In [3]:
```
# This tells matplotlib not to try opening a new window for each plot.
%matplotlib inline

import pandas as pd
import urllib.request
import numpy as np
import matplotlib as plt
from IPython.display import display

from IPython.core.interactiveshell import InteractiveShell
InteractiveShell.ast_node_interactivity = "all"
```

In [4]:
```
print('Loading merged data ...')
mutations_raw = pd.read_csv("pancancer_mutations_merged.csv",
                        usecols=['cancer_type', 'bcr_patient_barcode', 'Hugo_Symbol', 'BIO
TYPE'])
print("done.")
print("Mutations count", mutations_raw['bcr_patient_barcode'].count())
```

```
Loading merged data ...
done.
Mutations count 3570876
```

In [5]:
```
mutations_raw.head()
```

Out[5]:

	Hugo_Symbol	BIOTYPE	cancer_type	bcr_patient_barcode
0	TACC2	protein_coding	GBM	TCGA-02-0003
1	JAKMIP3	protein_coding	GBM	TCGA-02-0003
2	PANX3	protein_coding	GBM	TCGA-02-0003
3	SPI1	protein_coding	GBM	TCGA-02-0003
4	NAALAD2	protein_coding	GBM	TCGA-02-0003

In [6]:
```
mutations = mutations_raw[mutations_raw['BIOTYPE'] == 'protein_coding']
mutations_non_coding_genes = mutations_raw[mutations_raw['BIOTYPE'] != 'protein_coding']

coding_genes = list(mutations['Hugo_Symbol'].unique())
non_coding_genes = list(mutations_non_coding_genes['Hugo_Symbol'].unique())
print("Number of coding genes:", len(coding_genes))
print("Number of non-coding genes:", len(non_coding_genes))
```

```
Number of coding genes: 19209
Number of non-coding genes: 2140
```

In [7]:
```
# Show the distribution of genes across patient tumors
gene_count = mutations.groupby(['Hugo_Symbol'])['bcr_patient_barcode'].nunique().reset_ind
ex(name='count')
gene_count.columns = ['gene', 'patient_count']
gene_count = gene_count.sort_values(['patient_count', 'gene'], ascending=[0,1])
print('Genes by patient frequency')
print("  mean:", int(gene_count['patient_count'].mean()))
print("  min: ", int(gene_count['patient_count'].min()))
print("  max: ", int(gene_count['patient_count'].max()))
gene_count.head(10)

ax = gene_count['patient_count'].hist(bins=200, figsize=(12,4))
ax.set_xlabel("Number of Genes")
ax.set_ylabel("Number of Patient Tumors (gene is present in)")
```

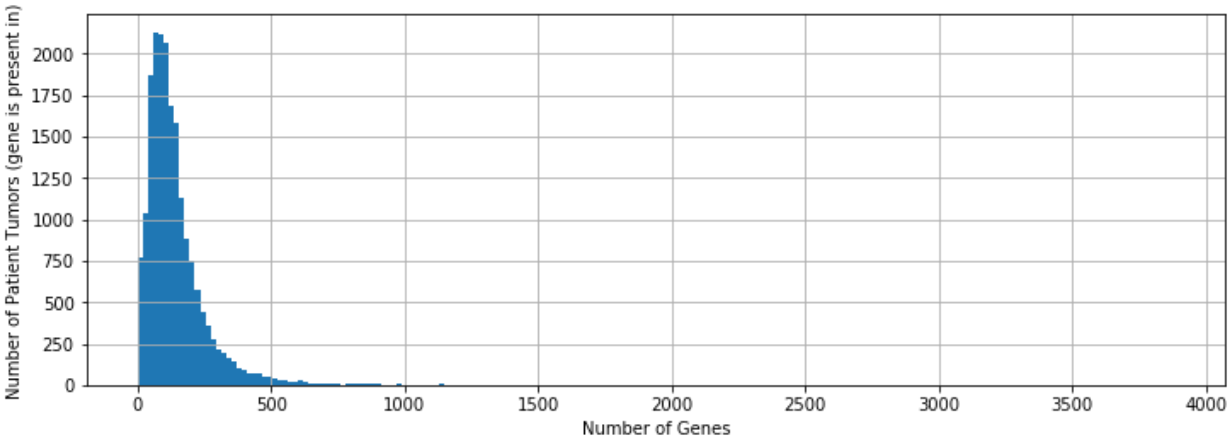
```
Genes by patient frequency
  mean: 141
  min:  1
  max:  3879
```

Out[7]:

	gene	patient_count
17222	TP53	3879
17606	TTN	3781
10315	MUC16	2415
3983	CSMD3	1610
14415	RYR2	1594
16203	SYNE1	1538
9210	LRP1B	1514
12362	PIK3CA	1428
6089	FLG	1399
17924	USH2A	1378

Out[7]: `Text(0.5, 0, 'Number of Genes')`

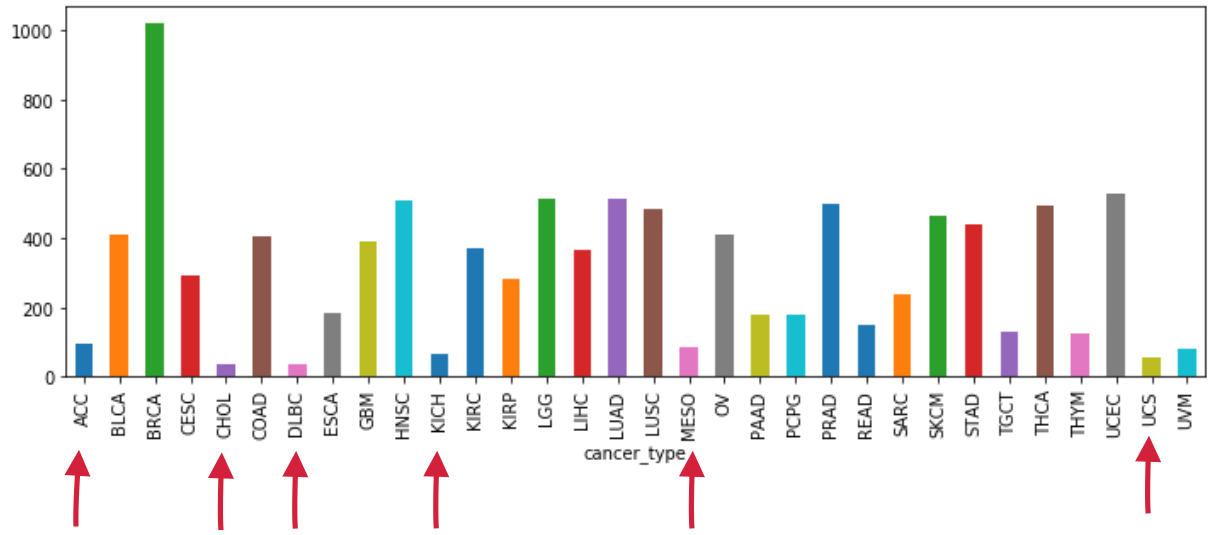
Out[7]: `Text(0, 0.5, 'Number of Patient Tumors (gene is present in)')`



In [8]:
```
# Print out the number of cancer types that are present in the
# mutations dataset
cancer_types = mutations['cancer_type'].unique()
print("\nNumber of cancer types", len(cancer_types))
print(np.sort(cancer_types))

# Get number of cases per cancer type
group_patients_by_cancer = mutations.groupby(['cancer_type'])['bcr_patient_barcode'].nuniq
ue()
print("\nNumber of patients", group_patients_by_cancer.sum())
group_patients_by_cancer.plot.bar(figsize=(12,4))
```

```
Number of cancer types 32
['ACC' 'BLCA' 'BRCA' 'CESC' 'CHOL' 'COAD' 'DLBC' 'ESCA' 'GBM' 'HNSC'
 'KICH' 'KIRC' 'KIRP' 'LGG' 'LIHC' 'LUAD' 'LUSC' 'MESO' 'OV' 'PAAD' 'PCPG'
 'PRAD' 'READ' 'SARC' 'SKCM' 'STAD' 'TGCT' 'THCA' 'THYM' 'UCEC' 'UCS'
 'UVM']

Number of patients 10008
```

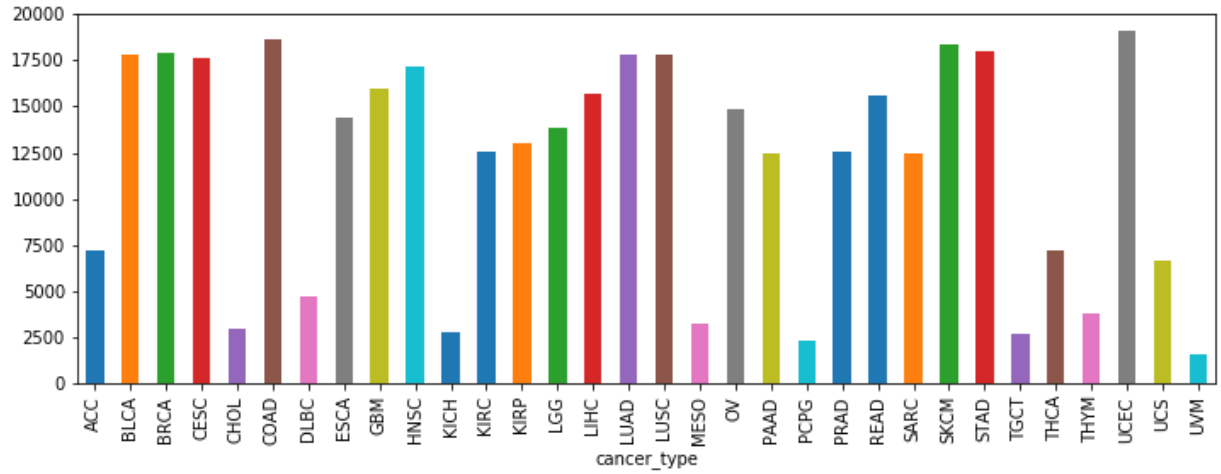
Out[8]: <matplotlib.axes._subplots.AxesSubplot at 0x11255f710>



In [9]:
```
# Get the unique genes per cancer type
group_genes_by_cancer = mutations.groupby(['cancer_type'])['Hugo_Symbol'].nunique();
group_genes_by_cancer.plot.bar(figsize=(12,4))
print("Mean number of genes represented for each cancer type:", int(np.round(group_genes_b
y_cancer.mean())))
print("Min number of genes represented for each cancer type:", int(np.round(group_genes_by
_cancer.min())))
print("Max number of genes represented for each cancer type:", int(np.round(group_genes_by
_cancer.max())))
```

Out[9]: <matplotlib.axes._subplots.AxesSubplot at 0x11f8da748>

```
Mean number of genes represented for each cancer type: 11831
Min number of genes represented for each cancer type: 1606
Max number of genes represented for each cancer type: 19090
```



In [72]:
```
# Write out a matrix; each row is a patient tumor; each column is a gene
def saveFeatureMatrix(mutations, feature_genes, gene_count):
    cases = list()
    grouped = mutations.groupby('bcr_patient_barcode')
    i = int(0)

    cols = ['case_id', 'cancer_type']
    for gene in feature_genes:
        cols.append(gene)


    for name, group in grouped:
        case = list()
        case.append(name)
        for cc in group.cancer_type.head(1):
            case.append(cc)

        for gene_flag  in feature_genes.isin(group.Hugo_Symbol.unique()):
            switch = 0
            if gene_flag == True:
                switch = 1
            case.append(switch)
        cases.append(case)


    cases_df = pd.DataFrame(cases)
    cases_df.columns = cols
    print("  number of rows in full dataset", cases_df.case_id.count())

    # Write out transformed data to csv
    fileName = "pancancer_case_features_" + str(gene_count) + ".csv"
    print("  writing", fileName, "...")
    cases_df.to_csv(fileName)
    print("  done.")
```

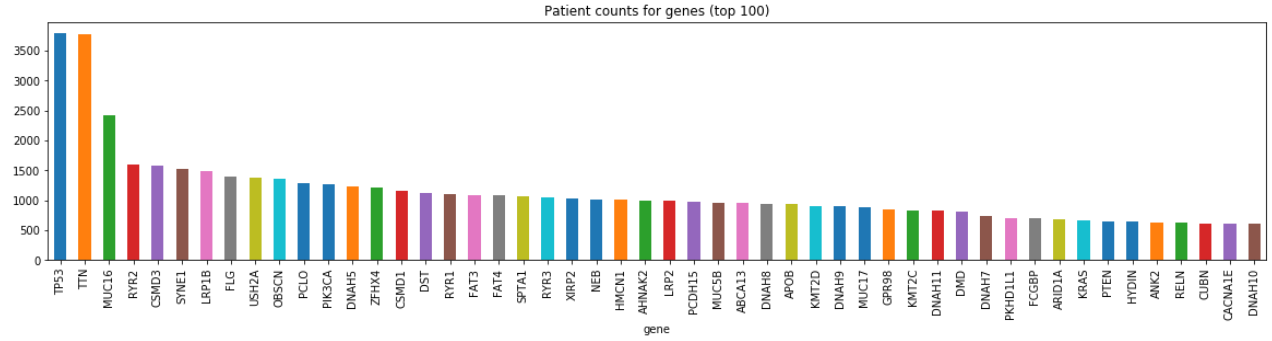
In [87]:
```
def showGenesAcrossCancerTypes(top_gene_cancer_matrix, top_n_gene_count, total_gene_count
):
    plt.rcParams["figure.figsize"] = (20,4)
    sums_by_cancer_type = top_gene_cancer_matrix.sum(axis=1, skipna=True, numeric_only=Tru
e)
    sorted = sums_by_cancer_type.sort_values(ascending=False).reindex()
    df = pd.DataFrame(sorted).reset_index()
    df.columns = ['gene', 'patient_count']
    df.reset_index()
    title = 'Patient counts for genes (top ' + str(top_n_gene_count) + ')';
    ax = df.head(50).plot.bar(x='gene', y='patient_count', legend=None, title=title)
```

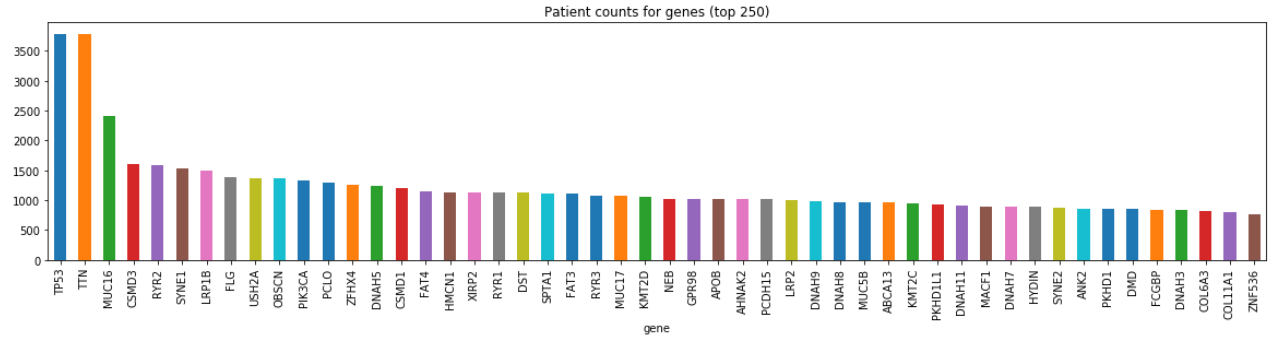
In [88]:

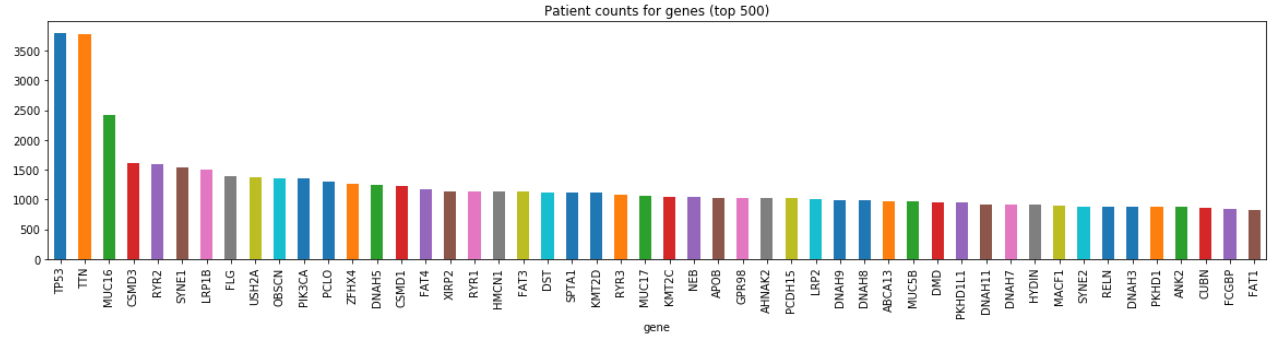
```
def createFeatureMatrix(top_n_gene_count):
    print("Formatting gene matrix with top ", top_n_gene_count, "genes from each cancer ty
pe")

    # Now try to find the most common genes per cancer type and
    # merge these together to come up with a master list
    cancer_gene_count = mutations.groupby(['cancer_type', 'Hugo_Symbol'])['bcr_patient_bar
code'].nunique().reset_index(name='count')
    cancer_gene_count.columns = ['cancer_type', 'gene', 'patient_count']



    # Now create a large matrix, row is the gene, column for each cancer type
    df = pd.DataFrame(cancer_gene_count, columns=['cancer_type', 'gene', 'patient_count'])
    gene_cancer_matrix = pd.pivot_table(df, values='patient_count', index=['gene'],
                         columns=['cancer_type'], aggfunc=np.sum, fill_value=0)


    # Now find the top n genes for each cancer type
    top_genes = []
    for cancer_type in gene_cancer_matrix.columns:
        sorted_genes = gene_cancer_matrix[cancer_type].sort_values(ascending=False)
        top_rows = sorted_genes[sorted_genes > 0].head(top_n_gene_count)
        for gene, patient_count in top_rows.items():
            top_genes.append(list([cancer_type, gene, patient_count]))


    # Turn this back into a matrix, row is gene, column for each cancer type
    top_df = pd.DataFrame(top_genes, columns=['cancer_type', 'gene', 'patient_count'])
    top_gene_cancer_matrix = pd.pivot_table(top_df, values='patient_count', index=['gene'
],
                         columns=['cancer_type'], aggfunc=np.sum, fill_value=0)
    print("  number of genes:", top_gene_cancer_matrix.shape[0])
    showGenesAcrossCancerTypes(top_gene_cancer_matrix, top_n_gene_count, top_gene_cancer_m
atrix.shape[0] )
    feature_genes = top_gene_cancer_matrix.index
    saveFeatureMatrix(mutations, feature_genes, top_n_gene_count)
```

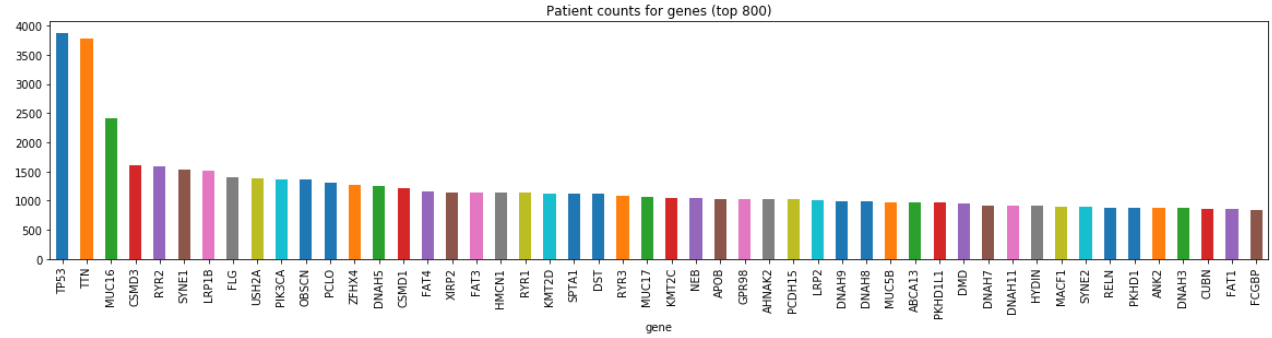
In [89]:
```
createFeatureMatrix(100)
createFeatureMatrix(250)
createFeatureMatrix(500)
createFeatureMatrix(800)
```

```
Formatting gene matrix with top  100 genes from each cancer type
  number of genes: 1063
  number of rows in full dataset 10008
  writing pancancer_case_features_100.csv ...
  done.
Formatting gene matrix with top  250 genes from each cancer type
  number of genes: 2530
  number of rows in full dataset 10008
  writing pancancer_case_features_250.csv ...
  done.
Formatting gene matrix with top  500 genes from each cancer type
  number of genes: 4778
  number of rows in full dataset 10008
  writing pancancer_case_features_500.csv ...
  done.
Formatting gene matrix with top  800 genes from each cancer type
  number of genes: 7184
  number of rows in full dataset 10008
  writing pancancer_case_features_800.csv ...
  done.
```








Patient counts for genes (top 800)
4000
3500
3000
2500
2000
1500
1000
500
0
TP53
TTN
MUC16
CSMD3
RYR2
SYNE1
LRP1B
FLG
USH2A
PIK3CA
OBSCN
PCLO
ZFHX4
DNAH5
CSMD1
FAT4
XIRP2
FAT3
HMCN1
RYR1
KMT2D
SPTA1
DST
RYR3
MUC17
KMT2C
NEB
APOB
GPR98
AHNAK2
PCDH15
LRP2
DNAH9
DNAH8
MUC5B
ABCA13
PKHD1L1
DMD
DNAH7
DNAH11
HYDIN
MACF1
SYNE2
RELN
PKHD1
ANK2
DNAH3
CUBN
FAT1
FCGBP
gene

In [ ]: