In [1]:
```python
from matplotlib import pyplot as plt
%matplotlib inline
import seaborn as sns; sns.set()
import pandas as pd
```

In [2]:
```python
url = "https://raw.githubusercontent.com/\
Stemanz/python_tutorials/master/datasets/gene_expression.csv"
data = pd.read_csv(url, index_col="gene symbol")
```
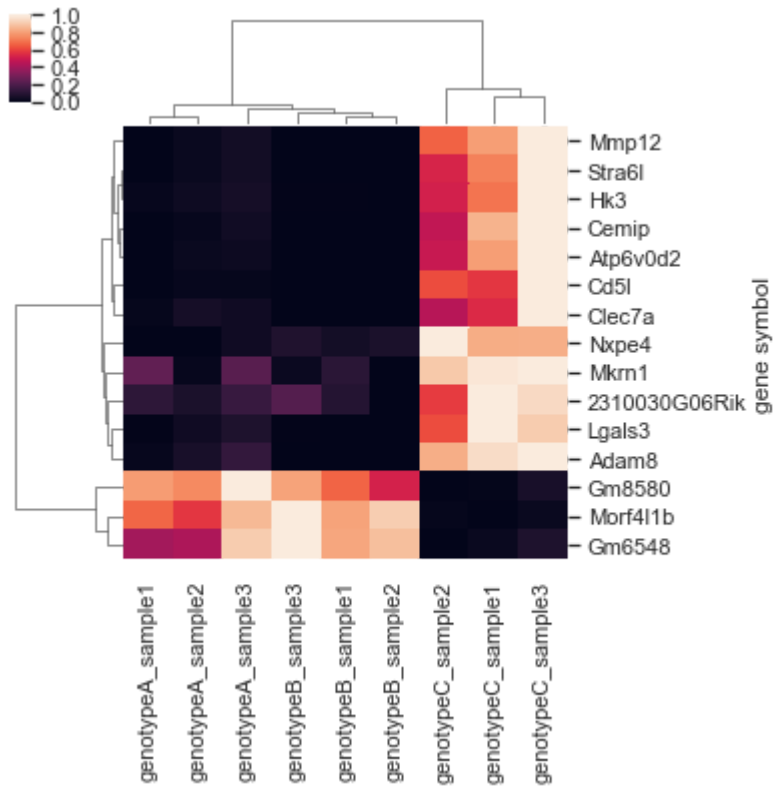
In [3]:
```python
data.head()
```

Out[3]:

gene symbol	genotypeA_sample1	genotypeA_sample2	genotypeA_sample3	genotypeB_sample1	gen
Gm8580	5.767900	5.455137	7.157003	4.900520	
Morf4l1b	109.484714	97.039848	134.512688	127.100854	
Gm6548	39.844572	40.872696	64.365084	59.735055	
Cemip	0.083976	1.620770	4.182101	0.114739	
Stra6l	0.041988	1.246746	2.193053	0.057370	

```
1  res = sns.clustermap(data, standard_scale=0, figsize=(5,5))
```

```
1  # from the doc:
2  # To access the reordered row indices, use: clustergrid.dendrogram_row.reordered
3  # Column indices, use: clustergrid.dendrogram_col.reordered_ind
4  print(res.dendrogram_row.reordered_ind)
```

```
[7, 4, 10, 3, 6, 5, 8, 13, 12, 14, 9, 11, 0, 1, 2]
```

In [6]:

```python
def extract_clustered_table(res, data):
    """
    input
    =====
    res:     <sns.matrix.ClusterGrid>  the clustermap object
    data:    <pd.DataFrame>            input table

    output
    ======
    returns: <pd.DataFrame>            reordered input table
    """

    # if sns.clustermap is run with row_cluster=False:
    if res.dendrogram_row.reordered_ind is None:
        print("Apparently, rows were not clustered.")
        return -1

    if res.dendrogram_col.reordered_ind is not None:
        # reordering index and columns
        new_cols = data.columns[res.dendrogram_col.reordered_ind]
        new_ind = data.index[res.dendrogram_row.reordered_ind]

        return data.loc[new_ind, new_cols]

    else:
        # reordering the index
        new_ind = data.index[res.dendrogram_row.reordered_ind]

        return data.loc[new_ind,:]
```

In [7]:

```python
ordered = extract_clustered_table(res, data)
```

```
1  ordered
```

Out[8]:

gene symbol	genotypeA_sample1	genotypeA_sample2	genotypeA_sample3	genotypeB_sample3
Mmp12	4.030854	27.366074	51.868253	2.077973
Stra6l	0.041988	1.246746	2.193053	0.000000
Hk3	7.179959	11.033702	15.198367	5.194933
Cemip	0.083976	1.620770	4.182101	0.074213
Atp6v0d2	1.007714	9.038908	12.240296	1.038987
Cd5l	3.568985	41.267291	34.833841	1.706907
Clec7a	6.088269	15.646662	12.750308	3.562240
Nxpe4	1.040044	1.088409	1.530037	2.077973
Mkrn1	65.249450	51.989306	63.904543	52.691467
2310030G06Rik	1.175666	0.997397	1.275031	1.558480
Lgals3	24.479041	63.958067	112.151708	21.892934
Adam8	8.691529	19.324562	34.884842	4.749653
Gm8580	5.767900	5.455137	7.157003	5.869533
Morf4l1b	109.484714	97.039848	134.512688	151.387781
Gm6548	39.844572	40.872696	64.365084	68.343802

In [ ]:

```
1
```