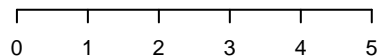
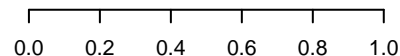


7tm_3	p=1.2E-01	n=3
AC_N	p=1.2E-01	n=2
Adaptin_N	p=1.2E-01	n=2
adh_short	p=1.2E-01	n=3
Ala_racemase_N	p=1.2E-01	n=1
Alpha-amylase_C	p=1.2E-01	n=1
Aminotran_5	p=1.2E-01	n=2
AP4E_app_platf	p=1.2E-01	n=1
Asp_Arg_Hydrox	p=1.2E-01	n=1
ATP-synt_F	p=1.2E-01	n=1
Auts2	p=1.2E-01	n=1
BAG6	p=1.2E-01	n=1
Biotin_lipoyl_2	p=1.2E-01	n=1
Bravo_FIGEY	p=1.2E-01	n=1
CAMSAP_CC1	p=1.2E-01	n=1
CAMSAP_CKK	p=1.2E-01	n=1
CBFB_NFYA	p=1.2E-01	n=1
CBM_48	p=1.2E-01	n=1
CDC37_C	p=1.2E-01	n=1
CDC37_M	p=1.2E-01	n=1
CDC37_N	p=1.2E-01	n=1
CNOT1_CAF1_bind	p=1.2E-01	n=1
CNOT1_HEAT	p=1.2E-01	n=1
CNOT1_TTP_bind	p=1.2E-01	n=1
Coatomer_g_Cpla	p=1.2E-01	n=1
COP-gamma_platf	p=1.2E-01	n=1
CortBP2	p=1.2E-01	n=1
CRAL_TRIO	p=1.2E-01	n=2
D-ser_dehydrat	p=1.2E-01	n=1
DnaJ	p=1.2E-01	n=4

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n=311/269 input genes with annotations

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fraction