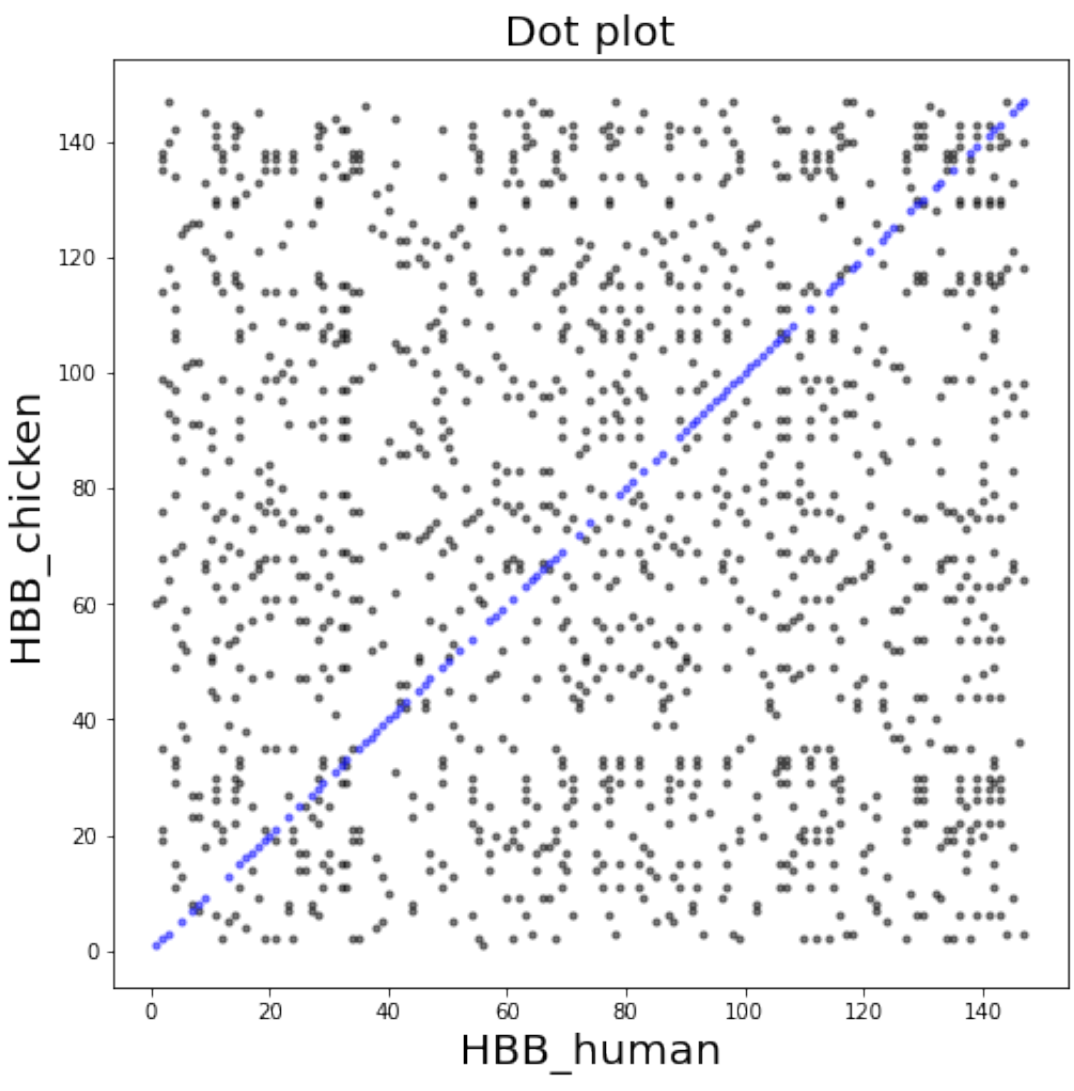
Question 1

In [4]:
```
%matplotlib inline
from DnaUtils import readFasta
import matplotlib.pyplot as plt
human = readFasta("human.fasta")[1][0]
chicken = readFasta("chicken.fasta")[1][0]
l = [(i,j) for i,h in enumerate(human, start = 1) for j,c in enumerate(chicken, start = 1) if h == c and i != j]
x,y = list(zip(*l))
plt.figure(figsize = (8,8))
plt.scatter(x,y, c = 'k', alpha = 0.5, s = 10)
l = [(i,j) for i,h in enumerate(human, start = 1) for j,c in enumerate(chicken, start = 1) if h == c and i == j]
x,y = list(zip(*l))
plt.scatter(x,y, c = 'b', alpha = 0.5, s = 10)
plt.title("Dot plot", fontsize = 20)
plt.xlabel("HBB_human", fontsize = 20)
plt.ylabel("HBB_chicken", fontsize = 20)
plt.show()
```



B)

In [2]:
```
print(f"Number of common residues = {len(x)}")
```

```
Number of common residues = 102
```

Question 2

In [3]:
```
def score(a,b):
    score = 0
    if a == b:
        score += 1
    elif '-' not in a+b:
        score -= 0
    else:
        score -= 1
    return score

def orig(s1,s2):
    from itertools import groupby
    score = 0
    for char,count in list(groupby(s1)):
        if char == '-':
            score -= 2
    for char,count in list(groupby(s2)):
        if char == '-':
            score -= 2

    return score

seq1 = "AATCTATA"
seq2 = "AAG--ATA"

print("score = ", sum([score(a,b) for a,b in zip(seq1,seq2)]) + orig(seq1,seq2))
```

```
score =  1
```

Question 3

Sequence 1 = AATCTATA
Sequence 2 = AAG--ATA

Number of matches = 5 (+5)
Number of mismatches = 3 (0)
Number of times gap was created = 1 (-2)
Length of Gaps = 2 (-2)

score = 5 + 0 - 2 - 2
score = 1

Question 4

In [4]:

```
import numpy as np
import pandas as pd
a = 'ACAGTCGAACG'
b = 'ACCGTCCG'
m = len(a)
n = len(b)
subs = lambda a,b : 2 if a == b else -1
table = [[0 for i in range(m+1)] for j in range(n+1)]
table[0] = [i * -2 for i in range(m+1)]
for j in range(n+1):
    table[j][0] = -2*j
for i in range(1,n+1):
    for j in range(1,m+1):
        table[i][j] = max(table[i-1][j-1] + subs(a[j-1],b[i-1]), table[i][j-1] - 2, table[i-1][j] - 2)
df = pd.DataFrame(np.matrix(table))
df.columns = ['-'] + [char for char in a]
df = df.T
df.columns = ['-'] + [char for char in b]
df.T
```

Out[4]:

	-	A	C	A	G	T	C	G	A	A	C	G
-	0	-2	-4	-6	-8	-10	-12	-14	-16	-18	-20	-22
A	-2	2	0	-2	-4	-6	-8	-10	-12	-14	-16	-18
C	-4	0	4	2	0	-2	-4	-6	-8	-10	-12	-14
C	-6	-2	2	3	1	-1	0	-2	-4	-6	-8	-10
G	-8	-4	0	1	5	3	1	2	0	-2	-4	-6
T	-10	-6	-2	-1	3	7	5	3	1	-1	-3	-5
C	-12	-8	-4	-3	1	5	9	7	5	3	1	-1
C	-14	-10	-6	-5	-1	3	7	8	6	4	5	3
G	-16	-12	-8	-7	-3	1	5	9	7	5	3	7

Question 5

	-	A	C	A	G	T	C	G	A	A	C	G
-	0	-2	-4	-6	-8	-10	-12	-14	-16	-18	-20	-22
A	-2	2	0	-2	-4	-6	-8	-10	-12	-14	-16	-18
C	-4	0	4	2	0	-2	-4	-6	-8	-10	-12	-14
C	-6	-2	2	3	1	-1	0	-2	-4	-6	-8	-10
G	-8	-4	0	1	5	3	1	2	0	-2	-4	-6
T	-10	-6	-2	-1	3	7	5	3	1	-1	-3	-5
C	-12	-8	-4	-3	1	5	9	7	5	3	1	-1
C	-14	-10	-6	-5	-1	3	7	8	6	4	5	3
G	-16	-12	-8	-7	-3	1	5	9	7	5	3	7