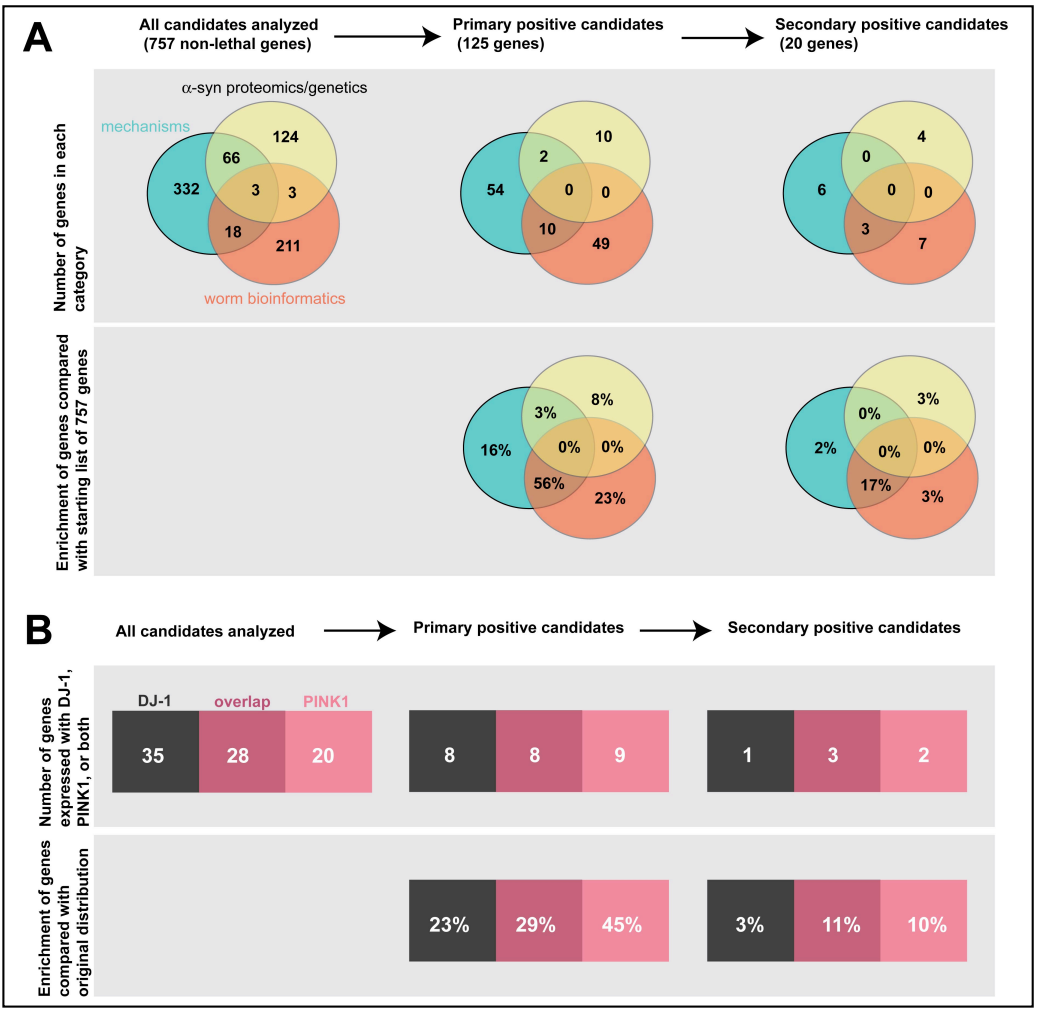
A
All candidates analyzed (757 non-lethal genes)
Primary positive candidates (125 genes)
Secondary positive candidates (20 genes)
α-syn proteomics/genetics
mechanisms
worm bioinformatics
Number of genes in each category
332
66
124
3
3
18
211
54
2
10
0
0
10
49
6
0
4
0
0
3
7
Enrichment of genes compared with starting list of 757 genes
16%
3%
8%
0%
0%
56%
23%
2%
0%
3%
0%
0%
17%
3%
B
All candidates analyzed
Primary positive candidates
Secondary positive candidates
Number of genes expressed with DJ-1, PINK1, or both
DJ-1
overlap
PINK1
35
28
20
8
8
9
1
3
2
Enrichment of genes compared with original distribution
23%
29%
45%
3%
11%
10%