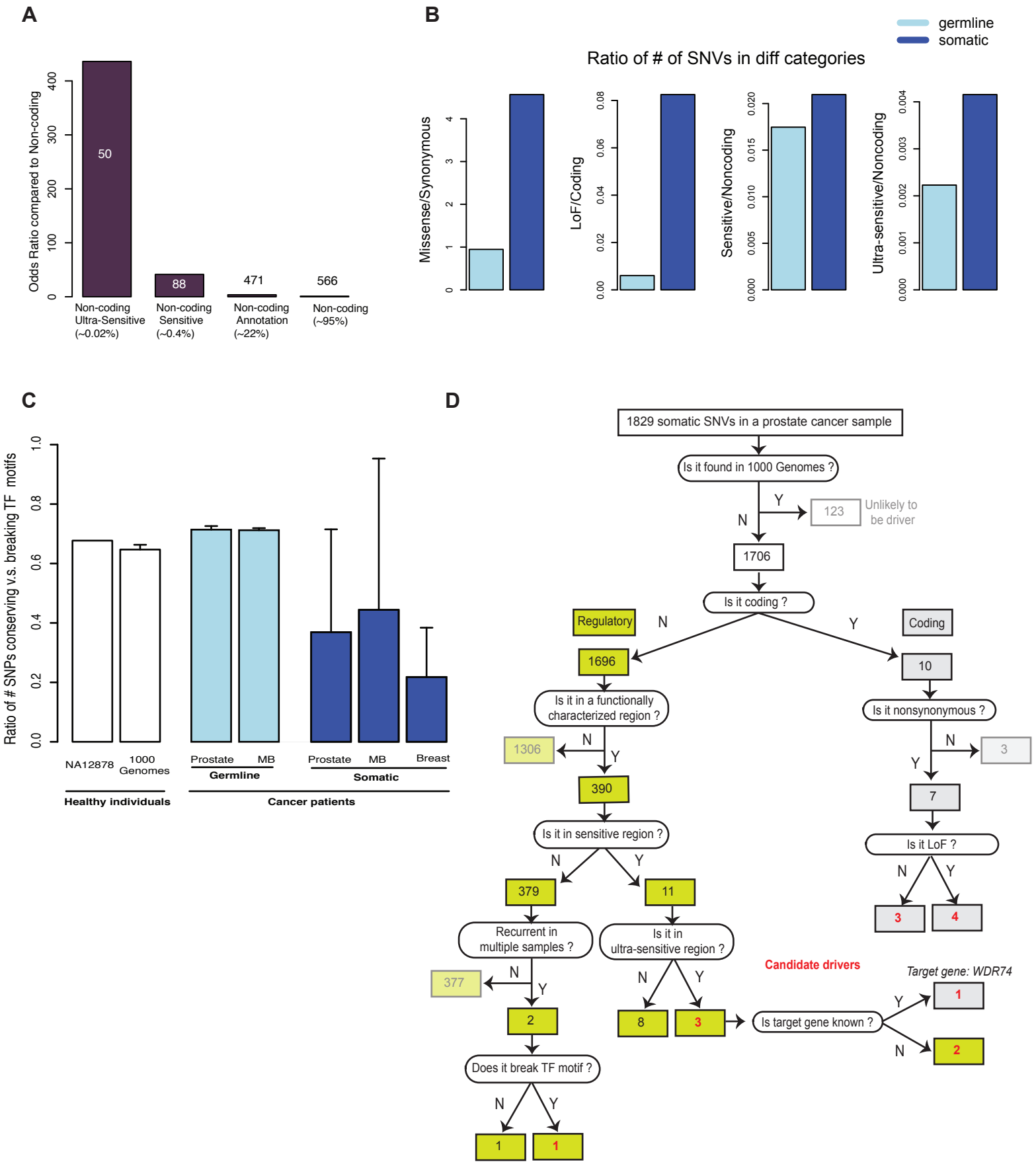
A
Odds Ratio compared to Non-coding
0
100
200
300
400
50
88
471
566
Non-coding Ultra-Sensitive (~0.02%)
Non-coding Sensitive (~0.4%)
Non-coding Annotation (~22%)
Non-coding (~95%)
B
germline
somatic
Ratio of # of SNVs in diff categories
Missense/Synonymous
LoF/Coding
Sensitive/Noncoding
Ultra-sensitive/Noncoding
C
Ratio of # SNPs conserving v.s. breaking TF motifs
0.0
0.2
0.4
0.6
0.8
1.0
NA12878
1000 Genomes
Prostate
MB
Germline
Prostate
MB
Breast
Somatic
Healthy individuals
Cancer patients
D
1829 somatic SNVs in a prostate cancer sample
Is it found in 1000 Genomes ?
Y
123
Unlikely to be driver
N
1706
Is it coding ?
Regulatory
N
Y
Coding
1696
10
Is it in a functionally characterized region ?
Is it nonsynonymous ?
N
1306
Y
N
3
Y
390
7
Is it in sensitive region ?
Is it LoF ?
N
Y
N
Y
379
11
3
4
Recurrent in multiple samples ?
Is it in ultra-sensitive region ?
Candidate drivers
Target gene: WDR74
N
377
Y
N
Y
Y
1
2
8
3
Is target gene known ?
N
2
Does it break TF motif ?
N
Y
1
1