.813	91	74	
503	909711	SCH	0.806	252	203	
894	1298162	K8	0.802	126	101	
402	907799	MC116	0.802	258	207	
714	949092	CP67-MEL	0.800	25	20	
378	907312	KU-19-19	0.793	222	176	

Check whether bad data are actually bad

In [42]:

```
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)
```

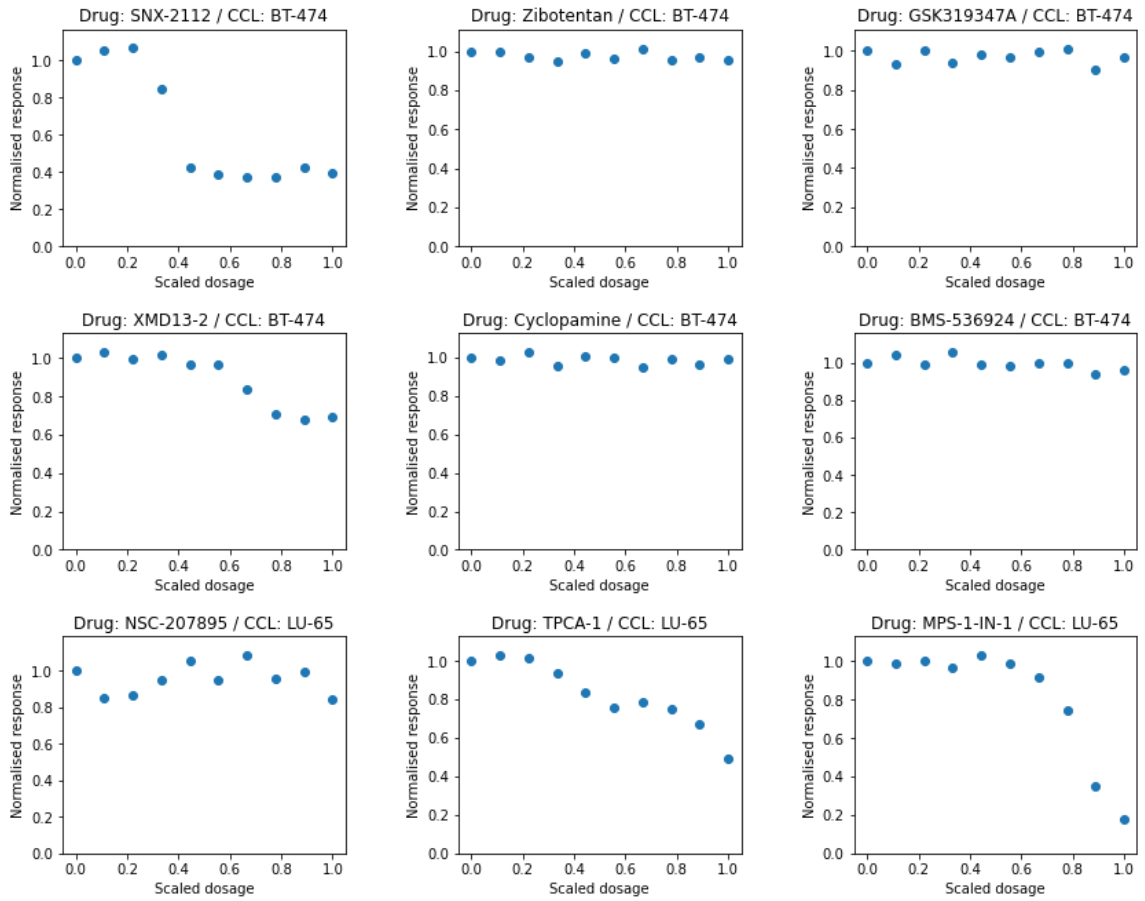


Samples with 2 bad responses

In [43]:

```
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)
```

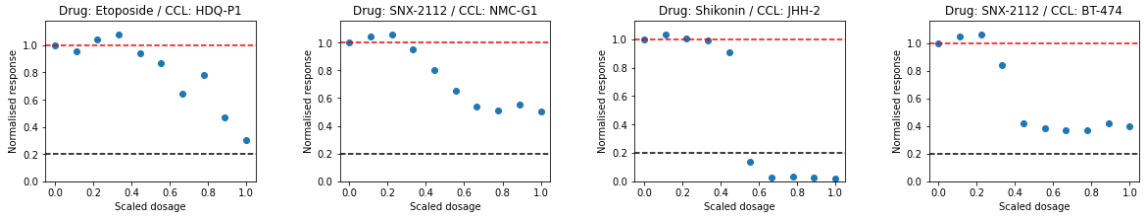
```
Number of samples with 2 bad responses: 28485
```



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

In [44]:

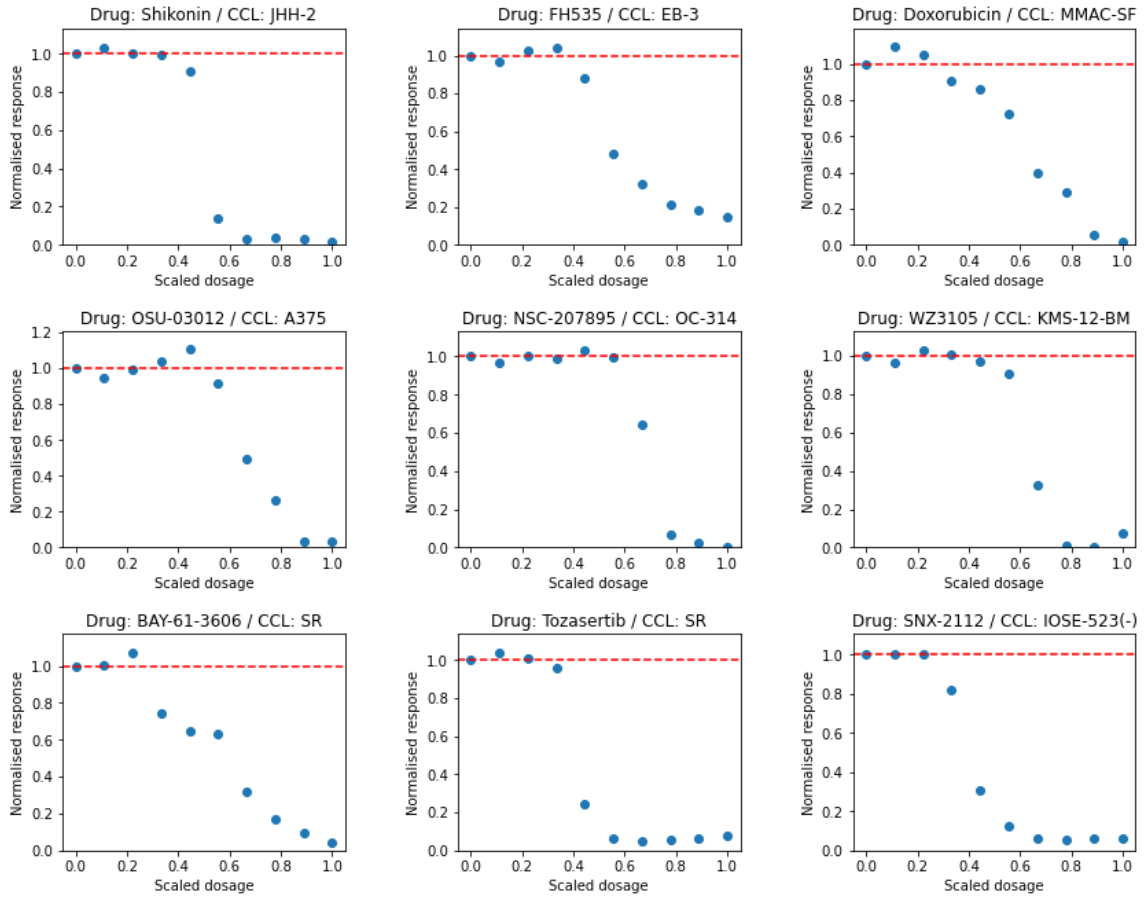
```
specific_samples = [("Etoposide", "HDQ-P1"),
                    ("SNX-2112", "NMC-G1"),
                    ("Shikonin", "JHH-2"),
                    ("SNX-2112", "BT-474")
                   ]
show_specific(bad_data, specific_samples, conc_columns, response_norm, upper_limit=1, lower_limit
```



In [45]:

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

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

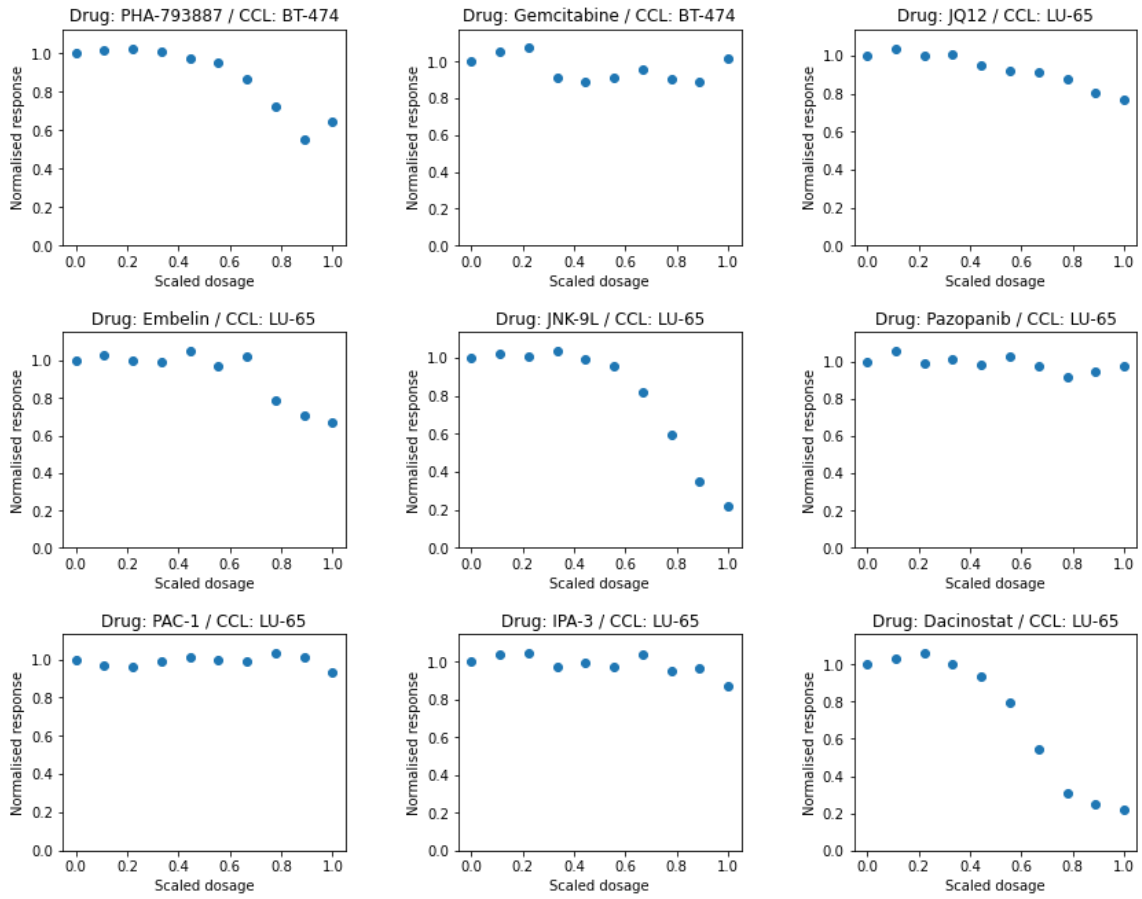
The question: What is the accuracy of measuring responses?
Can we treat samples with responses up to 1.01 as valid ones?

Samples with 3 bad responses

In [46]:

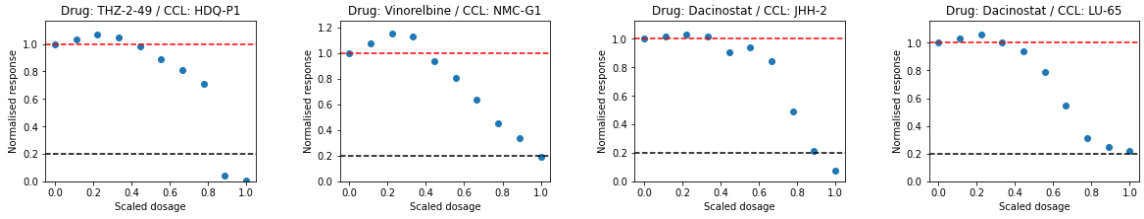
```
N = 3
df = bad_data[bad_data["high_responses"]==N]
print("Number of samples with %d bad responses: %d" % (N, df.shape[0]))

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 [47]:

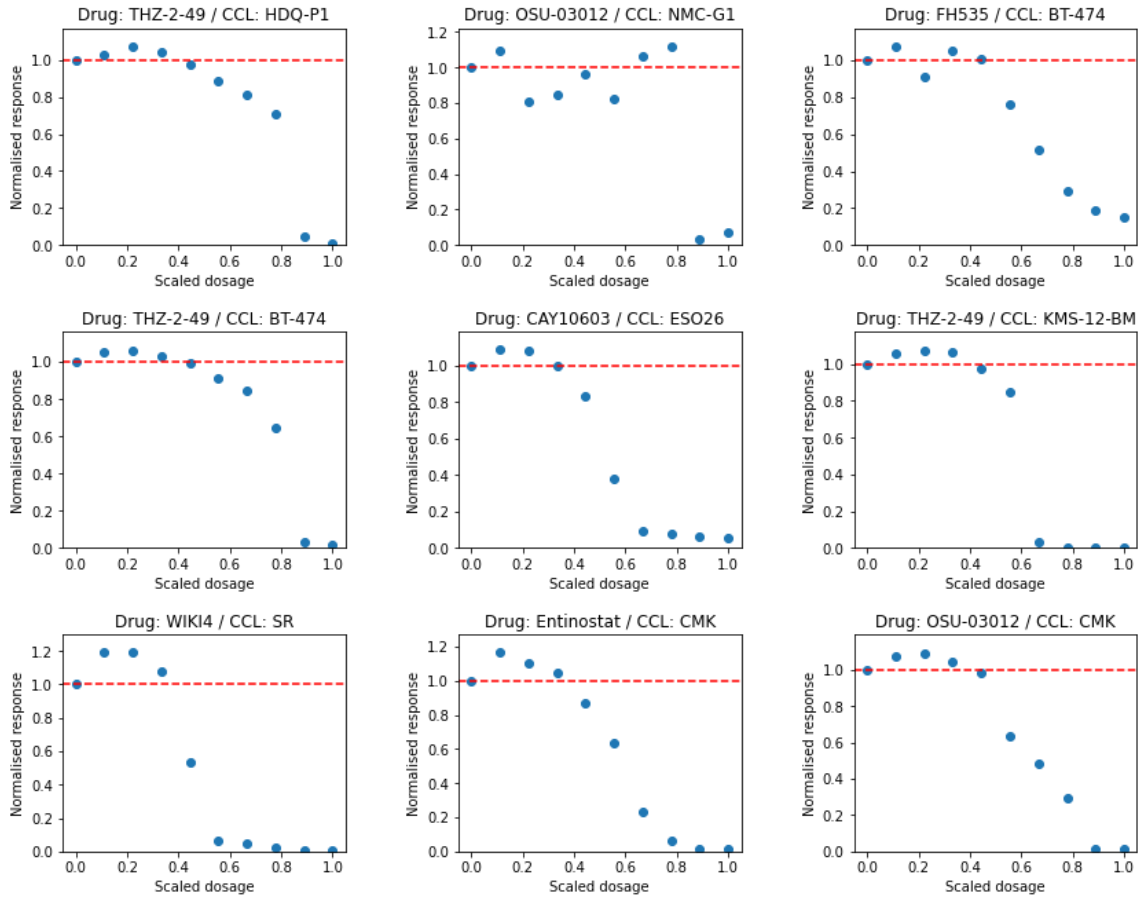
```
specific_samples = [("THZ-2-49", "HDQ-P1"),
                    ("Vinorelbine", "NMC-G1"),
                    ("Dacinostat", "JHH-2"),
                    ("Dacinostat", "LU-65")
                   ]
show_specific(bad_data, specific_samples, conc_columns, response_norm, upper_limit=1, lower_limit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



In [48]:

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

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

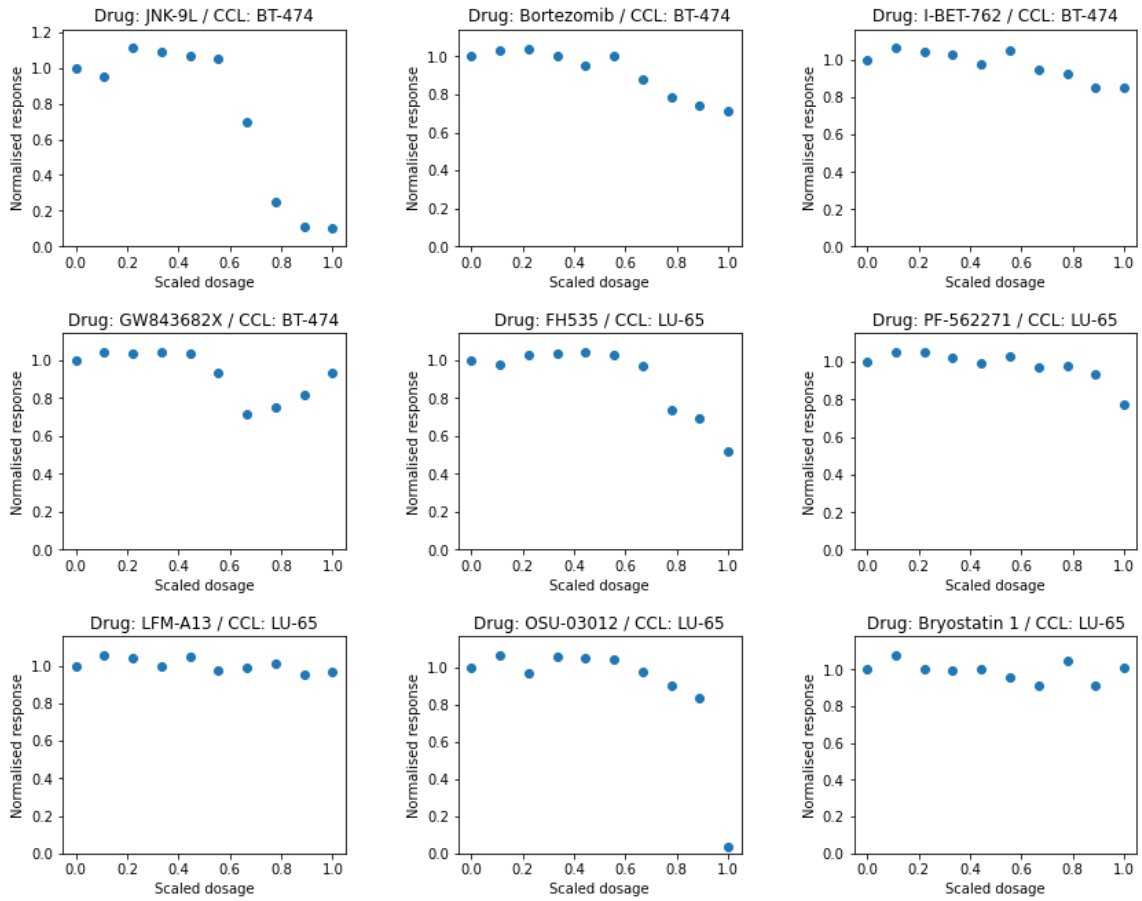


Samples with 4 bad responses

In [49]:

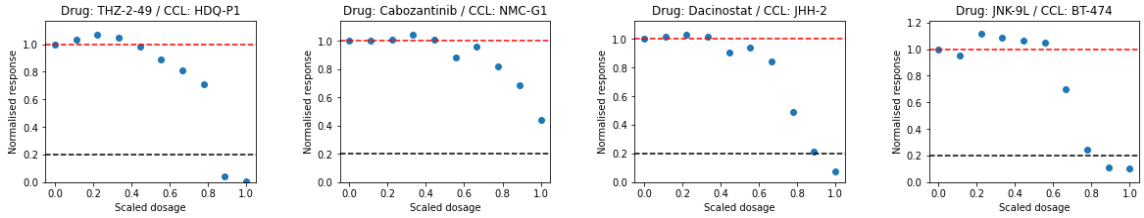
```
N = 4
df = bad_data[bad_data["high_responses"]==N]
print("Number of samples with %d bad responses: %d" % (N, df.shape[0]))

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 [50]:

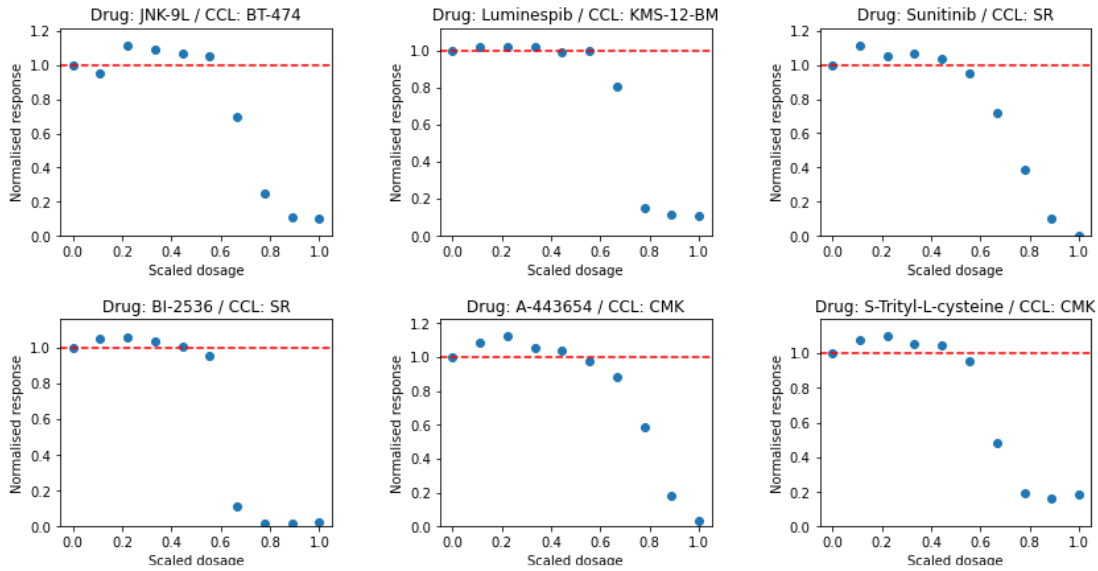
```
specific_samples = [("THZ-2-49", "HDQ-P1"),
                    ("Cabozantinib", "NMC-G1"),
                    ("Dacinostat", "JHH-2"),
                    ("JNK-9L", "BT-474")
                   ]
show_specific(bad_data, specific_samples, conc_columns, response_norm, upper_limit=1, lower_limit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



In [51]:

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

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: 8
79
```

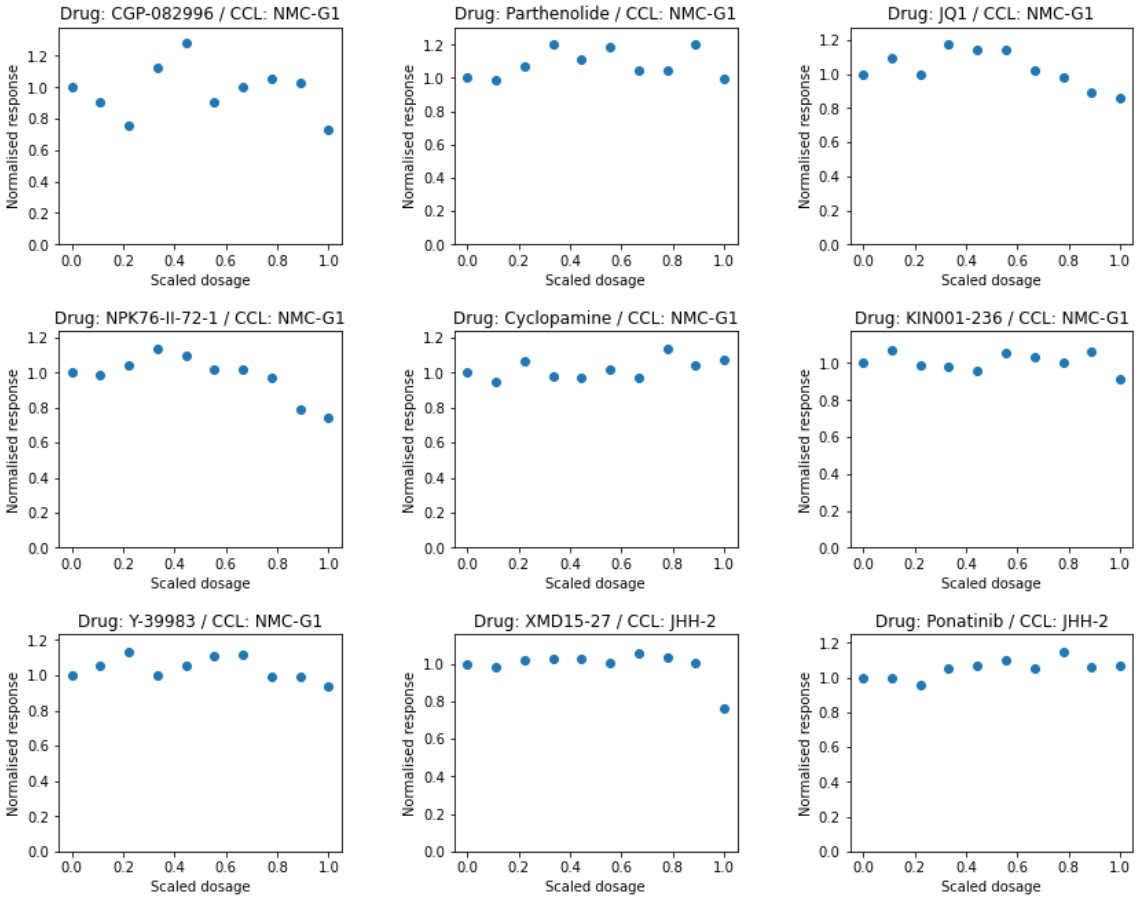


Samples with 5+ bad responses

In [52]:

```
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)
```

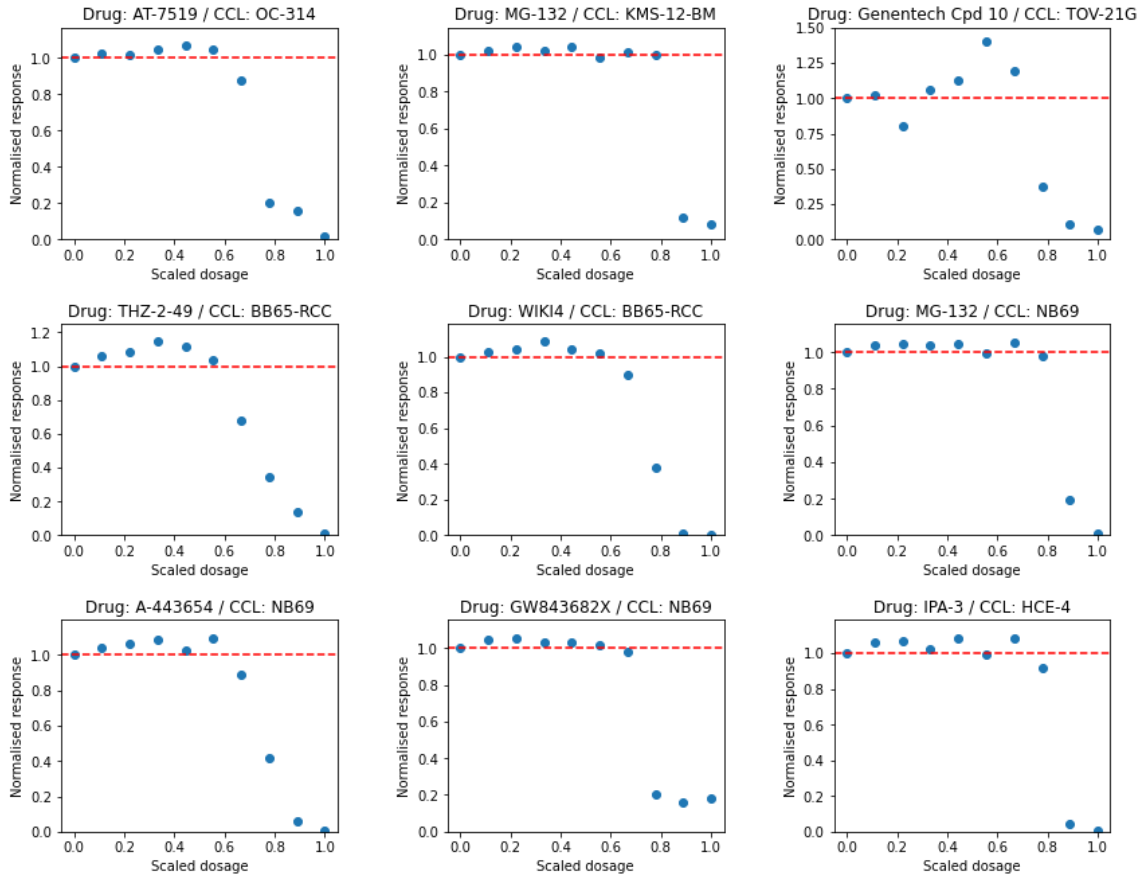
```
Number of samples with more than 5 bad responses: 54756
```



In [53]:

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

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)
```

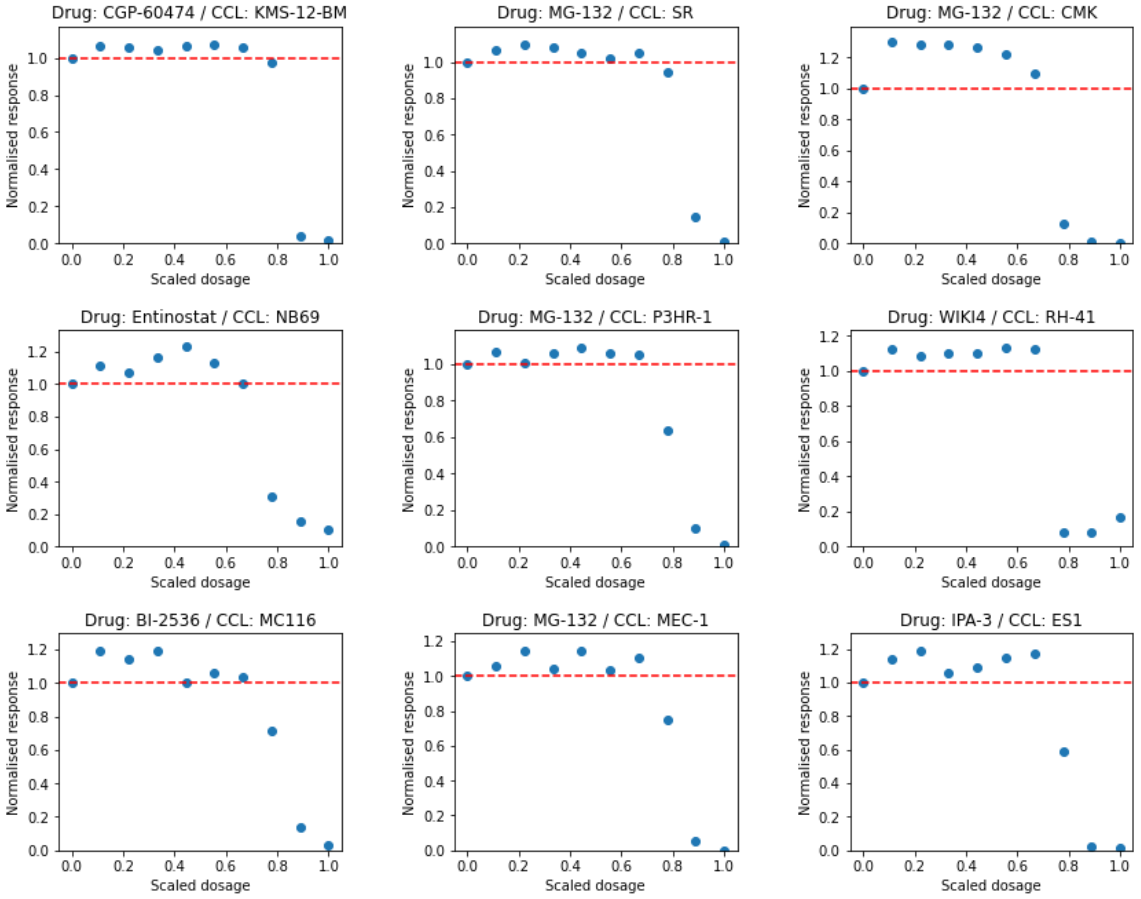
```
Number of samples with 5 bad responses, but with 2 last responses below 0.2: 441
```



In [54]:

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

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)
```

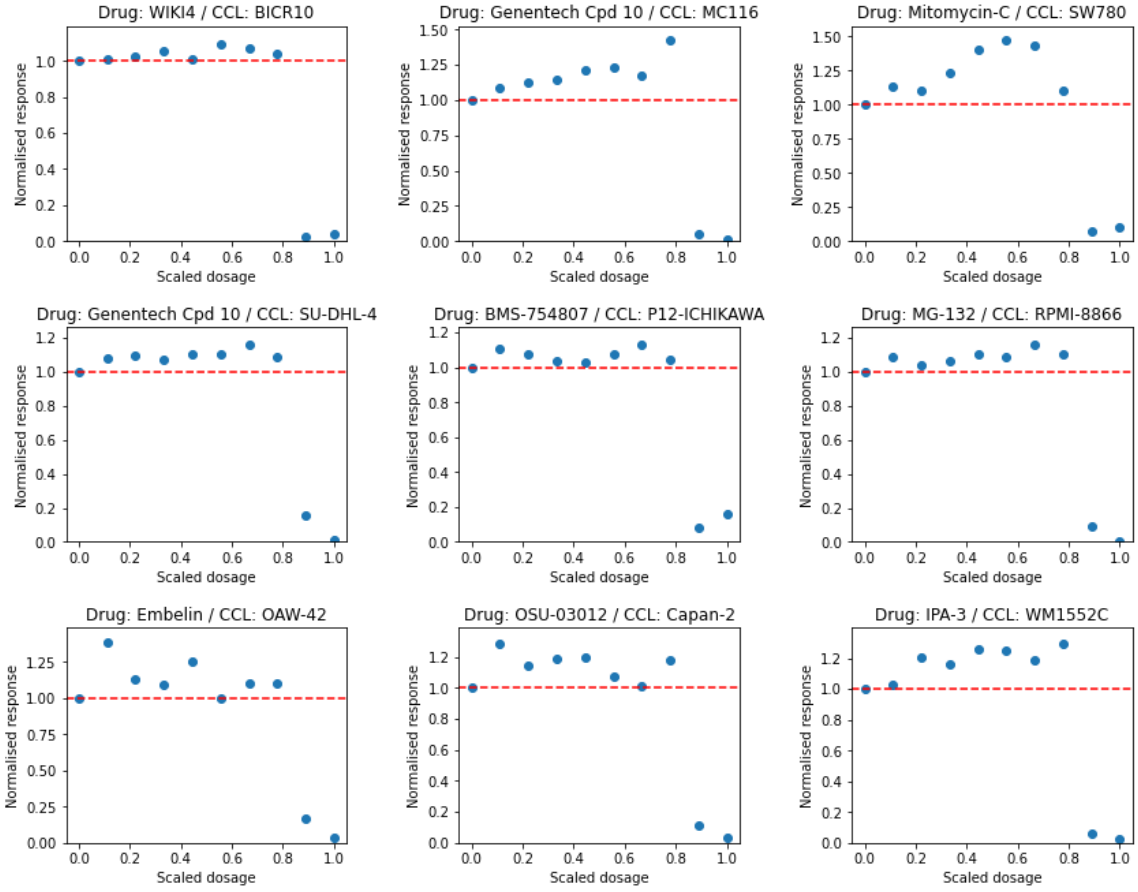
```
Number of samples with 6 bad responses, but with 2 last responses below 0.2: 135
```



In [55]:

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

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



In [56]:

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

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 8 bad responses, but with 2 last responses below 0.2: 0

<Figure size 1008x792 with 0 Axes>
```

In [57]:

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

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 1008x792 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 [58]:

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

```
CPU times: user 44 ms, sys: 21.2 ms, total: 65.2 ms
Wall time: 62.7 ms
```

In [59]:

```
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 [60]:

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

Out[60]:

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

In [61]:

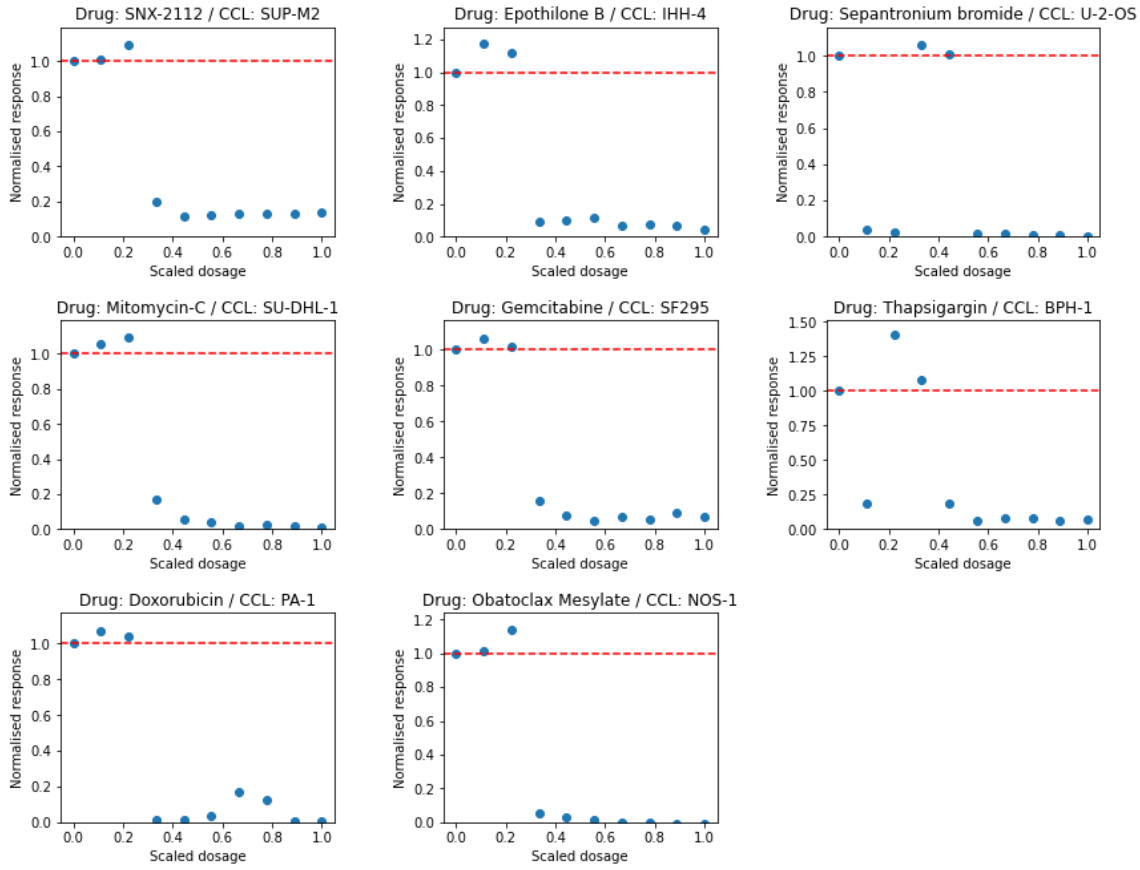
```
not_bad_04["low_response_04"].value_counts()
```

Out[61]:

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

In [62]:

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

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)
```



Part 5: Repeat with an additional constrain

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

In [63]:

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

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()
```

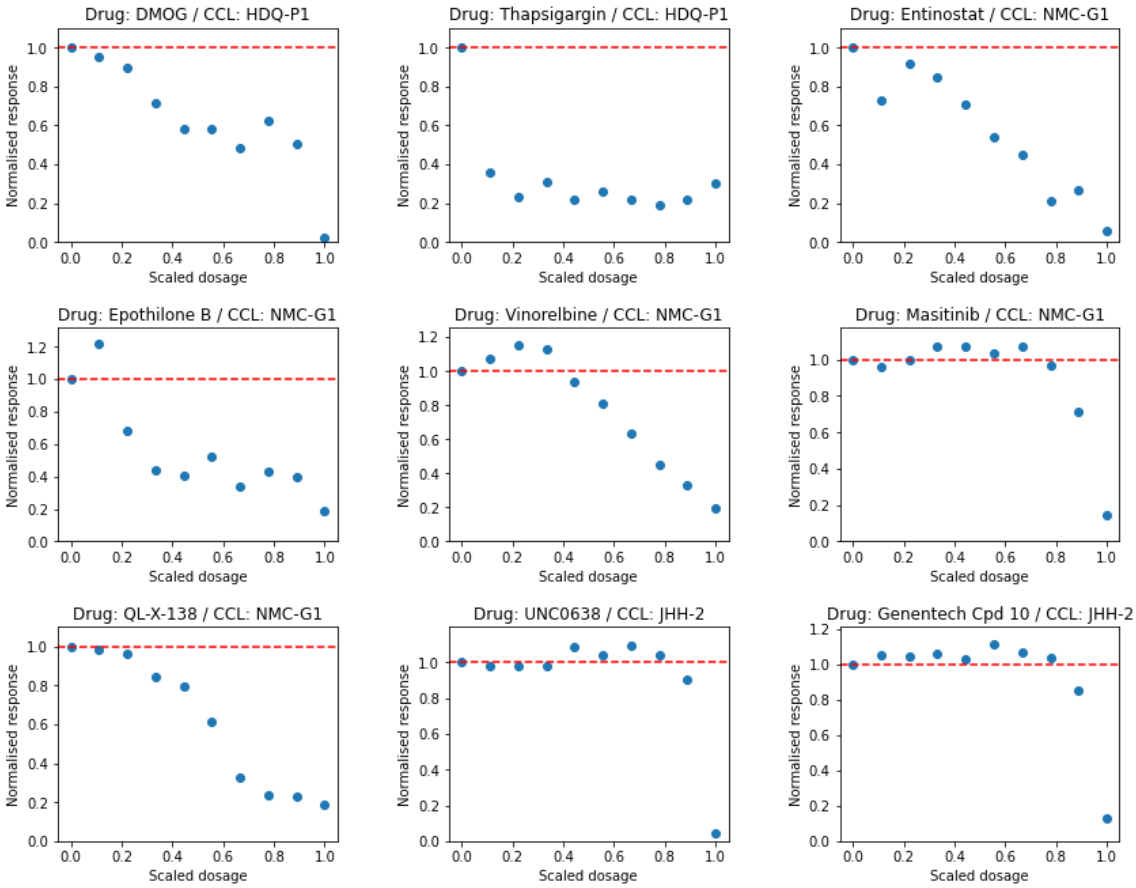
```
Before filtration: 16438, After filtration: 190245
```

Out[63]:

```
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 [64]:

```
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)
```



Further ideas

```
Possible Scenarios for predicting drug response curves:
    1. predict each point one-by-one
    2. predict coefficents of some fitting sigmoid function
    (actually, that is equal to
         - classification of whether there was response to drugs or not
         - for good data prediction of coefficients
    3. classify all the data into 3 categories:
        no response/not valid data
        some response
        perfect sigmoid which we can treat with an average sigmoid function
```