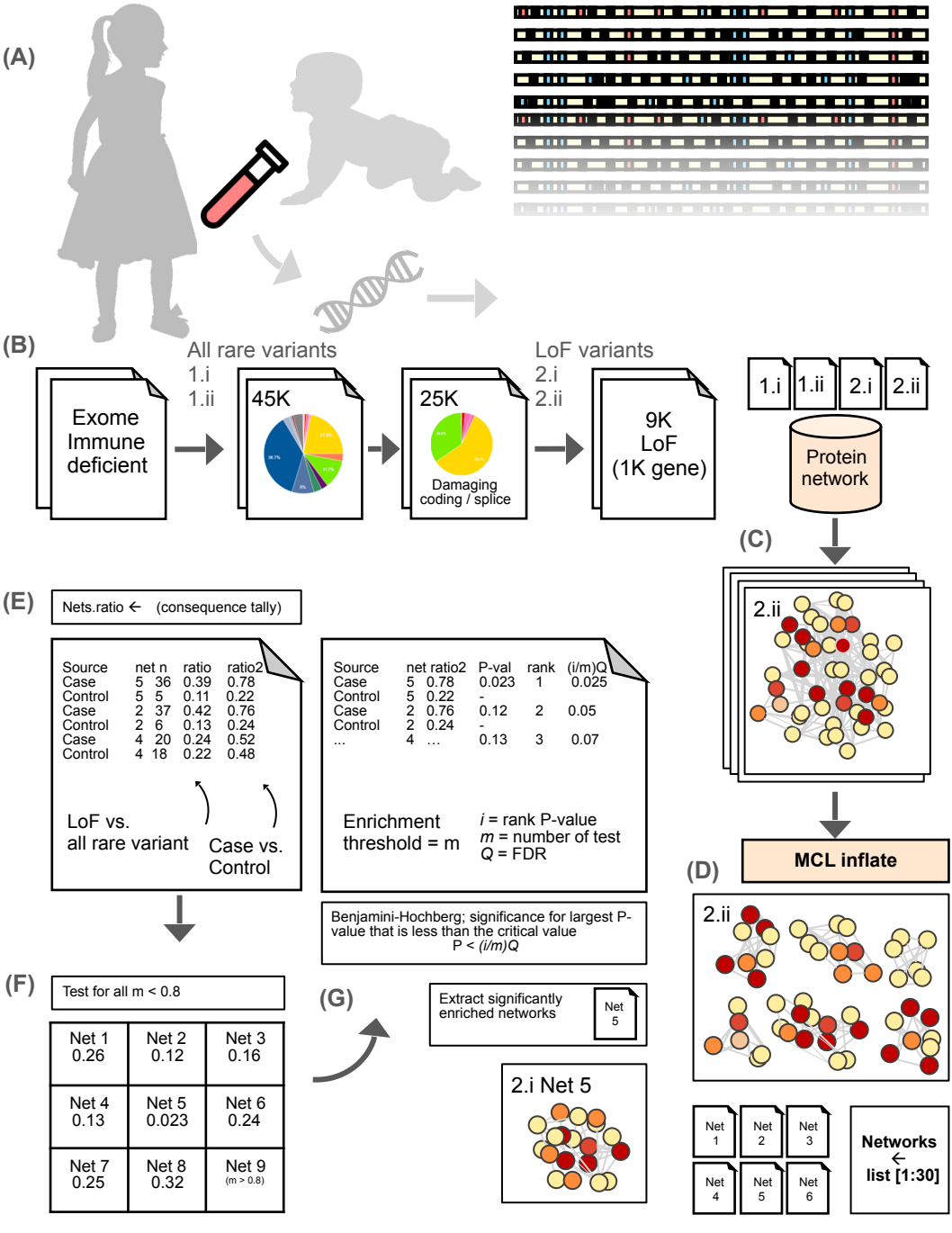
(A)
(B)
All rare variants
1.i
1.ii
LoF variants
2.i
2.ii
Exome
Immune
deficient
45K
25K
Damaging
coding / splice
9K
LoF
(1K gene)
1.i
1.ii
2.i
2.ii
Protein
network
(C)
2.ii
MCL inflate
(D)
2.ii
(E)
Nets.ratio ← (consequence tally)
Source net n ratio ratio2
Case 5 36 0.39 0.78
Control 5 5 0.11 0.22
Case 2 37 0.42 0.76
Control 2 6 0.13 0.24
Case 4 20 0.24 0.52
Control 4 18 0.22 0.48
LoF vs.
all rare variant
Case vs.
Control
Source net ratio2 P-val rank (i/m)Q
Case 5 0.78 0.023 1 0.025
Control 5 0.22 -
Case 2 0.76 0.12 2 0.05
Control 2 0.24 -
... 4 … 0.13 3 0.07
Enrichment
threshold = m
i = rank P-value
m = number of test
Q = FDR
Benjamini-Hochberg; significance for largest P-value that is less than the critical value
P < (i/m)Q
(F)
Test for all m < 0.8
Net 1 0.26
Net 2 0.12
Net 3 0.16
Net 4 0.13
Net 5 0.023
Net 6 0.24
Net 7 0.25
Net 8 0.32
Net 9 (m > 0.8)
(G)
Extract significantly enriched networks
Net 5
2.i Net 5
Net 1
Net 2
Net 3
Net 4
Net 5
Net 6
Networks ← list [1:30]