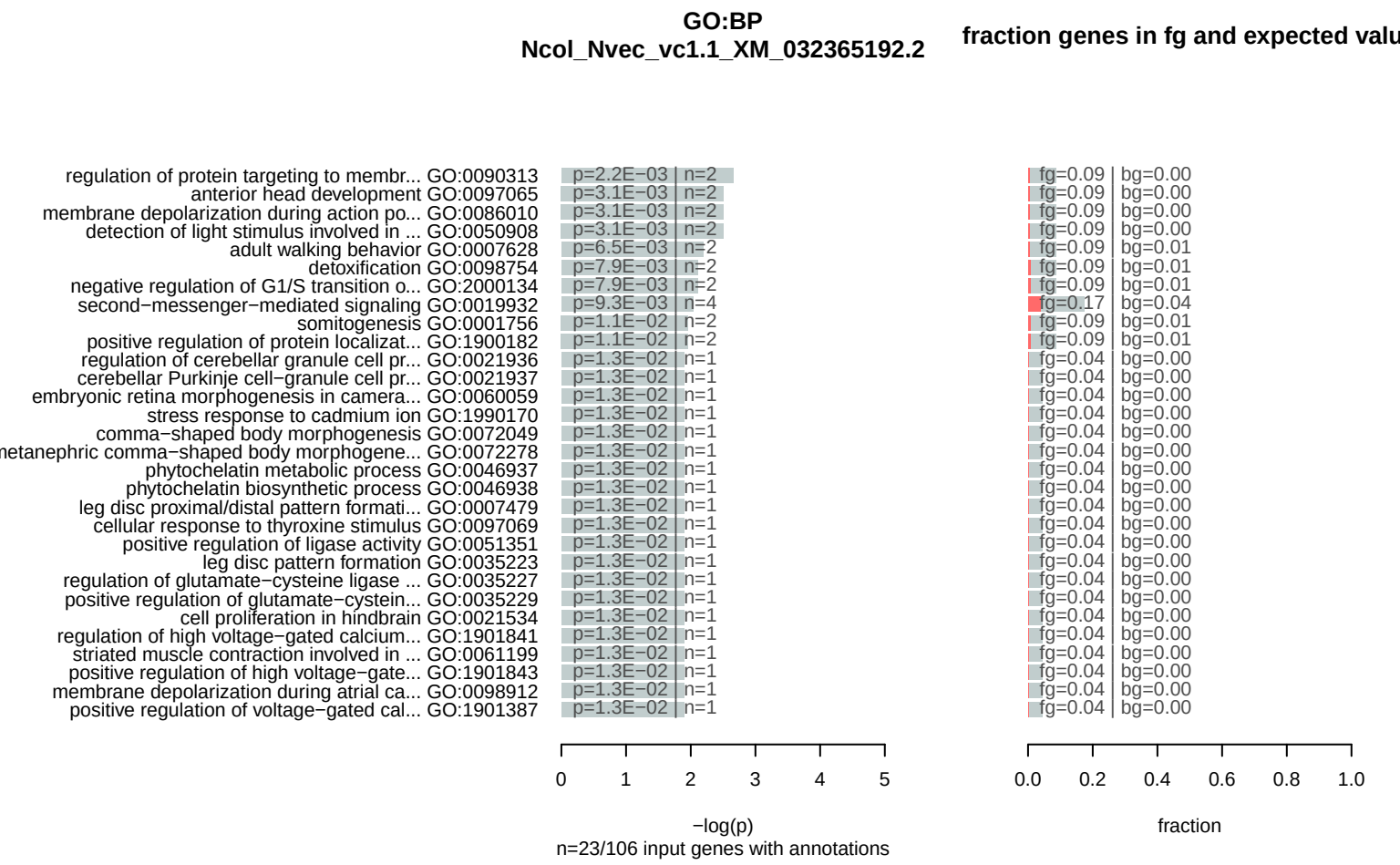
GO:BP
Ncol_Nvec_vc1.1_XM_032365192.2
fraction genes in fg and expected valu
regulation of protein targeting to membr... GO:0090313 p=2.2E−03 n=2 fg=0.09 bg=0.00
anterior head development GO:0097065 p=3.1E−03 n=2 fg=0.09 bg=0.00
membrane depolarization during action po... GO:0086010 p=3.1E−03 n=2 fg=0.09 bg=0.00
detection of light stimulus involved in ... GO:0050908 p=3.1E−03 n=2 fg=0.09 bg=0.00
adult walking behavior GO:0007628 p=6.5E−03 n=2 fg=0.09 bg=0.01
detoxification GO:0098754 p=7.9E−03 n=2 fg=0.09 bg=0.01
negative regulation of G1/S transition o... GO:2000134 p=7.9E−03 n=2 fg=0.09 bg=0.01
second−messenger−mediated signaling GO:0019932 p=9.3E−03 n=4 fg=0.17 bg=0.04
somitogenesis GO:0001756 p=1.1E−02 n=2 fg=0.09 bg=0.01
positive regulation of protein localizat... GO:1900182 p=1.1E−02 n=2 fg=0.09 bg=0.01
regulation of cerebellar granule cell pr... GO:0021936 p=1.3E−02 n=1 fg=0.04 bg=0.00
cerebellar Purkinje cell−granule cell pr... GO:0021937 p=1.3E−02 n=1 fg=0.04 bg=0.00
embryonic retina morphogenesis in camera... GO:0060059 p=1.3E−02 n=1 fg=0.04 bg=0.00
stress response to cadmium ion GO:1990170 p=1.3E−02 n=1 fg=0.04 bg=0.00
comma−shaped body morphogenesis GO:0072049 p=1.3E−02 n=1 fg=0.04 bg=0.00
metanephric comma−shaped body morphogene... GO:0072278 p=1.3E−02 n=1 fg=0.04 bg=0.00
phytochelatin metabolic process GO:0046937 p=1.3E−02 n=1 fg=0.04 bg=0.00
phytochelatin biosynthetic process GO:0046938 p=1.3E−02 n=1 fg=0.04 bg=0.00
leg disc proximal/distal pattern formati... GO:0007479 p=1.3E−02 n=1 fg=0.04 bg=0.00
cellular response to thyroxine stimulus GO:0097069 p=1.3E−02 n=1 fg=0.04 bg=0.00
positive regulation of ligase activity GO:0051351 p=1.3E−02 n=1 fg=0.04 bg=0.00
leg disc pattern formation GO:0035223 p=1.3E−02 n=1 fg=0.04 bg=0.00
regulation of glutamate−cysteine ligase ... GO:0035227 p=1.3E−02 n=1 fg=0.04 bg=0.00
positive regulation of glutamate−cystein... GO:0035229 p=1.3E−02 n=1 fg=0.04 bg=0.00
cell proliferation in hindbrain GO:0021534 p=1.3E−02 n=1 fg=0.04 bg=0.00
regulation of high voltage−gated calcium... GO:1901841 p=1.3E−02 n=1 fg=0.04 bg=0.00
striated muscle contraction involved in ... GO:0061199 p=1.3E−02 n=1 fg=0.04 bg=0.00
positive regulation of high voltage−gate... GO:1901843 p=1.3E−02 n=1 fg=0.04 bg=0.00
membrane depolarization during atrial ca... GO:0098912 p=1.3E−02 n=1 fg=0.04 bg=0.00
positive regulation of voltage−gated cal... GO:1901387 p=1.3E−02 n=1 fg=0.04 bg=0.00
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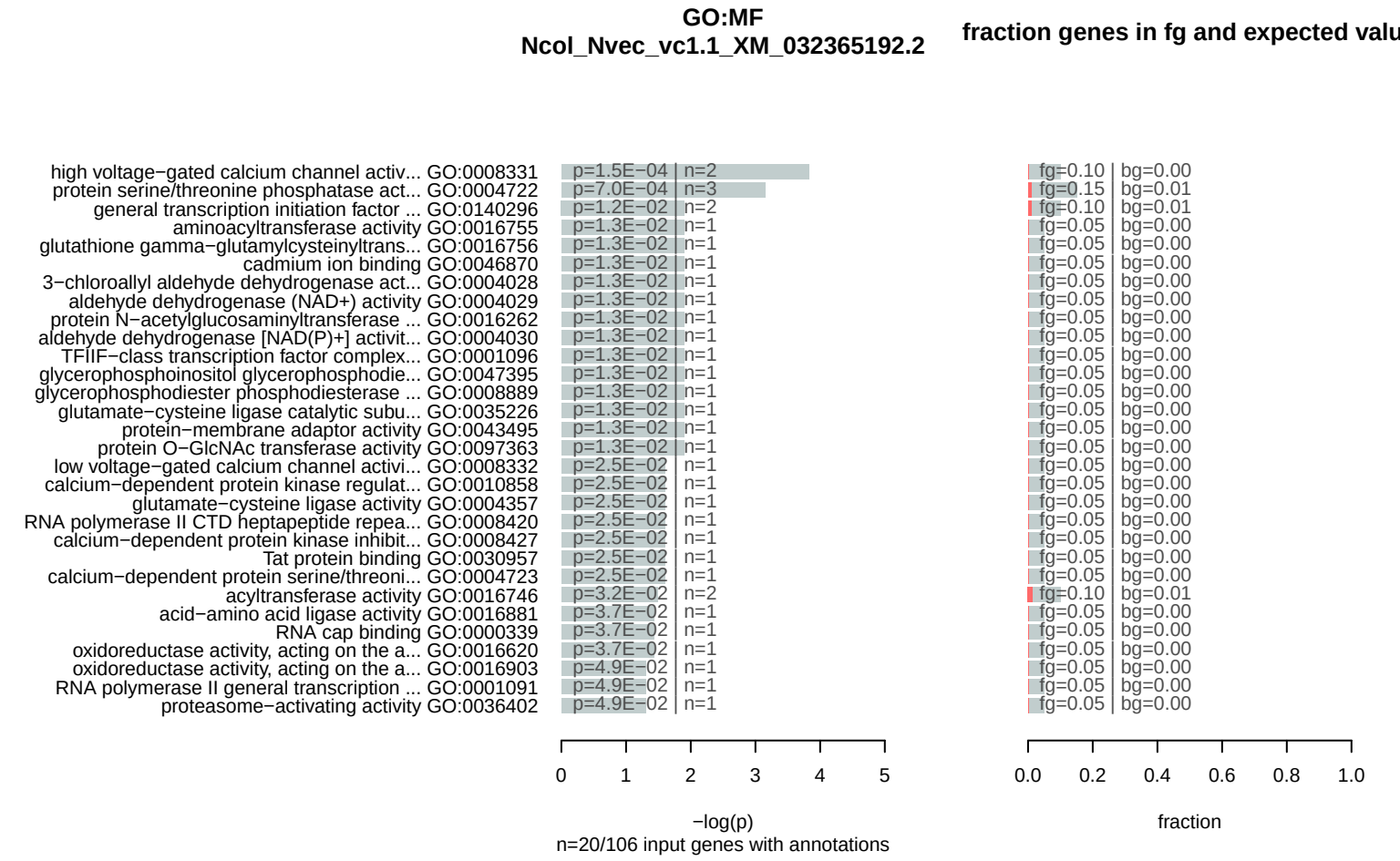
−log(p)
n=23/106 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction


GO:MF
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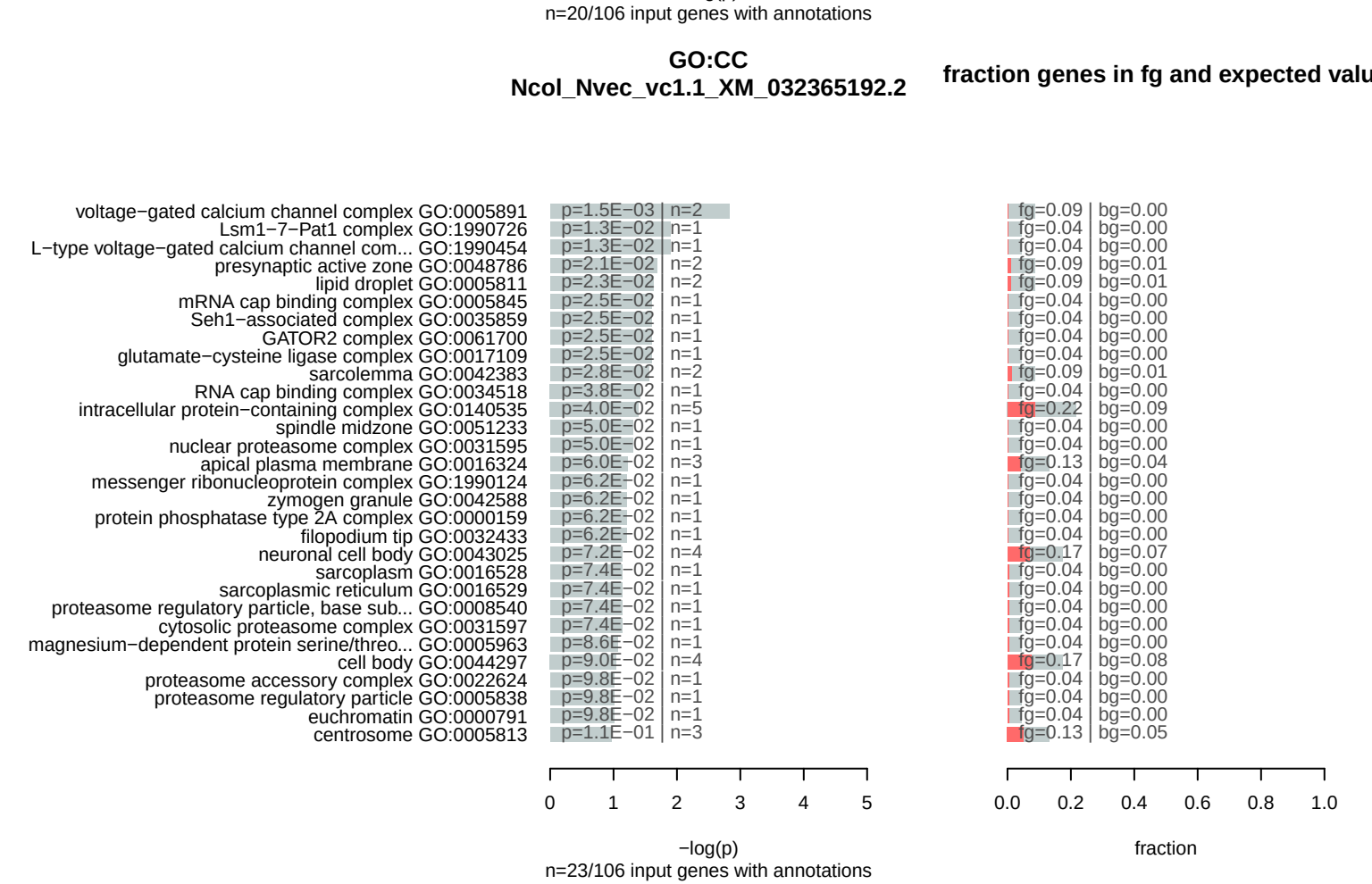
fraction genes in fg and expected valu
high voltage−gated calcium channel activ... GO:0008331 p=1.5E−04 n=2 fg=0.10 bg=0.00
protein serine/threonine phosphatase act... GO:0004722 p=7.0E−04 n=3 fg=0.15 bg=0.01
general transcription initiation factor ... GO:0140296 p=1.2E−02 n=2 fg=0.10 bg=0.01
aminoacyltransferase activity GO:0016755 p=1.3E−02 n=1 fg=0.05 bg=0.00
glutathione gamma−glutamylcysteinyltrans... GO:0016756 p=1.3E−02 n=1 fg=0.05 bg=0.00
cadmium ion binding GO:0046870 p=1.3E−02 n=1 fg=0.05 bg=0.00
3−chloroallyl aldehyde dehydrogenase act... GO:0004028 p=1.3E−02 n=1 fg=0.05 bg=0.00
aldehyde dehydrogenase (NAD+) activity GO:0004029 p=1.3E−02 n=1 fg=0.05 bg=0.00
protein N−acetylglucosaminyltransferase ... GO:0016262 p=1.3E−02 n=1 fg=0.05 bg=0.00
aldehyde dehydrogenase [NAD(P)+] activit... GO:0004030 p=1.3E−02 n=1 fg=0.05 bg=0.00
TFIIF−class transcription factor complex... GO:0001096 p=1.3E−02 n=1 fg=0.05 bg=0.00
glycerophosphoinositol glycerophosphodie... GO:0047395 p=1.3E−02 n=1 fg=0.05 bg=0.00
glycerophosphodiester phosphodiesterase ... GO:0008889 p=1.3E−02 n=1 fg=0.05 bg=0.00
glutamate−cysteine ligase catalytic subu... GO:0035226 p=1.3E−02 n=1 fg=0.05 bg=0.00
protein−membrane adaptor activity GO:0043495 p=1.3E−02 n=1 fg=0.05 bg=0.00
protein O−GlcNAc transferase activity GO:0097363 p=1.3E−02 n=1 fg=0.05 bg=0.00
low voltage−gated calcium channel activi... GO:0008332 p=2.5E−02 n=1 fg=0.05 bg=0.00
calcium−dependent protein kinase regulat... GO:0010858 p=2.5E−02 n=1 fg=0.05 bg=0.00
glutamate−cysteine ligase activity GO:0004357 p=2.5E−02 n=1 fg=0.05 bg=0.00
RNA polymerase II CTD heptapeptide repea... GO:0008420 p=2.5E−02 n=1 fg=0.05 bg=0.00
calcium−dependent protein kinase inhibit... GO:0008427 p=2.5E−02 n=1 fg=0.05 bg=0.00
Tat protein binding GO:0030957 p=2.5E−02 n=1 fg=0.05 bg=0.00
calcium−dependent protein serine/threoni... GO:0004723 p=2.5E−02 n=1 fg=0.05 bg=0.00
acyltransferase activity GO:0016746 p=3.2E−02 n=2 fg=0.10 bg=0.01
acid−amino acid ligase activity GO:0016881 p=3.7E−02 n=1 fg=0.05 bg=0.00
RNA cap binding GO:0000339 p=3.7E−02 n=1 fg=0.05 bg=0.00
oxidoreductase activity, acting on the a... GO:0016620 p=3.7E−02 n=1 fg=0.05 bg=0.00
oxidoreductase activity, acting on the a... GO:0016903 p=4.9E−02 n=1 fg=0.05 bg=0.00
RNA polymerase II general transcription ... GO:0001091 p=4.9E−02 n=1 fg=0.05 bg=0.00
proteasome−activating activity GO:0036402 p=4.9E−02 n=1 fg=0.05 bg=0.00
0 1 2 3 4 5
−log(p)
n=20/106 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction


GO:CC
Ncol_Nvec_vc1.1_XM_032365192.2
fraction genes in fg and expected valu
voltage−gated calcium channel complex GO:0005891 p=1.5E−03 n=2 fg=0.09 bg=0.00
Lsm1−7−Pat1 complex GO:1990726 p=1.3E−02 n=1 fg=0.04 bg=0.00
L−type voltage−gated calcium channel com... GO:1990454 p=1.3E−02 n=1 fg=0.04 bg=0.00
presynaptic active zone GO:0048786 p=2.1E−02 n=2 fg=0.09 bg=0.01
lipid droplet GO:0005811 p=2.3E−02 n=2 fg=0.09 bg=0.01
mRNA cap binding complex GO:0005845 p=2.5E−02 n=1 fg=0.04 bg=0.00
Seh1−associated complex GO:0035859 p=2.5E−02 n=1 fg=0.04 bg=0.00
GATOR2 complex GO:0061700 p=2.5E−02 n=1 fg=0.04 bg=0.00
glutamate−cysteine ligase complex GO:0017109 p=2.5E−02 n=1 fg=0.04 bg=0.00
sarcolemma GO:0042383 p=2.8E−02 n=2 fg=0.09 bg=0.01
RNA cap binding complex GO:0034518 p=3.8E−02 n=1 fg=0.04 bg=0.00
intracellular protein−containing complex GO:0140535 p=4.0E−02 n=5 fg=0.22 bg=0.09
spindle midzone GO:0051233 p=5.0E−02 n=1 fg=0.04 bg=0.00
nuclear proteasome complex GO:0031595 p=5.0E−02 n=1 fg=0.04 bg=0.00
apical plasma membrane GO:0016324 p=6.0E−02 n=3 fg=0.13 bg=0.04
messenger ribonucleoprotein complex GO:1990124 p=6.2E−02 n=1 fg=0.04 bg=0.00
zymogen granule GO:0042588 p=6.2E−02 n=1 fg=0.04 bg=0.00
protein phosphatase type 2A complex GO:0000159 p=6.2E−02 n=1 fg=0.04 bg=0.00
filopodium tip GO:0032433 p=6.2E−02 n=1 fg=0.04 bg=0.00
neuronal cell body GO:0043025 p=7.2E−02 n=4 fg=0.17 bg=0.07
sarcoplasm GO:0016528 p=7.4E−02 n=1 fg=0.04 bg=0.00
sarcoplasmic reticulum GO:0016529 p=7.4E−02 n=1 fg=0.04 bg=0.00
proteasome regulatory particle, base sub... GO:0008540 p=7.4E−02 n=1 fg=0.04 bg=0.00
cytosolic proteasome complex GO:0031597 p=7.4E−02 n=1 fg=0.04 bg=0.00
magnesium−dependent protein serine/threo... GO:0005963 p=8.6E−02 n=1 fg=0.04 bg=0.00
cell body GO:0044297 p=9.0E−02 n=4 fg=0.17 bg=0.08
proteasome accessory complex GO:0022624 p=9.8E−02 n=1 fg=0.04 bg=0.00
proteasome regulatory particle GO:0005838 p=9.8E−02 n=1 fg=0.04 bg=0.00
euchromatin GO:0000791 p=9.8E−02 n=1 fg=0.04 bg=0.00
centrosome GO:0005813 p=1.1E−01 n=3 fg=0.13 bg=0.05
0 1 2 3 4 5
−log(p)
n=23/106 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction