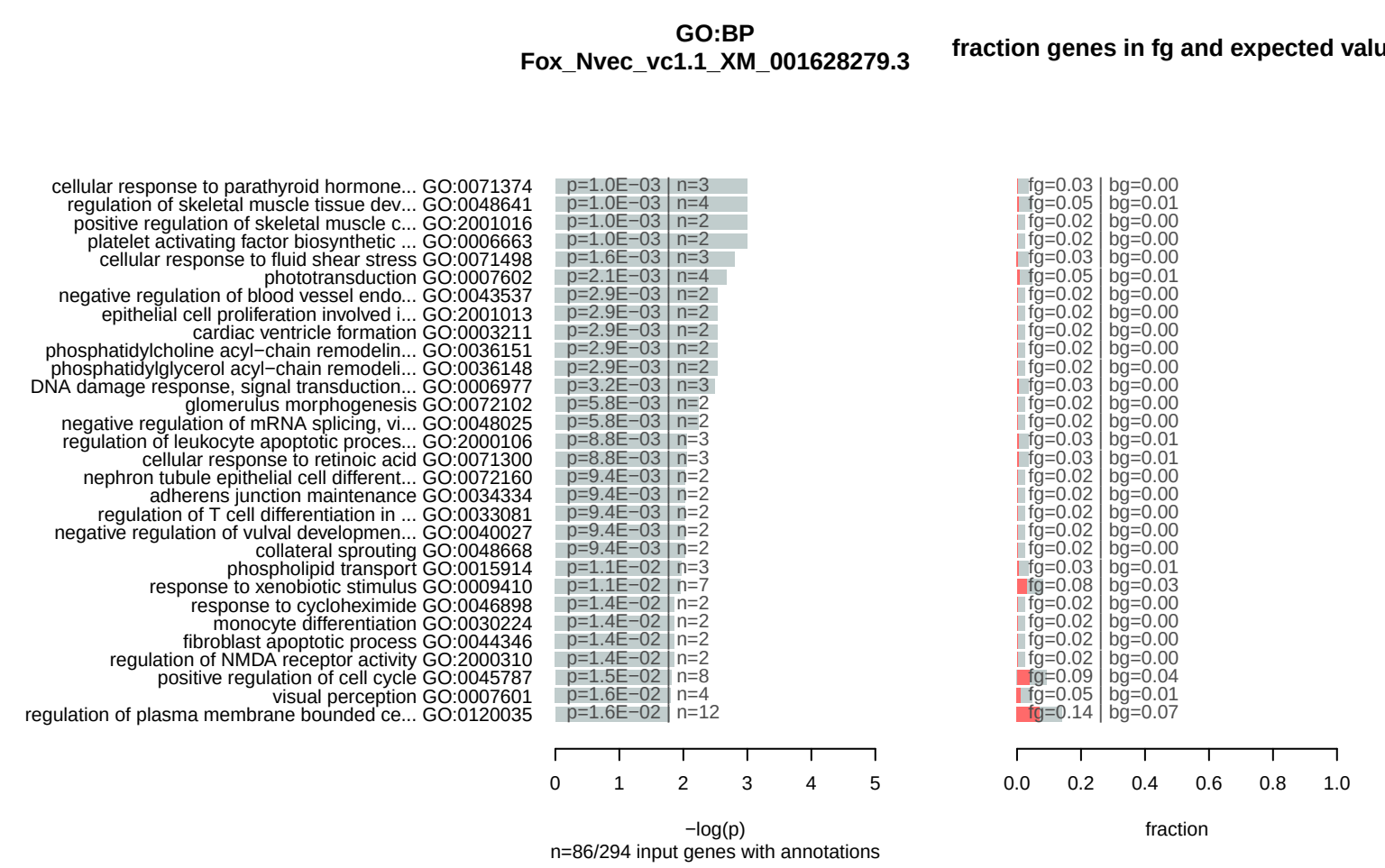
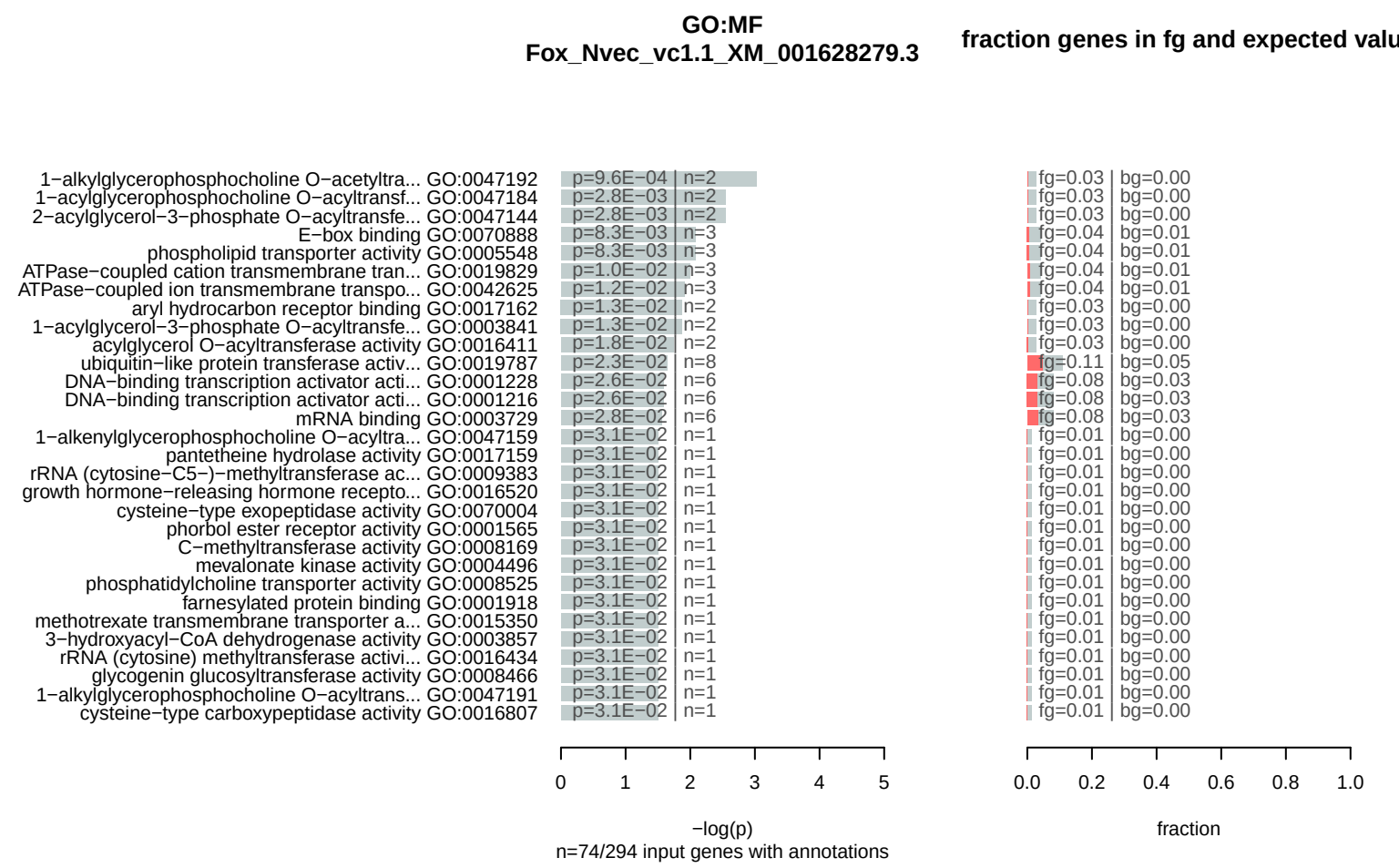
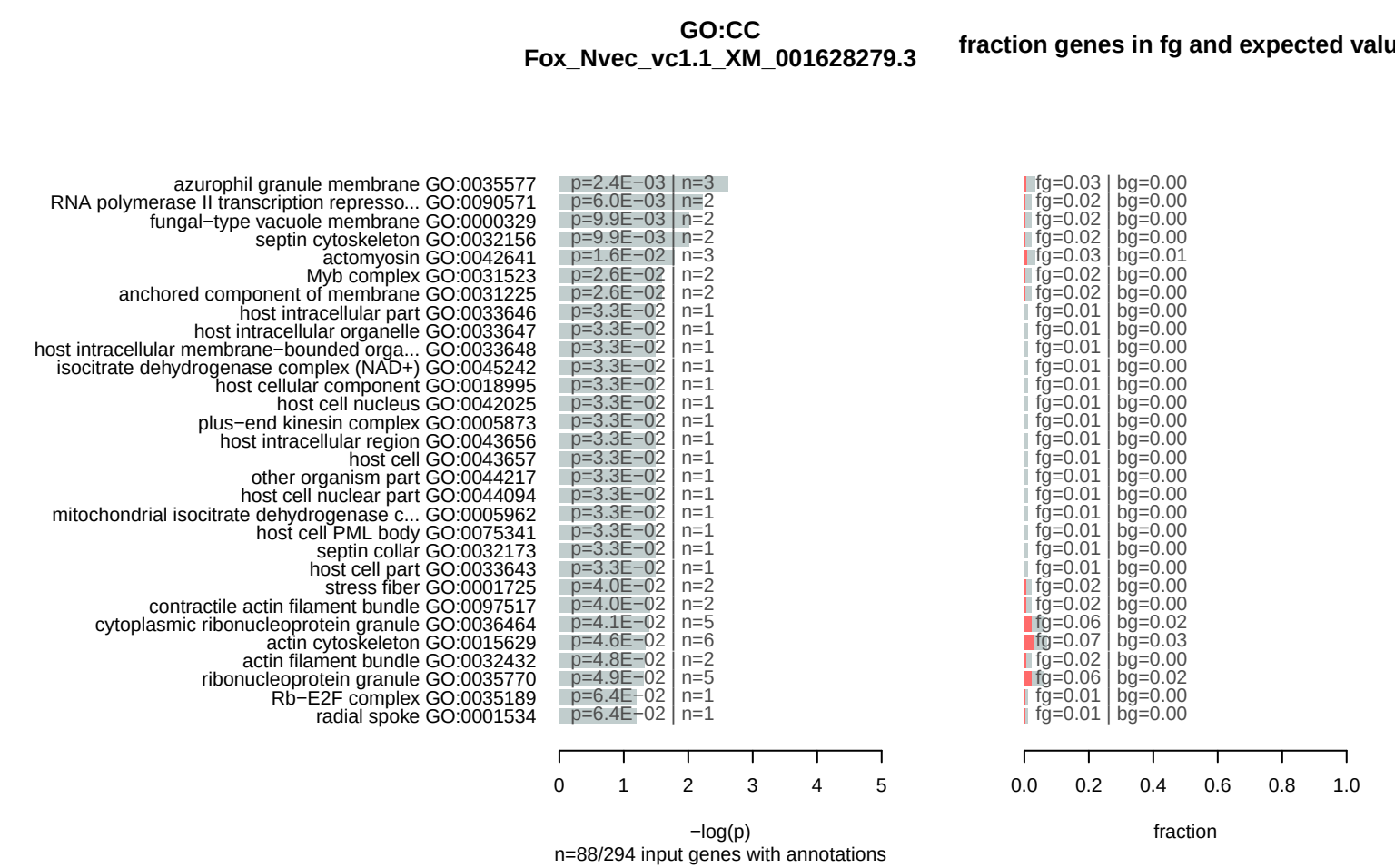

GO:BP
Fox_Nvec_vc1.1_XM_001628279.3
fraction genes in fg and expected valu
cellular response to parathyroid hormone... GO:0071374 p=1.0E−03 n=3 fg=0.03 bg=0.00
regulation of skeletal muscle tissue dev... GO:0048641 p=1.0E−03 n=4 fg=0.05 bg=0.01
positive regulation of skeletal muscle c... GO:2001016 p=1.0E−03 n=2 fg=0.02 bg=0.00
platelet activating factor biosynthetic ... GO:0006663 p=1.0E−03 n=2 fg=0.02 bg=0.00
cellular response to fluid shear stress GO:0071498 p=1.6E−03 n=3 fg=0.03 bg=0.00
phototransduction GO:0007602 p=2.1E−03 n=4 fg=0.05 bg=0.01
negative regulation of blood vessel endo... GO:0043537 p=2.9E−03 n=2 fg=0.02 bg=0.00
epithelial cell proliferation involved i... GO:2001013 p=2.9E−03 n=2 fg=0.02 bg=0.00
cardiac ventricle formation GO:0003211 p=2.9E−03 n=2 fg=0.02 bg=0.00
phosphatidylcholine acyl−chain remodelin... GO:0036151 p=2.9E−03 n=2 fg=0.02 bg=0.00
phosphatidylglycerol acyl−chain remodeli... GO:0036148 p=2.9E−03 n=2 fg=0.02 bg=0.00
DNA damage response, signal transduction... GO:0006977 p=3.2E−03 n=3 fg=0.03 bg=0.00
glomerulus morphogenesis GO:0072102 p=5.8E−03 n=2 fg=0.02 bg=0.00
negative regulation of mRNA splicing, vi... GO:0048025 p=5.8E−03 n=2 fg=0.02 bg=0.00
regulation of leukocyte apoptotic proces... GO:2000106 p=8.8E−03 n=3 fg=0.03 bg=0.01
cellular response to retinoic acid GO:0071300 p=8.8E−03 n=3 fg=0.03 bg=0.01
nephron tubule epithelial cell different... GO:0072160 p=9.4E−03 n=2 fg=0.02 bg=0.00
adherens junction maintenance GO:0034334 p=9.4E−03 n=2 fg=0.02 bg=0.00
regulation of T cell differentiation in ... GO:0033081 p=9.4E−03 n=2 fg=0.02 bg=0.00
negative regulation of vulval developmen... GO:0040027 p=9.4E−03 n=2 fg=0.02 bg=0.00
collateral sprouting GO:0048668 p=9.4E−03 n=2 fg=0.02 bg=0.00
phospholipid transport GO:0015914 p=1.1E−02 n=3 fg=0.03 bg=0.01
response to xenobiotic stimulus GO:0009410 p=1.1E−02 n=7 fg=0.08 bg=0.03
response to cycloheximide GO:0046898 p=1.4E−02 n=2 fg=0.02 bg=0.00
monocyte differentiation GO:0030224 p=1.4E−02 n=2 fg=0.02 bg=0.00
fibroblast apoptotic process GO:0044346 p=1.4E−02 n=2 fg=0.02 bg=0.00
regulation of NMDA receptor activity GO:2000310 p=1.4E−02 n=2 fg=0.02 bg=0.00
positive regulation of cell cycle GO:0045787 p=1.5E−02 n=8 fg=0.09 bg=0.04
visual perception GO:0007601 p=1.6E−02 n=4 fg=0.05 bg=0.01
regulation of plasma membrane bounded ce... GO:0120035 p=1.6E−02 n=12 fg=0.14 bg=0.07
0 1 2 3 4 5
−log(p)
n=86/294 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction


GO:MF
Fox_Nvec_vc1.1_XM_001628279.3
fraction genes in fg and expected valu
1−alkylglycerophosphocholine O−acetyltra... GO:0047192 p=9.6E−04 n=2 fg=0.03 bg=0.00
1−acylglycerophosphocholine O−acyltransf... GO:0047184 p=2.8E−03 n=2 fg=0.03 bg=0.00
2−acylglycerol−3−phosphate O−acyltransfe... GO:0047144 p=2.8E−03 n=2 fg=0.03 bg=0.00
E−box binding GO:0070888 p=8.3E−03 n=3 fg=0.04 bg=0.01
phospholipid transporter activity GO:0005548 p=8.3E−03 n=3 fg=0.04 bg=0.01
ATPase−coupled cation transmembrane tran... GO:0019829 p=1.0E−02 n=3 fg=0.04 bg=0.01
ATPase−coupled ion transmembrane transpo... GO:0042625 p=1.2E−02 n=3 fg=0.04 bg=0.01
aryl hydrocarbon receptor binding GO:0017162 p=1.3E−02 n=2 fg=0.03 bg=0.00
1−acylglycerol−3−phosphate O−acyltransfe... GO:0003841 p=1.3E−02 n=2 fg=0.03 bg=0.00
acylglycerol O−acyltransferase activity GO:0016411 p=1.8E−02 n=2 fg=0.03 bg=0.00
ubiquitin−like protein transferase activ... GO:0019787 p=2.3E−02 n=8 fg=0.11 bg=0.05
DNA−binding transcription activator acti... GO:0001228 p=2.6E−02 n=6 fg=0.08 bg=0.03
DNA−binding transcription activator acti... GO:0001216 p=2.6E−02 n=6 fg=0.08 bg=0.03
mRNA binding GO:0003729 p=2.8E−02 n=6 fg=0.08 bg=0.03
1−alkenylglycerophosphocholine O−acyltra... GO:0047159 p=3.1E−02 n=1 fg=0.01 bg=0.00
pantetheine hydrolase activity GO:0017159 p=3.1E−02 n=1 fg=0.01 bg=0.00
rRNA (cytosine−C5−)−methyltransferase ac... GO:0009383 p=3.1E−02 n=1 fg=0.01 bg=0.00
growth hormone−releasing hormone recepto... GO:0016520 p=3.1E−02 n=1 fg=0.01 bg=0.00
cysteine−type exopeptidase activity GO:0070004 p=3.1E−02 n=1 fg=0.01 bg=0.00
phorbol ester receptor activity GO:0001565 p=3.1E−02 n=1 fg=0.01 bg=0.00
C−methyltransferase activity GO:0008169 p=3.1E−02 n=1 fg=0.01 bg=0.00
mevalonate kinase activity GO:0004496 p=3.1E−02 n=1 fg=0.01 bg=0.00
phosphatidylcholine transporter activity GO:0008525 p=3.1E−02 n=1 fg=0.01 bg=0.00
farnesylated protein binding GO:0001918 p=3.1E−02 n=1 fg=0.01 bg=0.00
methotrexate transmembrane transporter a... GO:0015350 p=3.1E−02 n=1 fg=0.01 bg=0.00
3−hydroxyacyl−CoA dehydrogenase activity GO:0003857 p=3.1E−02 n=1 fg=0.01 bg=0.00
rRNA (cytosine) methyltransferase activi... GO:0016434 p=3.1E−02 n=1 fg=0.01 bg=0.00
glycogenin glucosyltransferase activity GO:0008466 p=3.1E−02 n=1 fg=0.01 bg=0.00
1−alkylglycerophosphocholine O−acyltrans... GO:0047191 p=3.1E−02 n=1 fg=0.01 bg=0.00
cysteine−type carboxypeptidase activity GO:0016807 p=3.1E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=74/294 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction


GO:CC
Fox_Nvec_vc1.1_XM_001628279.3
fraction genes in fg and expected valu
azurophil granule membrane GO:0035577 p=2.4E−03 n=3 fg=0.03 bg=0.00
RNA polymerase II transcription represso... GO:0090571 p=6.0E−03 n=2 fg=0.02 bg=0.00
fungal−type vacuole membrane GO:0000329 p=9.9E−03 n=2 fg=0.02 bg=0.00
septin cytoskeleton GO:0032156 p=9.9E−03 n=2 fg=0.02 bg=0.00
actomyosin GO:0042641 p=1.6E−02 n=3 fg=0.03 bg=0.01
Myb complex GO:0031523 p=2.6E−02 n=2 fg=0.02 bg=0.00
anchored component of membrane GO:0031225 p=2.6E−02 n=2 fg=0.02 bg=0.00
host intracellular part GO:0033646 p=3.3E−02 n=1 fg=0.01 bg=0.00
host intracellular organelle GO:0033647 p=3.3E−02 n=1 fg=0.01 bg=0.00
host intracellular membrane−bounded orga... GO:0033648 p=3.3E−02 n=1 fg=0.01 bg=0.00
isocitrate dehydrogenase complex (NAD+) GO:0045242 p=3.3E−02 n=1 fg=0.01 bg=0.00
host cellular component GO:0018995 p=3.3E−02 n=1 fg=0.01 bg=0.00
host cell nucleus GO:0042025 p=3.3E−02 n=1 fg=0.01 bg=0.00
plus−end kinesin complex GO:0005873 p=3.3E−02 n=1 fg=0.01 bg=0.00
host intracellular region GO:0043656 p=3.3E−02 n=1 fg=0.01 bg=0.00
host cell GO:0043657 p=3.3E−02 n=1 fg=0.01 bg=0.00
other organism part GO:0044217 p=3.3E−02 n=1 fg=0.01 bg=0.00
host cell nuclear part GO:0044094 p=3.3E−02 n=1 fg=0.01 bg=0.00
mitochondrial isocitrate dehydrogenase c... GO:0005962 p=3.3E−02 n=1 fg=0.01 bg=0.00
host cell PML body GO:0075341 p=3.3E−02 n=1 fg=0.01 bg=0.00
septin collar GO:0032173 p=3.3E−02 n=1 fg=0.01 bg=0.00
host cell part GO:0033643 p=3.3E−02 n=1 fg=0.01 bg=0.00
stress fiber GO:0001725 p=4.0E−02 n=2 fg=0.02 bg=0.00
contractile actin filament bundle GO:0097517 p=4.0E−02 n=2 fg=0.02 bg=0.00
cytoplasmic ribonucleoprotein granule GO:0036464 p=4.1E−02 n=5 fg=0.06 bg=0.02
actin cytoskeleton GO:0015629 p=4.6E−02 n=6 fg=0.07 bg=0.03
actin filament bundle GO:0032432 p=4.8E−02 n=2 fg=0.02 bg=0.00
ribonucleoprotein granule GO:0035770 p=4.9E−02 n=5 fg=0.06 bg=0.02
Rb−E2F complex GO:0035189 p=6.4E−02 n=1 fg=0.01 bg=0.00
radial spoke GO:0001534 p=6.4E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=88/294 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction