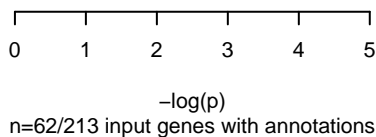


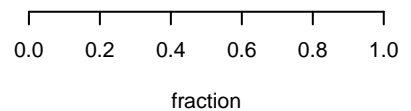
GO:BP  
Elav\_Nvec\_vc1.1\_XM\_001633156.3

fraction genes in fg and expected value

nucleoside diphosphate phosphorylation	GO:0006165	p=2.6E-03	n=4
lactate oxidation	GO:0019516	p=3.4E-03	n=2
propionate catabolic process	GO:0019543	p=3.4E-03	n=2
glucose catabolic process to lactate via...	GO:0019661	p=3.4E-03	n=2
nitrogenous compound fermentation	GO:0019666	p=3.4E-03	n=2
glycerol biosynthetic process from pyruv...	GO:0046327	p=3.4E-03	n=2
glycine metabolic process	GO:0006544	p=3.4E-03	n=2
erythrocyte maturation	GO:0043249	p=3.4E-03	n=2
kidney interstitial fibroblast different...	GO:0072071	p=3.4E-03	n=2
malate transport	GO:0015743	p=3.4E-03	n=2
lactate biosynthetic process	GO:0019249	p=3.4E-03	n=2
cellular response to potassium ion starv...	GO:0051365	p=3.4E-03	n=2
response to methionine	GO:1904640	p=3.4E-03	n=2
regulation of transcription by glucose	GO:0046015	p=3.4E-03	n=2
cellular response to fructose stimulus	GO:0071332	p=3.4E-03	n=2
positive regulation of transcription fro...	GO:0061402	p=3.4E-03	n=2
glycerol catabolic process	GO:0019563	p=3.4E-03	n=2
regulation of gluconeogenesis	GO:0006111	p=5.2E-03	n=3
metanephric renal vesicle morphogenesis	GO:0072283	p=6.6E-03	n=2
alanine metabolic process	GO:0006522	p=6.6E-03	n=2
aspartate metabolic process	GO:0006531	p=6.6E-03	n=2
hepatocyte differentiation	GO:0070365	p=6.6E-03	n=2
antibiotic catabolic process	GO:0017001	p=6.6E-03	n=2
NADH oxidation	GO:0006116	p=6.6E-03	n=2
response to cycloheximide	GO:0046898	p=6.6E-03	n=2
cellular response to peptide hormone sti...	GO:0071375	p=7.9E-03	n=7
programmed cell death	GO:0012501	p=8.8E-03	n=17
nematode larval development	GO:0002119	p=9.2E-03	n=7
carbohydrate derivative metabolic proces...	GO:1901135	p=1.0E-02	n=13
NADH regeneration	GO:0006735	p=1.1E-02	n=2



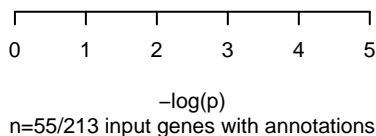
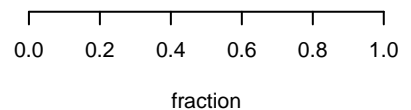
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**GO:MF**  
**Elav\_Nvec\_vc1.1\_XM\_001633156.3**

fraction genes in fg and expected value

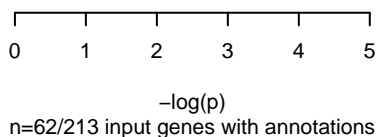
nucleoside diphosphate kinase activity	GO:0004550	p=1.5E-04	n=3
phosphoenolpyruvate carboxykinase (GTP) ...	GO:0004613	p=3.4E-03	n=2
lactate dehydrogenase activity	GO:0004457	p=3.4E-03	n=2
inosine kinase activity	GO:0008906	p=3.4E-03	n=2
DNA binding domain binding	GO:0050692	p=3.4E-03	n=2
oxidoreductase activity, acting on the C...	GO:0016899	p=3.4E-03	n=2
catecholamine binding	GO:1901338	p=1.1E-02	n=2
epinephrine binding	GO:0051379	p=1.1E-02	n=2
monosaccharide binding	GO:0048029	p=1.1E-02	n=2
core promoter sequence-specific DNA bind...	GO:0001046	p=1.6E-02	n=3
potassium ion transmembrane transporter ...	GO:0015079	p=1.9E-02	n=3
protein-disulfide reductase (NAD(P)) act...	GO:0047134	p=2.2E-02	n=2
oxidoreductase activity, acting on a sul...	GO:0016668	p=2.2E-02	n=2
DNA-binding transcription factor activit...	GO:0000981	p=2.7E-02	n=8
sphingolipid transfer activity	GO:0120016	p=3.5E-02	n=1
ceramide transfer activity	GO:0120017	p=3.5E-02	n=1
methylmalonyl-CoA mutase activity	GO:0004494	p=3.5E-02	n=1
protein N-acetylglucosaminyltransferase ...	GO:0016262	p=3.5E-02	n=1
cation:chloride symporter activity	GO:0015377	p=3.5E-02	n=1
potassium:chloride symporter activity	GO:0015379	p=3.5E-02	n=1
ceramide binding	GO:0097001	p=3.5E-02	n=1
glycerol-3-phosphate O-acyltransferase a...	GO:0004366	p=3.5E-02	n=1
8-oxo-dGDP phosphatase activity	GO:0044715	p=3.5E-02	n=1
protein O-GlcNAc transferase activity	GO:0097363	p=3.5E-02	n=1
polynucleotide phosphatase activity	GO:0098518	p=3.5E-02	n=1
dCMP deaminase activity	GO:0004132	p=3.5E-02	n=1
panthetheine-phosphate adenyllyltransferas...	GO:0004595	p=3.5E-02	n=1
anion:cation symporter activity	GO:0015296	p=3.5E-02	n=1
cobalamin binding	GO:0031419	p=3.5E-02	n=1
polynucleotide 5'-phosphatase activity	GO:0004651	p=3.5E-02	n=1

[illegible]

**GO:CC**  
**Elav\_Nvec\_vc1.1\_XM\_001633156.3**

fraction genes in fg and expected value

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	euchromatin	GO:0000791	p=2.8E-02	n=2
	fusome	GO:0045169	p=2.8E-02	n=2
	spectrin	GO:0008091	p=3.4E-02	n=1
	extrinsic component of mitochondrial inn...	GO:0031314	p=3.4E-02	n=1
Ric1-Rgp1	guanyl-nucleotide exchange fac...	GO:0034066	p=3.4E-02	n=1
	proteasome storage granule	GO:0034515	p=3.4E-02	n=1
	Rb-E2F complex	GO:0035189	p=3.4E-02	n=1
	outer dynein arm	GO:0036157	p=3.4E-02	n=1
	spectrosome	GO:0045170	p=3.4E-02	n=1
	sperm cytoplasmic droplet	GO:0097598	p=3.4E-02	n=1
	nuclear membrane	GO:0031965	p=3.5E-02	n=4
	intercellular bridge	GO:0045171	p=6.1E-02	n=2
	NELF complex	GO:0032021	p=6.7E-02	n=1
	female germline ring canal	GO:0035324	p=6.7E-02	n=1
	intrinsic component of nuclear inner memb...	GO:0031229	p=6.7E-02	n=1
	nuclear stress granule	GO:0097165	p=6.7E-02	n=1
	ESCRT I complex	GO:0000813	p=6.7E-02	n=1
	integral component of nuclear inner memb...	GO:0005639	p=6.7E-02	n=1
	transcription repressor complex	GO:0017053	p=7.1E-02	n=2
	NuRD complex	GO:0016581	p=9.9E-02	n=1
	guanyl-nucleotide exchange factor comple...	GO:0032045	p=9.9E-02	n=1
	axonemal dynein complex	GO:0005858	p=9.9E-02	n=1
	CHD-type complex	GO:0090545	p=9.9E-02	n=1
	germline ring canal	GO:0045172	p=9.9E-02	n=1
	Cul4A-RING E3 ubiquitin ligase complex	GO:0031464	p=9.9E-02	n=1
	Hrd1p ubiquitin ligase ERAD-L complex	GO:0000839	p=9.9E-02	n=1
	mitotic spindle	GO:0072686	p=1.1E-01	n=2
	mitochondrial matrix	GO:0005759	p=1.2E-01	n=5
	transcription regulator complex	GO:0005667	p=1.2E-01	n=5



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