```python
#!/usr/bin/env python
# -*- coding: utf-8 -*-

import sys
from Bio import SeqIO

fasta_file = sys.argv[1]   # Input fasta file
wanted_file = sys.argv[2]  # Input wanted file, one gene name per line
result_file = sys.argv[3]  # Output fasta file

wanted = set()
with open(wanted_file) as f:
    for line in f:
        line = line.strip()
        if line != "":
            wanted.add(line)

fasta_sequences = SeqIO.parse(open(fasta_file),'fasta')

print(type(fasta_sequences))

with open(result_file, "w") as f:
    for s in fasta_sequences:
        name = s.id
        if name in wanted and len(s.seq.tostring()) > 0:
            wanted.remove(name) # Output only the first appearance for a name
            SeqIO.write([s], f, "fasta")
```