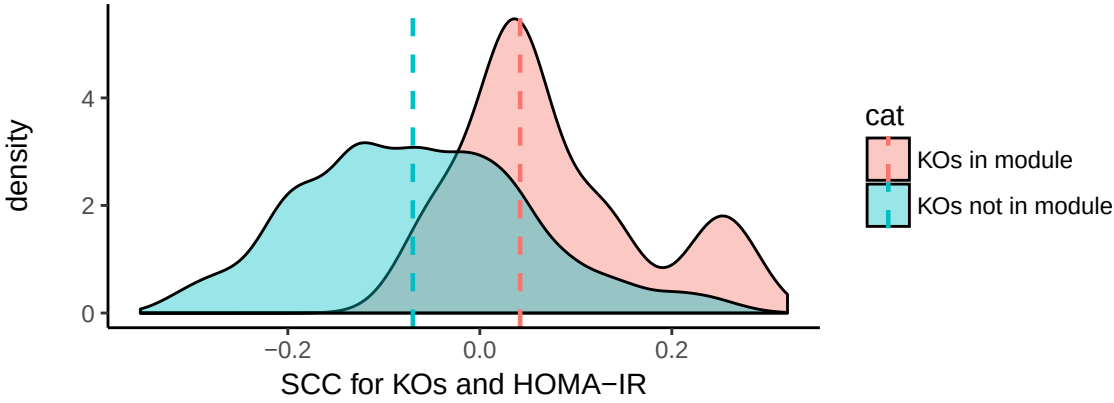
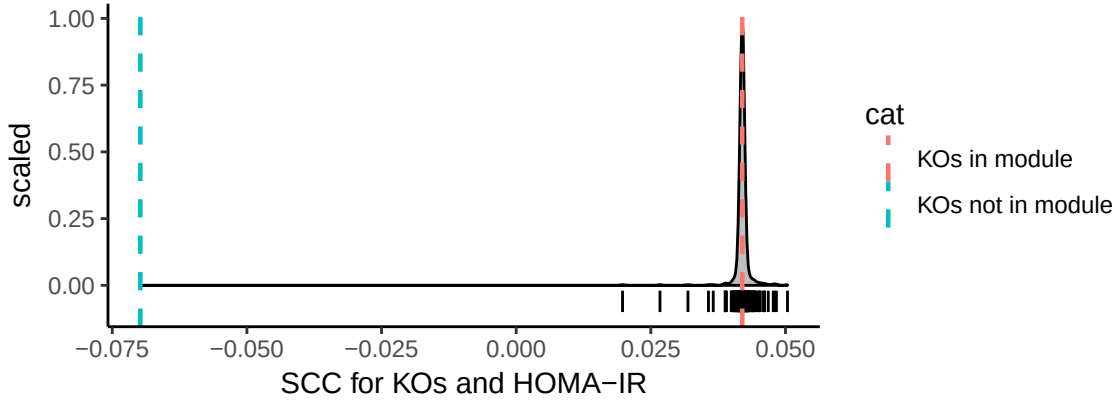
a

KEGG module: M00124
Pyridoxal biosynthesis
6 KOs in module vs all remaining 6752 KOs



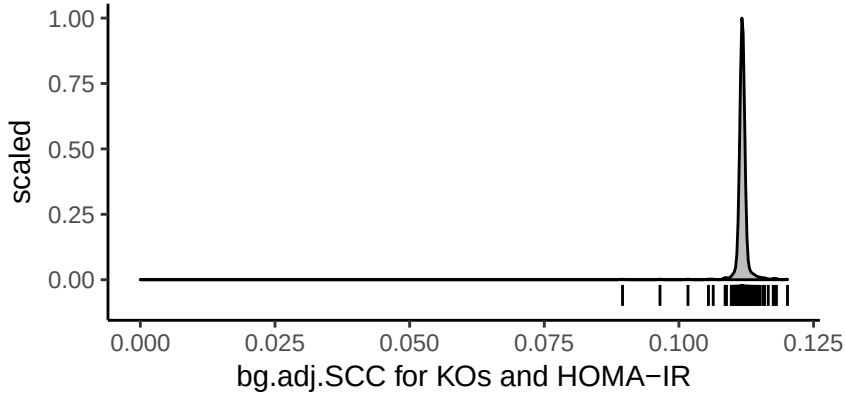
b

KEGG module: M00124
Pyridoxal biosynthesis
SCC for leave−1−MGS−out
Number of MGSs = 573



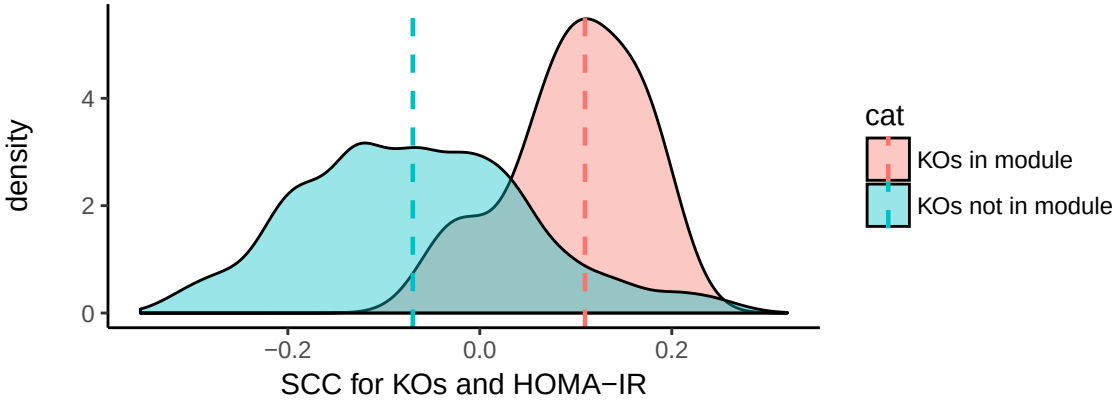
c

KEGG module: M00124
Pyridoxal biosynthesis
bg.adj.SCC for leave−1−MGS−out
Number of MGSs = 573



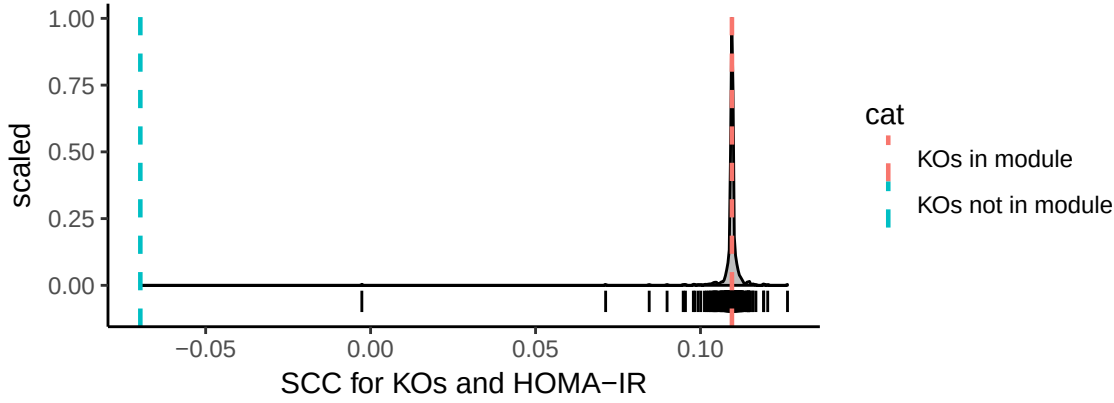
a

KEGG module: M00570
Isoleucine biosynthesis
7 KOs in module vs all remaining 6751 KOs



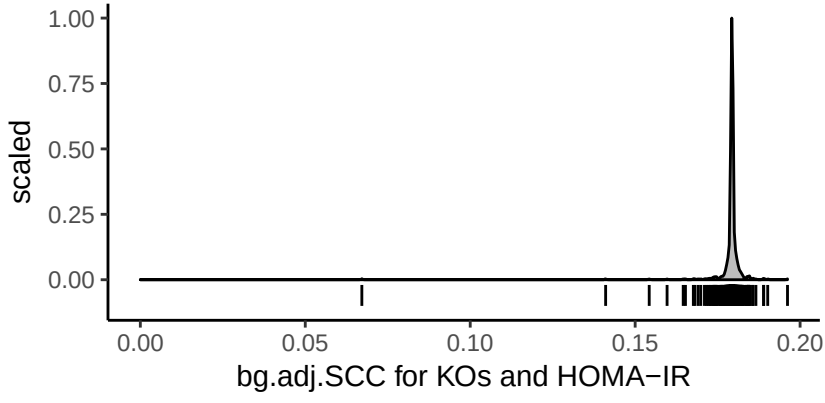
b

KEGG module: M00570
Isoleucine biosynthesis
SCC for leave−1−MGS−out
Number of MGSs = 617



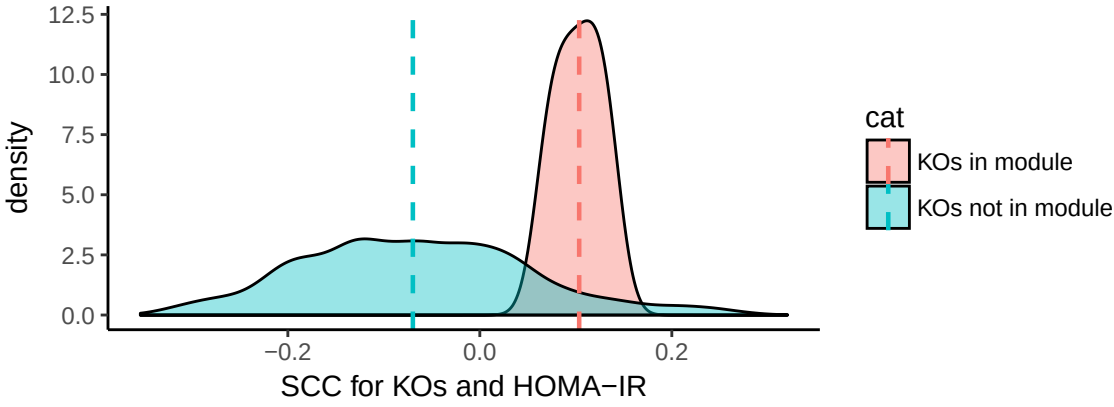
c

KEGG module: M00570
Isoleucine biosynthesis
bg.adj.SCC for leave−1−MGS−out
Number of MGSs = 617



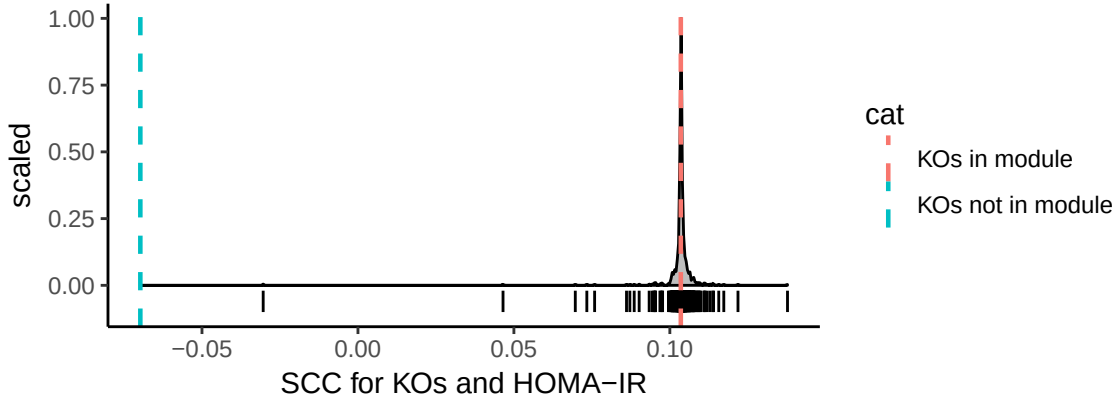
a

KEGG module: M00432
Leucine biosynthesis
5 KOs in module vs all remaining 6753 KOs



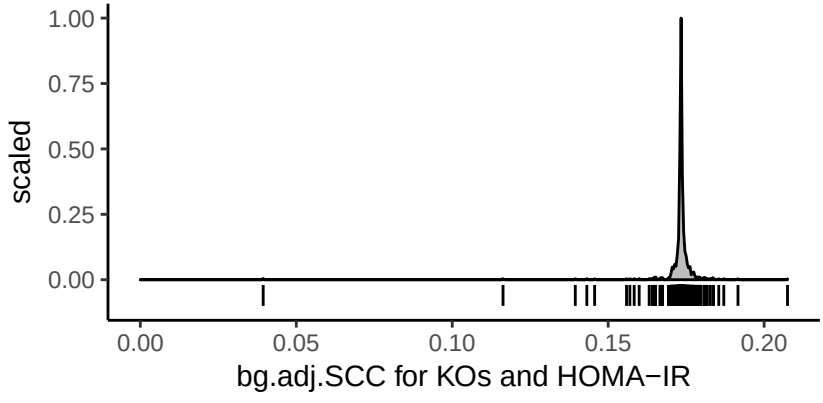
b

KEGG module: M00432
Leucine biosynthesis
SCC for leave−1−MGS−out
Number of MGSs = 523



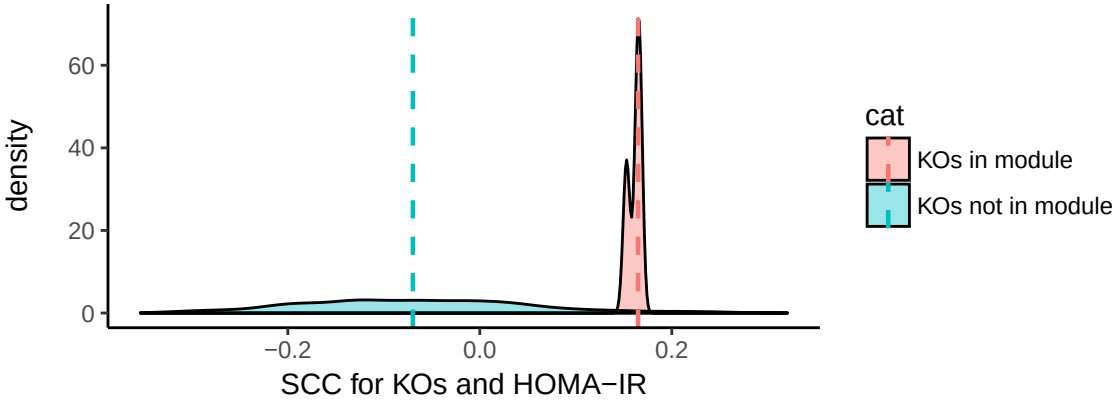
c

KEGG module: M00432
Leucine biosynthesis
bg.adj.SCC for leave−1−MGS−out
Number of MGSs = 523



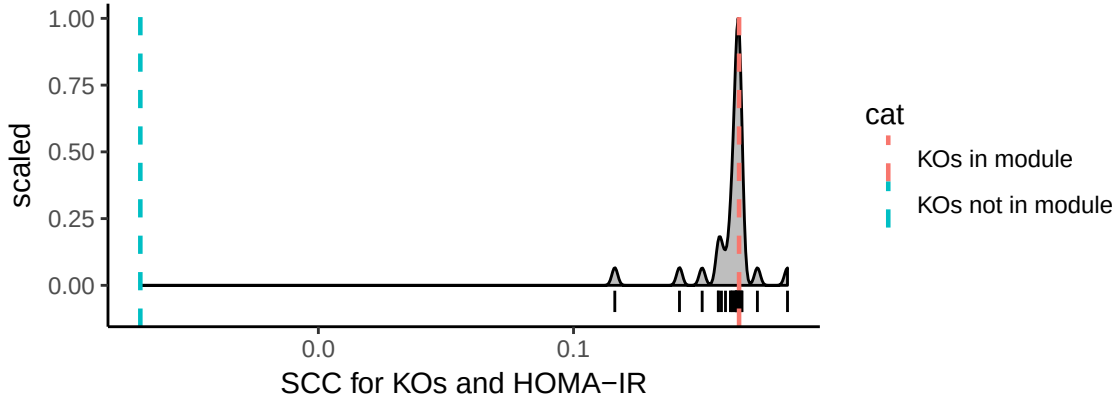
a

KEGG module: M00208
Glycine betaine/proline transport system
3 KOs in module vs all remaining 6755 KOs



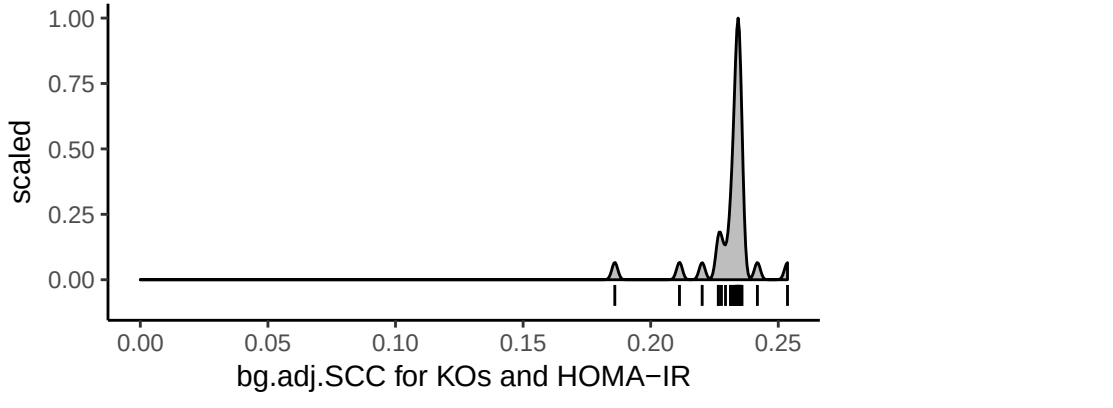
b

KEGG module: M00208
Glycine betaine/proline transport system
SCC for leave−1−MGS−out
Number of MGSs = 31



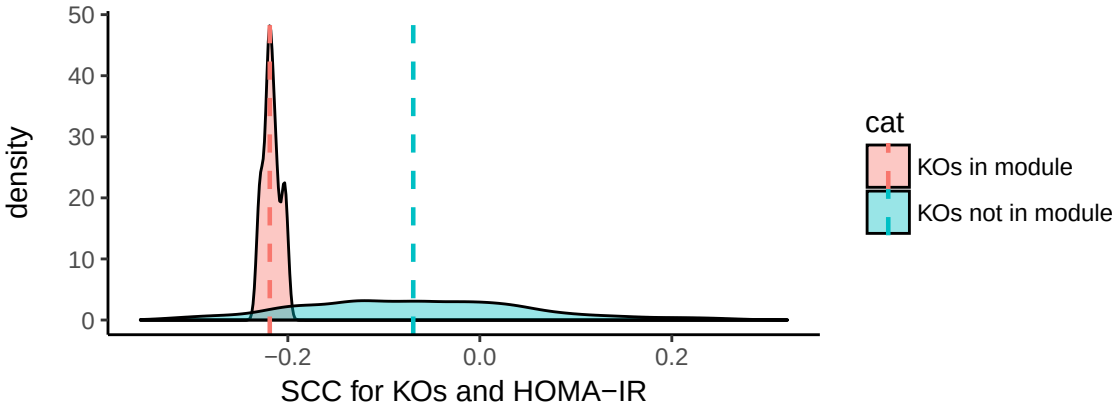
c

KEGG module: M00208
Glycine betaine/proline transport system
bg.adj.SCC for leave−1−MGS−out
Number of MGSs = 31



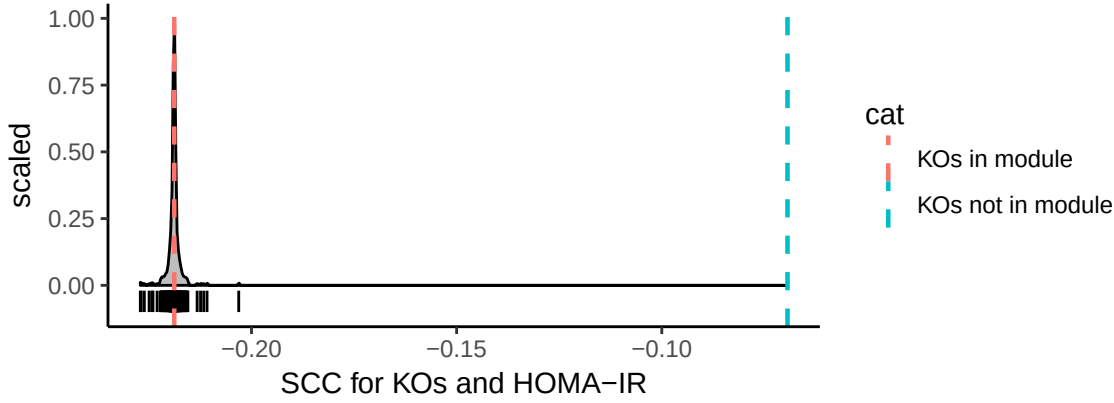
a

KEGG module: M00237
Branched−chain amino acid transport system
5 KOs in module vs all remaining 6753 KOs



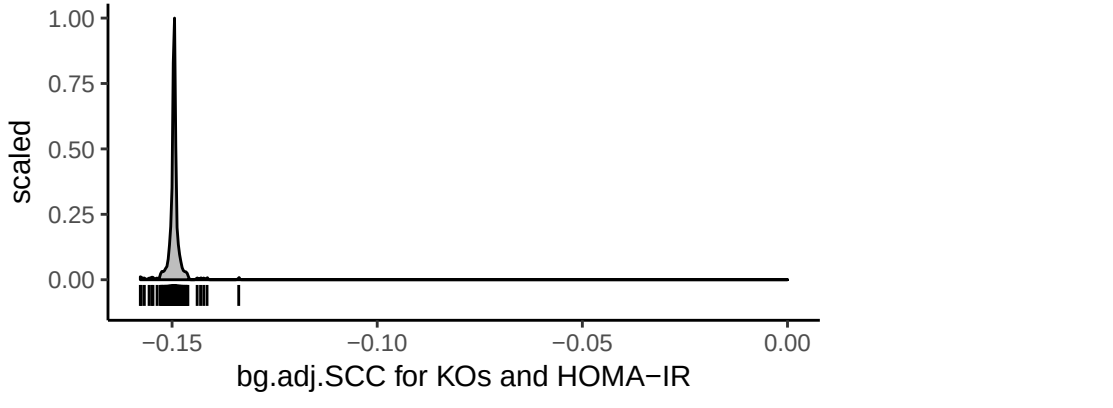
b

KEGG module: M00237
Branched−chain amino acid transport system
SCC for leave−1−MGS−out
Number of MGSs = 328



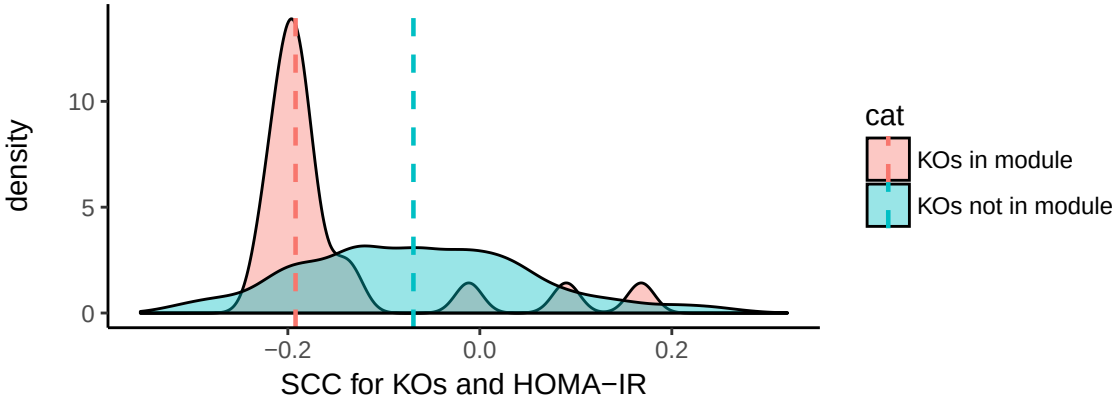
c

KEGG module: M00237
Branched−chain amino acid transport system
bg.adj.SCC for leave−1−MGS−out
Number of MGSs = 328



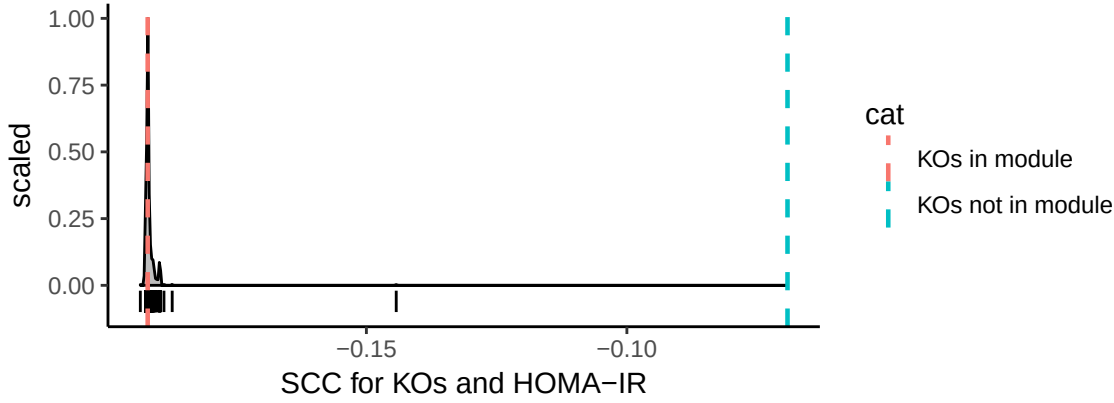
a

KEGG module: M00357
Methanogenesis
21 KOs in module vs all remaining 6737 KOs



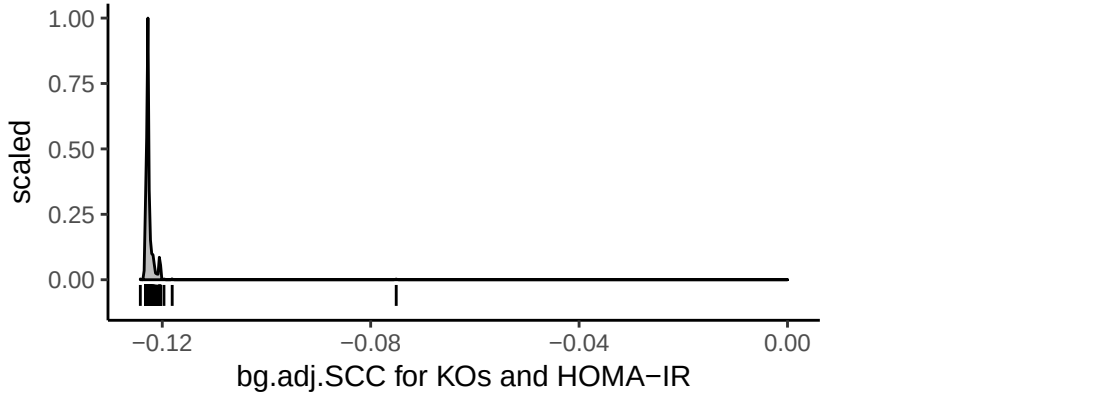
b

KEGG module: M00357
Methanogenesis
SCC for leave−1−MGS−out
Number of MGSs = 686



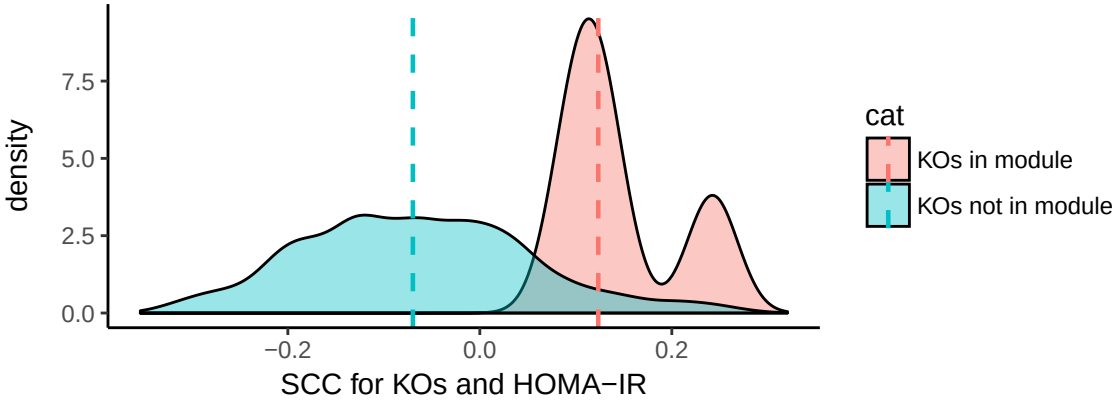
c

KEGG module: M00357
Methanogenesis
bg.adj.SCC for leave−1−MGS−out
Number of MGSs = 686



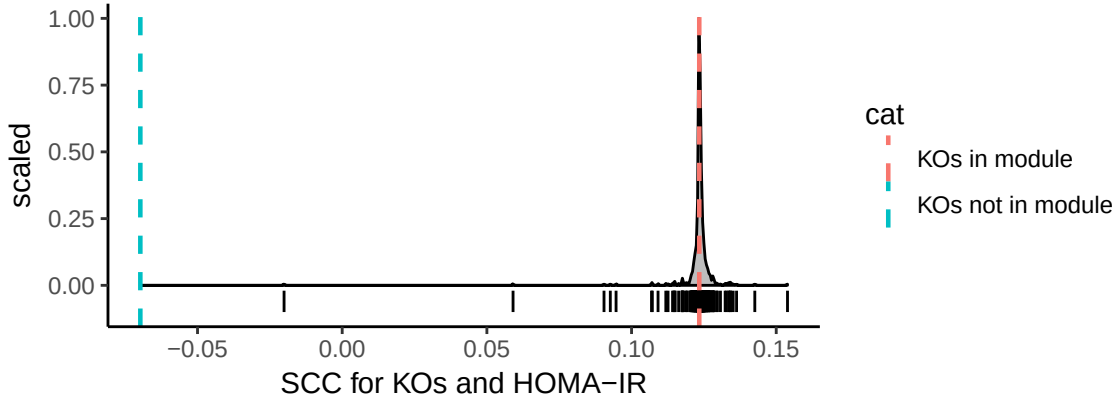
a

KEGG module: M00535
Isoleucine biosynthesis
4 KOs in module vs all remaining 6754 KOs



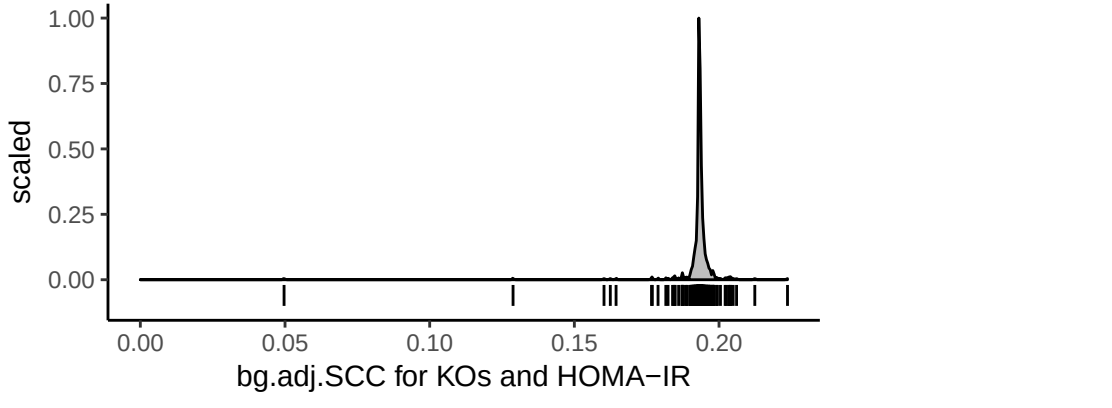
b

KEGG module: M00535
Isoleucine biosynthesis
SCC for leave−1−MGS−out
Number of MGSs = 478



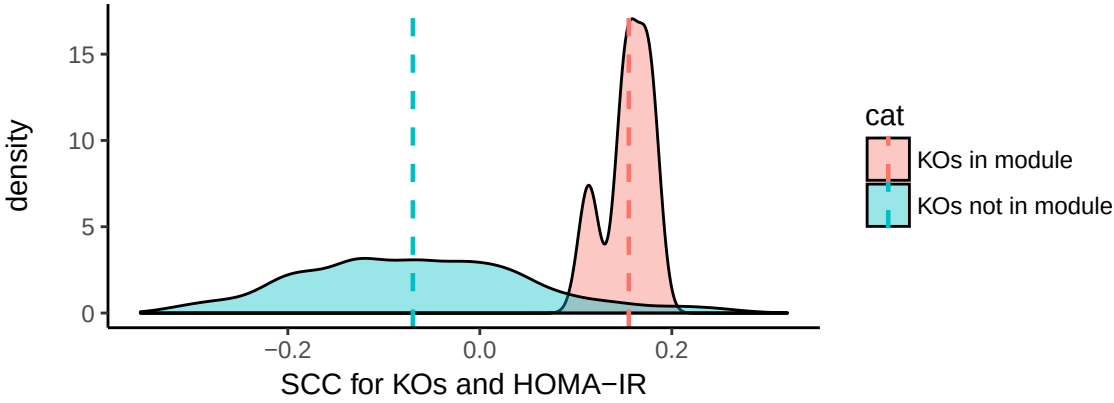
c

KEGG module: M00535
Isoleucine biosynthesis
bg.adj.SCC for leave−1−MGS−out
Number of MGSs = 478



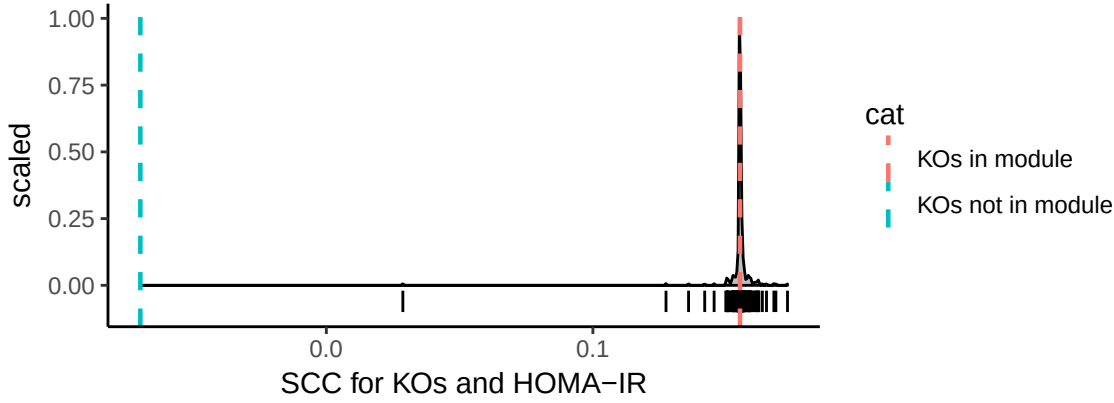
a

KEGG module: M00061
Uronic acid metabolism
7 KOs in module vs all remaining 6751 KOs



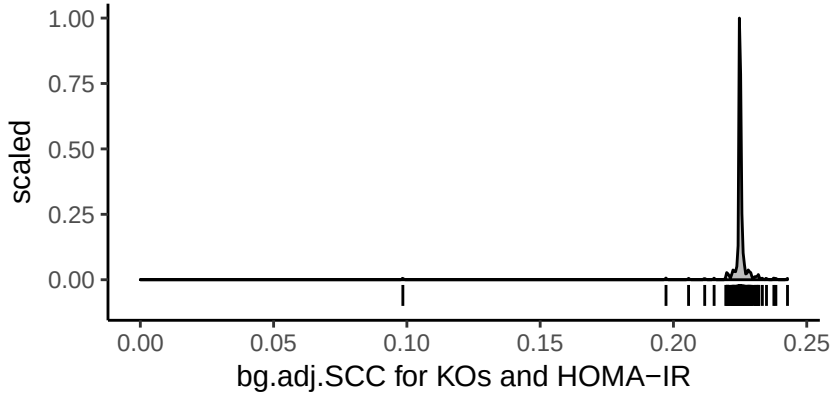
b

KEGG module: M00061
Uronic acid metabolism
SCC for leave−1−MGS−out
Number of MGSs = 332



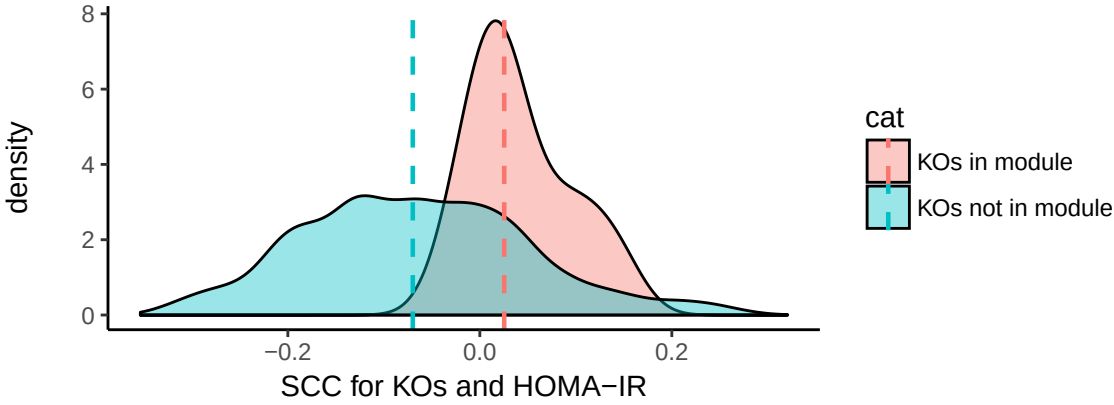
c

KEGG module: M00061
Uronic acid metabolism
bg.adj.SCC for leave−1−MGS−out
Number of MGSs = 332



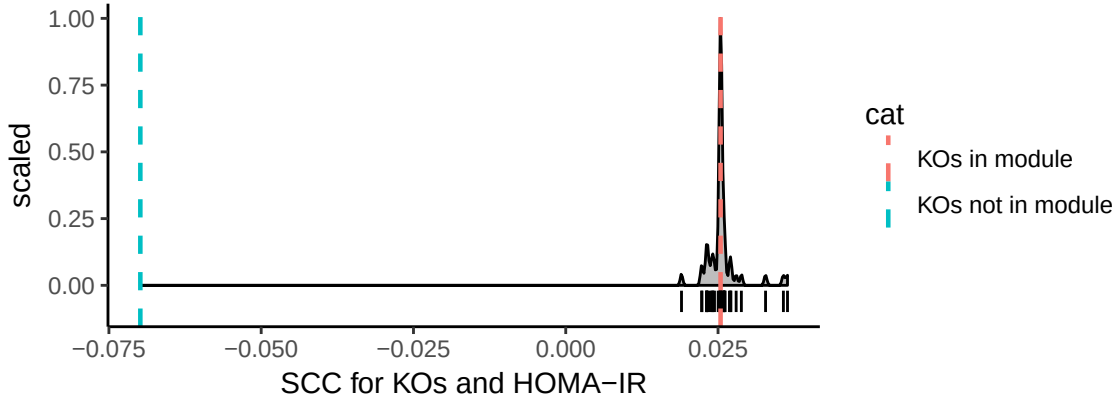
a

KEGG module: M00530
Dissimilatory nitrate reduction
10 KOs in module vs all remaining 6748 KOs



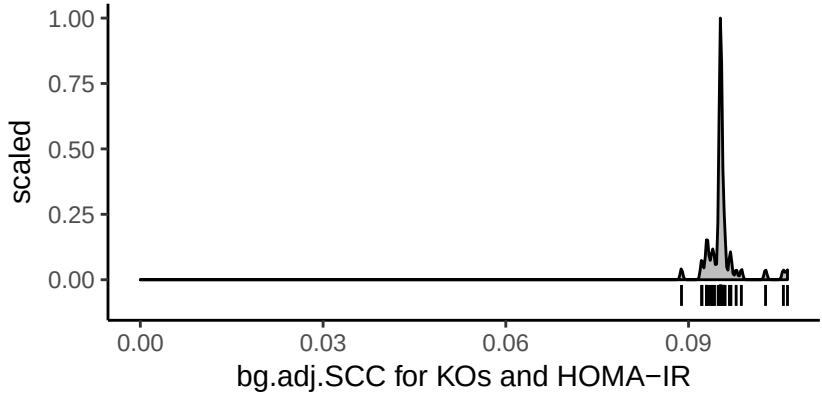
b

KEGG module: M00530
Dissimilatory nitrate reduction
SCC for leave−1−MGS−out
Number of MGSs = 54



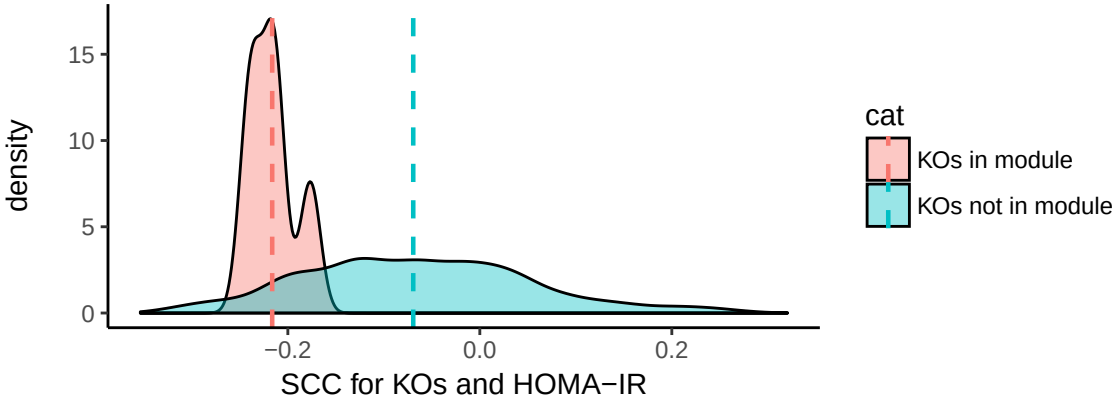
c

KEGG module: M00530
Dissimilatory nitrate reduction
bg.adj.SCC for leave−1−MGS−out
Number of MGSs = 54



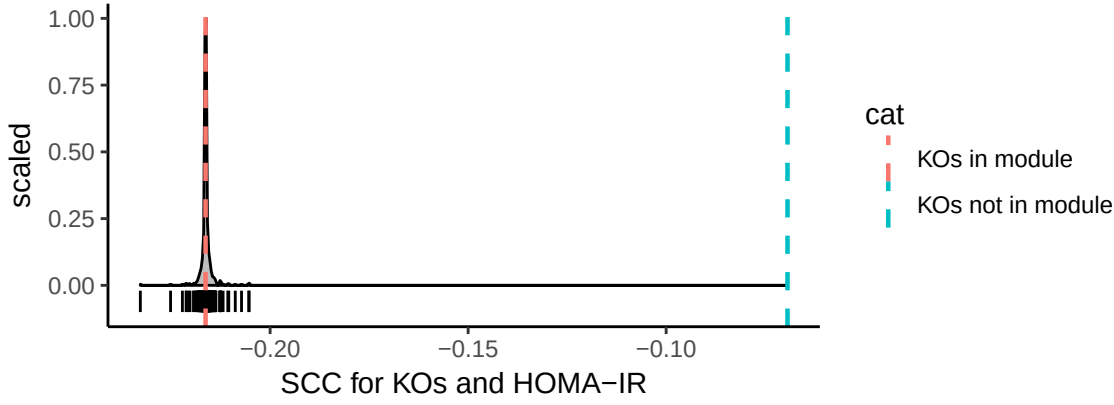
a

KEGG module: M00239
Peptides/nickel transport system
5 KOs in module vs all remaining 6753 KOs



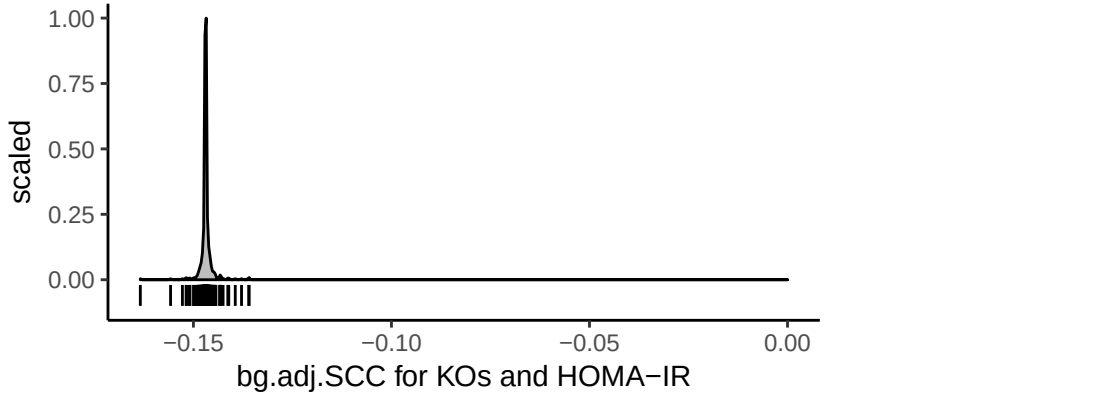
b

KEGG module: M00239
Peptides/nickel transport system
SCC for leave−1−MGS−out
Number of MGSs = 432



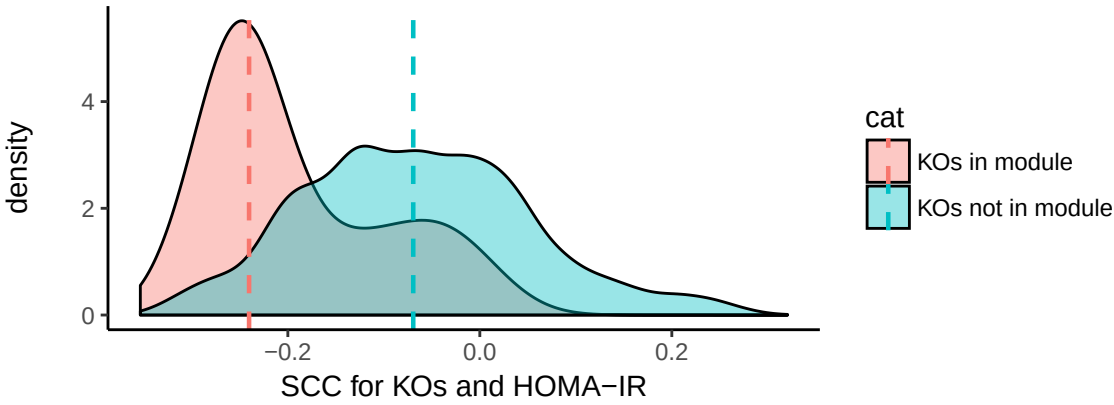
c

KEGG module: M00239
Peptides/nickel transport system
bg.adj.SCC for leave−1−MGS−out
Number of MGSs = 432



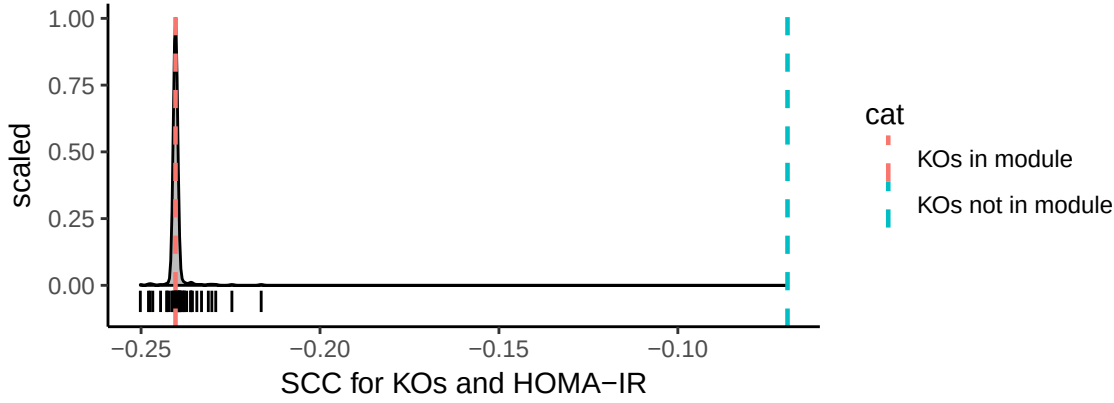
a

KEGG module: M00307
Pyruvate oxidation
9 KOs in module vs all remaining 6749 KOs



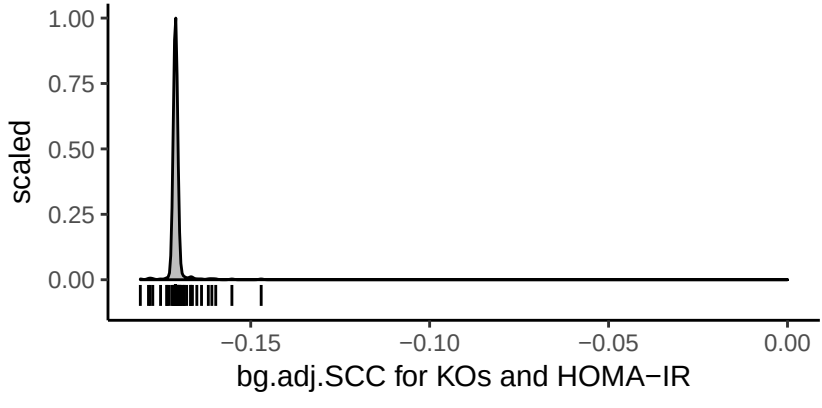
b

KEGG module: M00307
Pyruvate oxidation
SCC for leave−1−MGS−out
Number of MGSs = 391



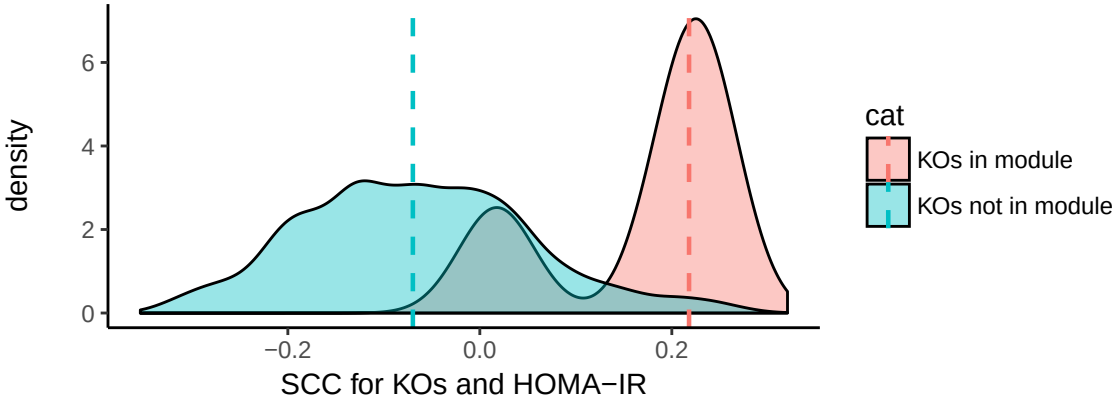
c

KEGG module: M00307
Pyruvate oxidation
bg.adj.SCC for leave−1−MGS−out
Number of MGSs = 391



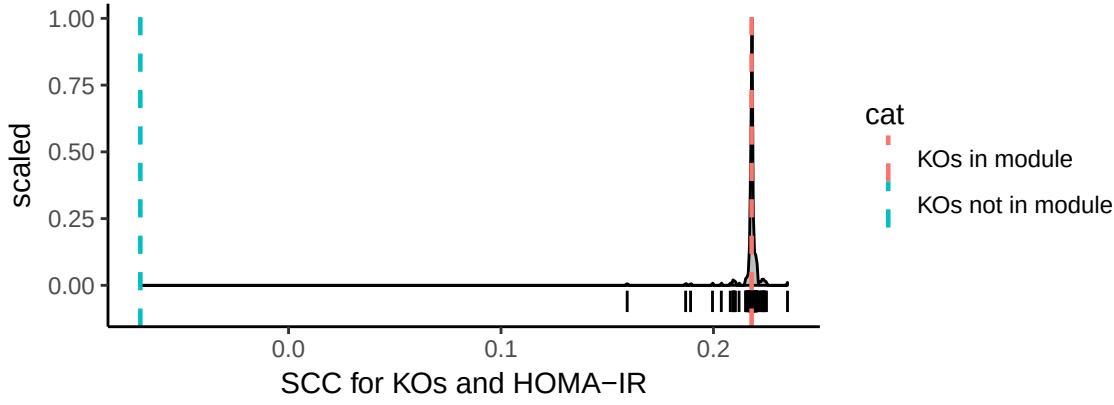
a

KEGG module: M00149
Succinate dehydrogenase
4 KOs in module vs all remaining 6754 KOs



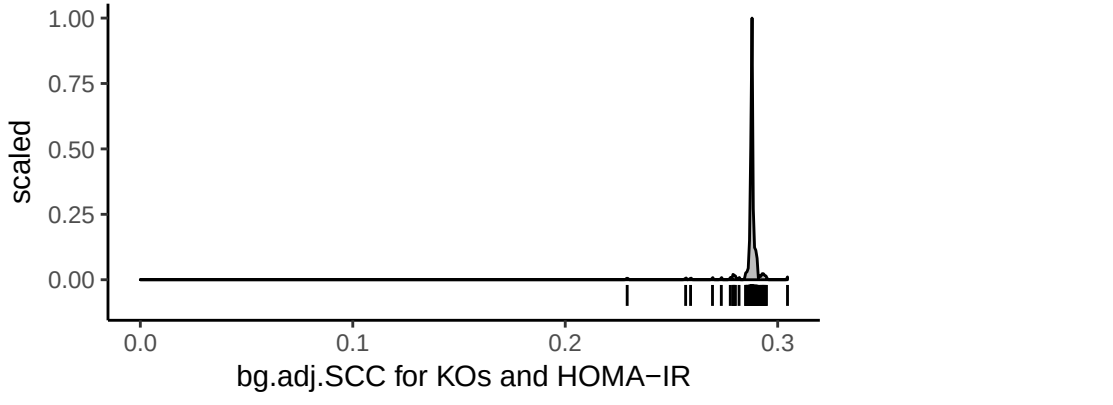
b

KEGG module: M00149
Succinate dehydrogenase
SCC for leave−1−MGS−out
Number of MGSs = 235



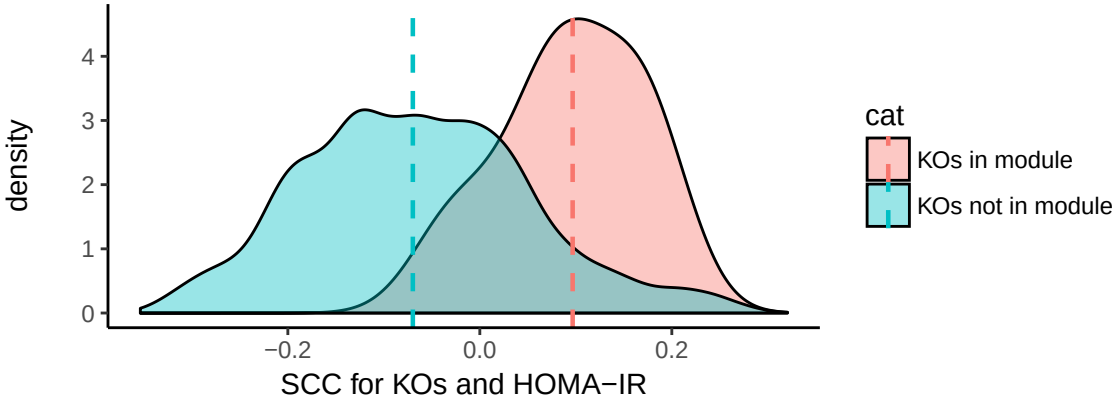
c

KEGG module: M00149
Succinate dehydrogenase
bg.adj.SCC for leave−1−MGS−out
Number of MGSs = 235



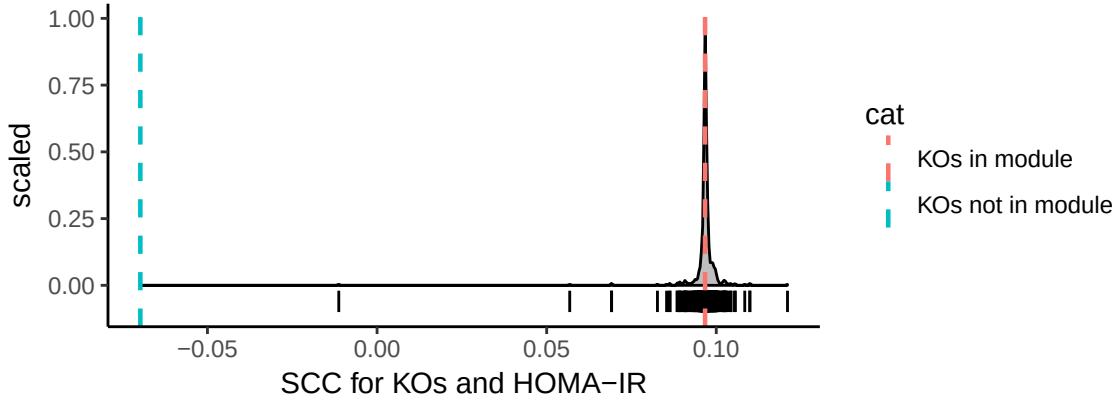
a

KEGG module: M00019
Valine/isoleucine biosynthesis
6 KOs in module vs all remaining 6752 KOs



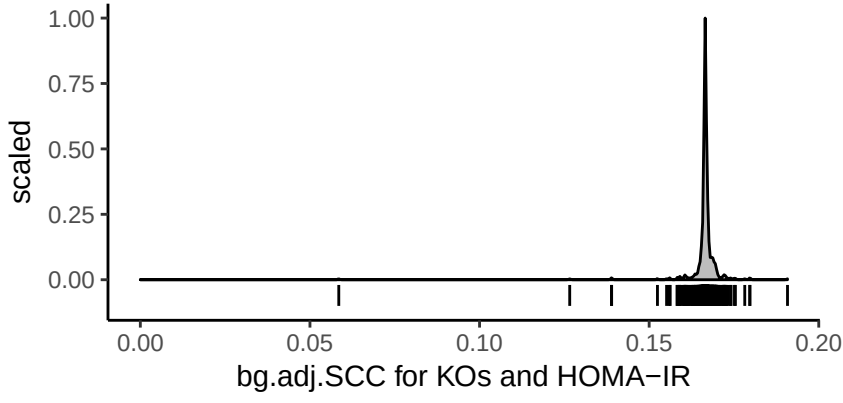
b

KEGG module: M00019
Valine/isoleucine biosynthesis
SCC for leave−1−MGS−out
Number of MGSs = 594



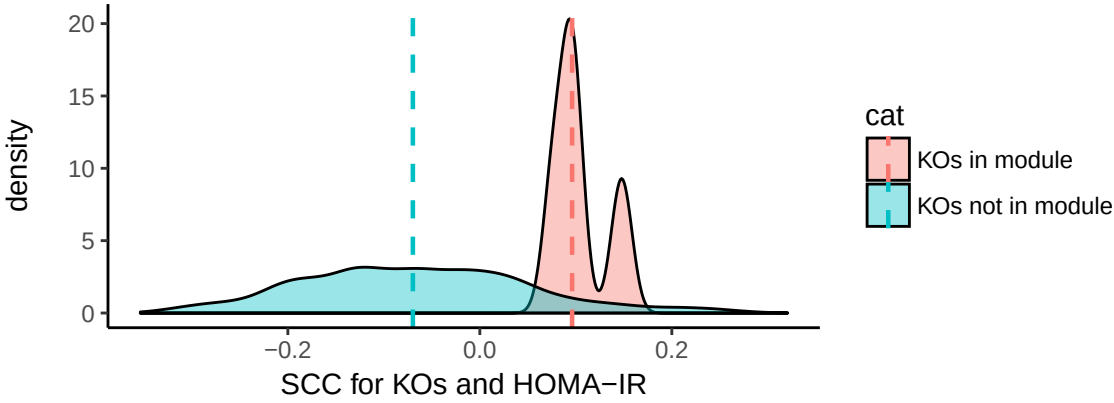
c

KEGG module: M00019
Valine/isoleucine biosynthesis
bg.adj.SCC for leave−1−MGS−out
Number of MGSs = 594



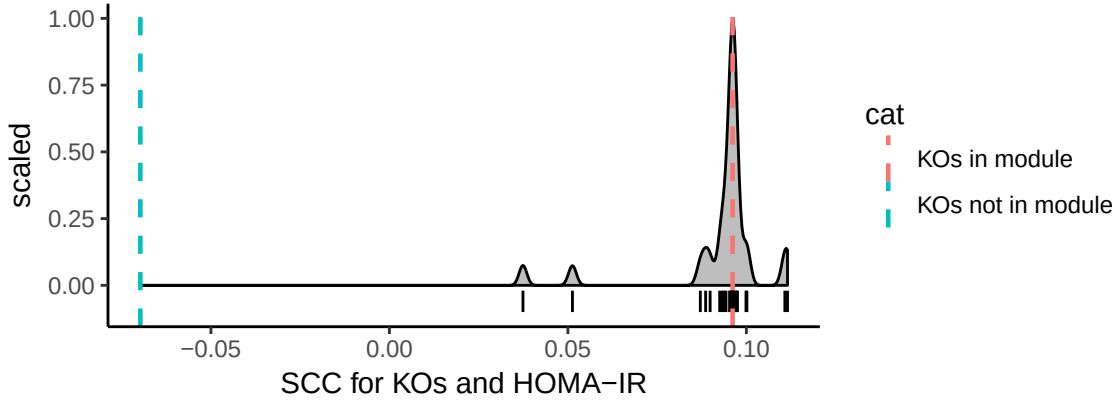
a

KEGG module: M00348
Glutathione transport system
4 KOs in module vs all remaining 6754 KOs



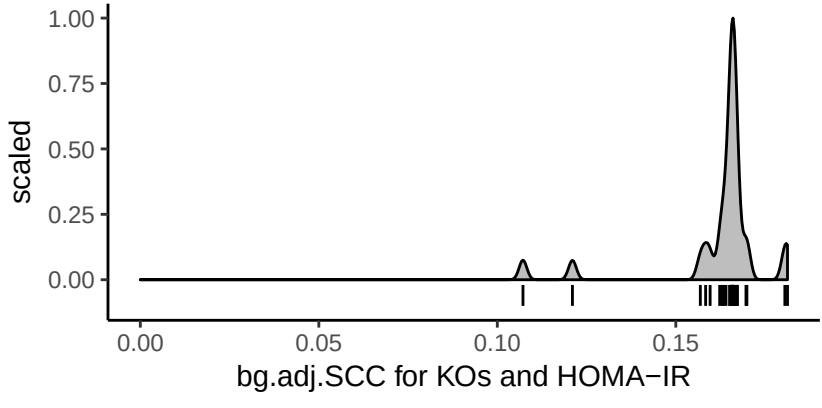
b

KEGG module: M00348
Glutathione transport system
SCC for leave−1−MGS−out
Number of MGSs = 28



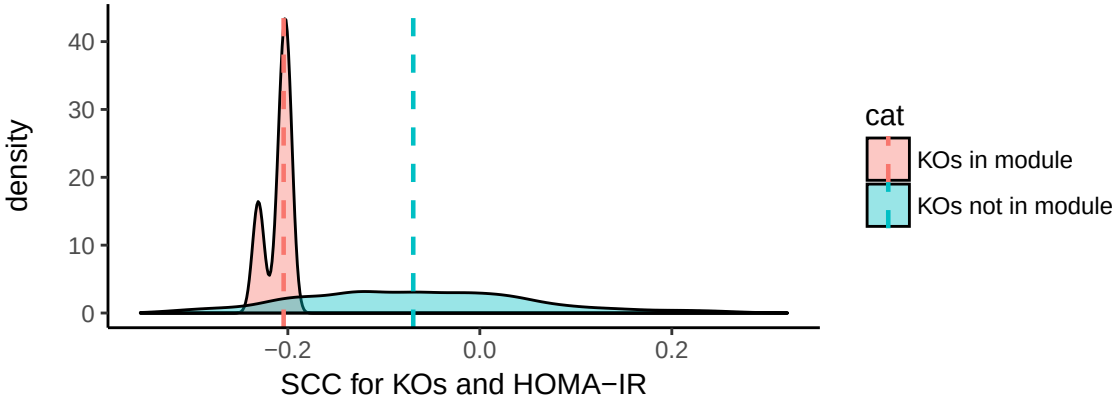
c

KEGG module: M00348
Glutathione transport system
bg.adj.SCC for leave−1−MGS−out
Number of MGSs = 28



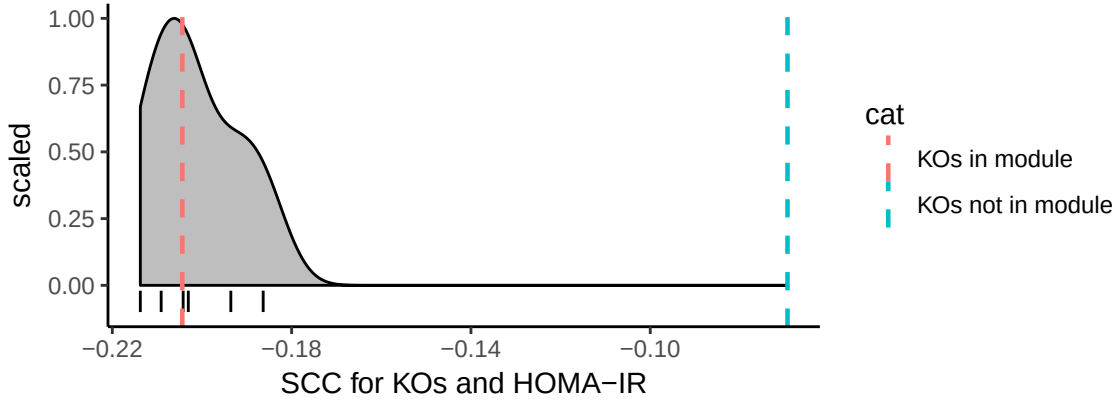
a

KEGG module: M00390
Exosome
4 KOs in module vs all remaining 6754 KOs



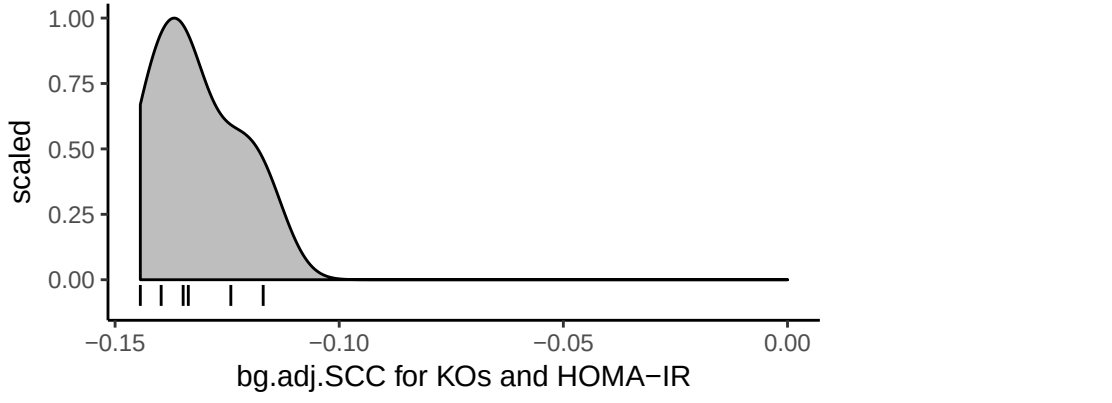
b

KEGG module: M00390
Exosome
SCC for leave−1−MGS−out
Number of MGSs = 6



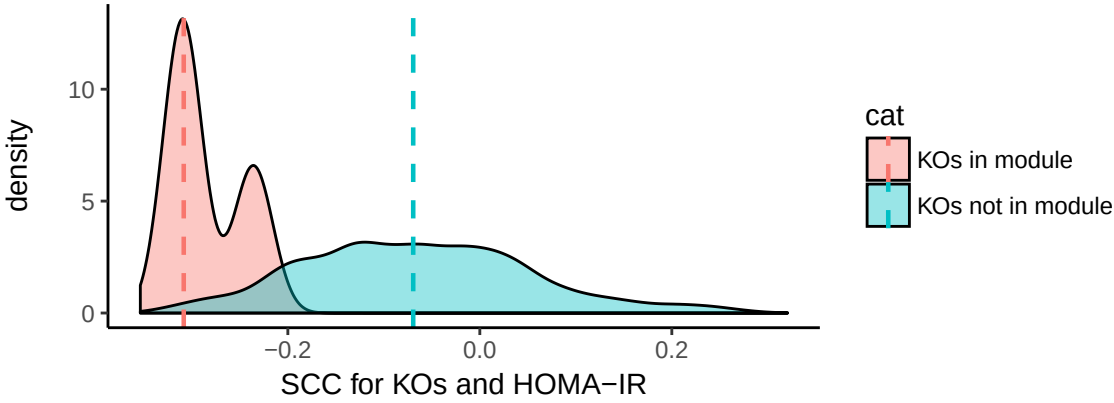
c

KEGG module: M00390
Exosome
bg.adj.SCC for leave−1−MGS−out
Number of MGSs = 6



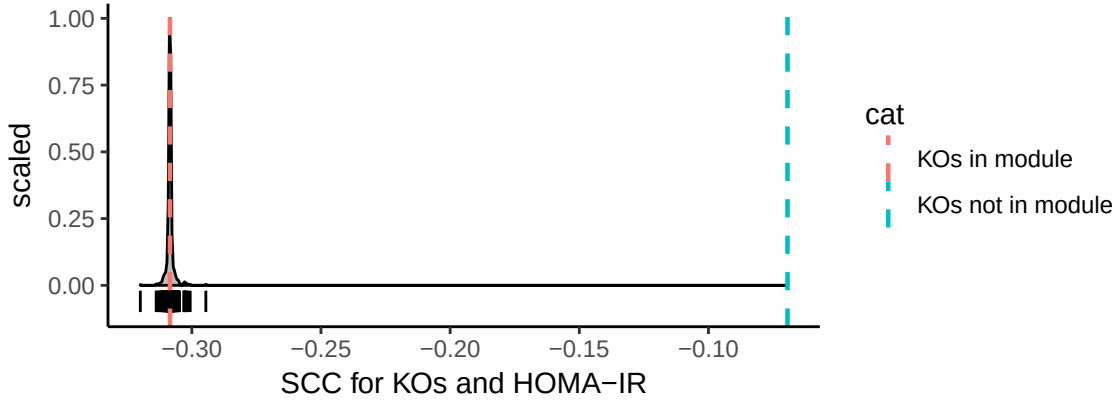
a

KEGG module: M00188
NitT/TauT family transport system
3 KOs in module vs all remaining 6755 KOs



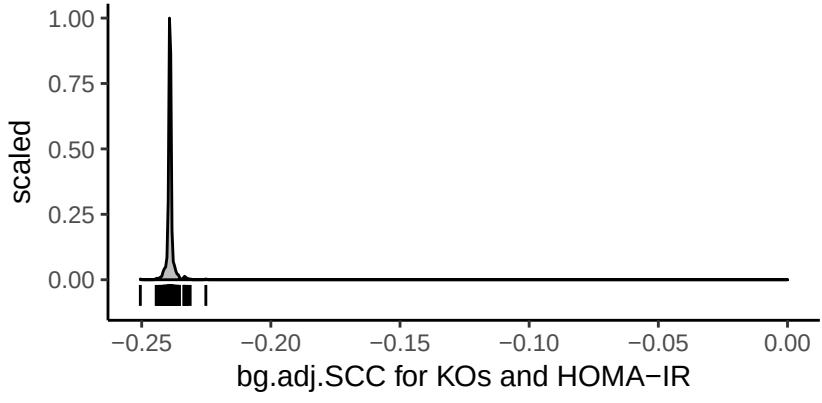
b

KEGG module: M00188
NitT/TauT family transport system
SCC for leave−1−MGS−out
Number of MGSs = 517



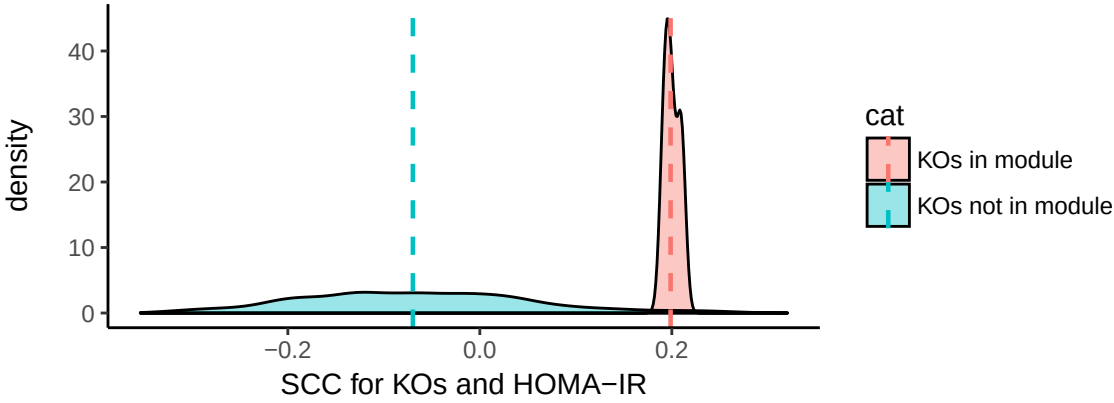
c

KEGG module: M00188
NitT/TauT family transport system
bg.adj.SCC for leave−1−MGS−out
Number of MGSs = 517



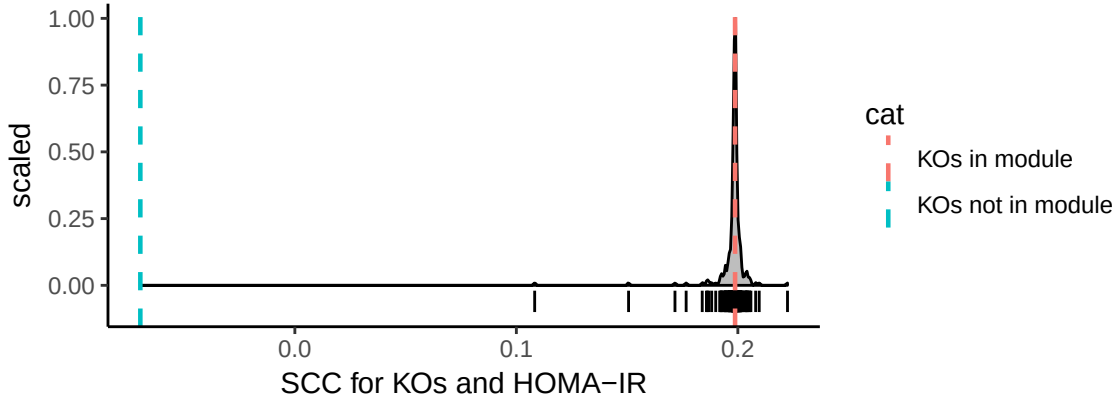
a

KEGG module: M00063
CMP−KDO biosynthesis
3 KOs in module vs all remaining 6755 KOs



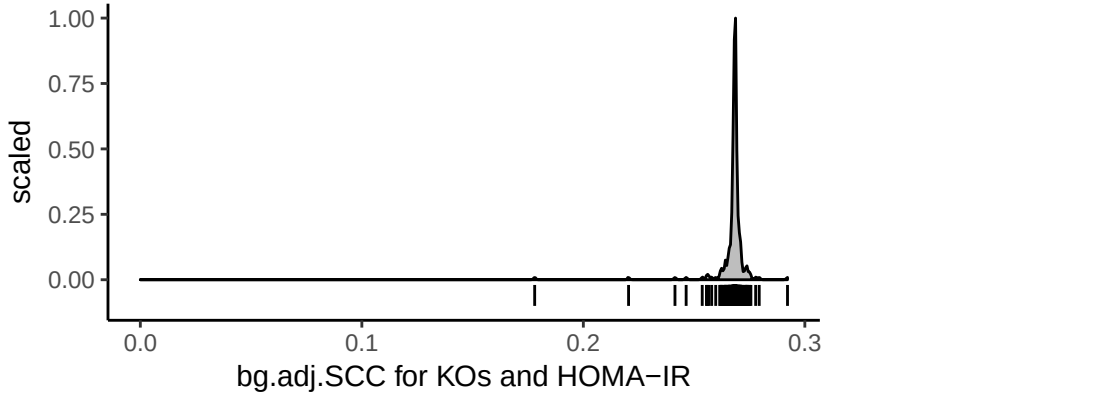
b

KEGG module: M00063
CMP−KDO biosynthesis
SCC for leave−1−MGS−out
Number of MGSs = 245



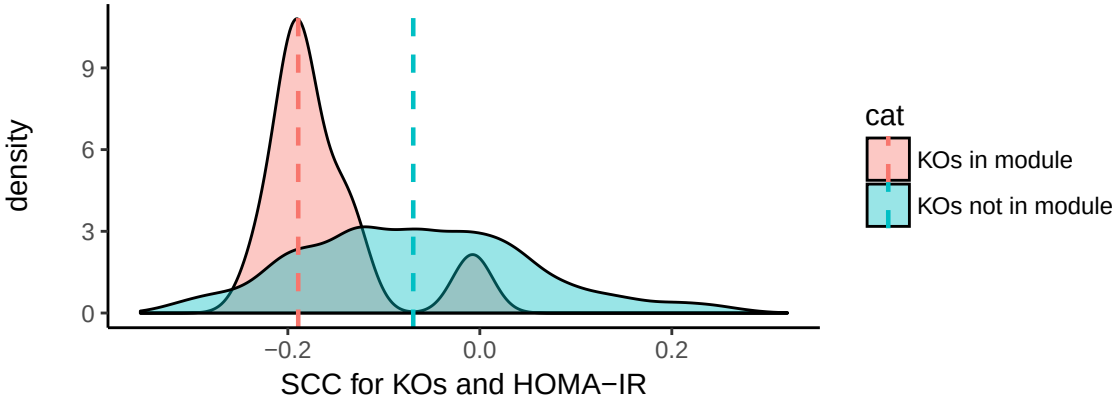
c

KEGG module: M00063
CMP−KDO biosynthesis
bg.adj.SCC for leave−1−MGS−out
Number of MGSs = 245



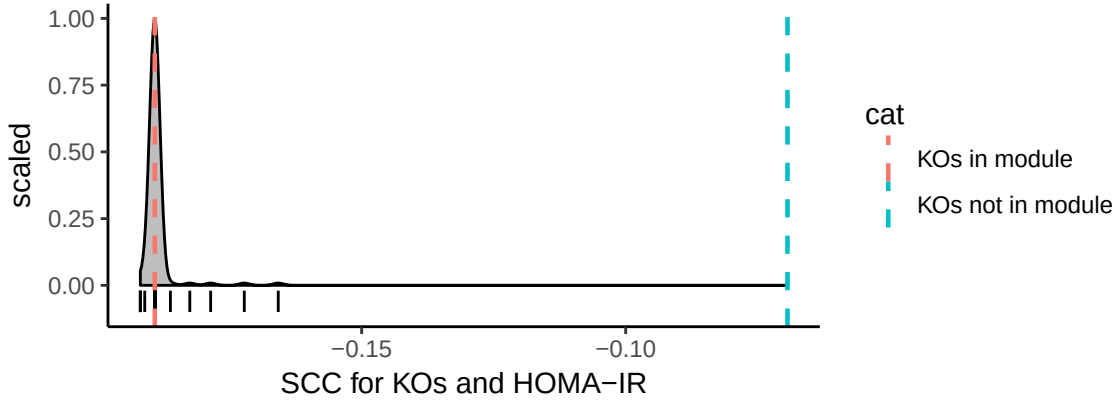
a

KEGG module: M00563
Methanogenesis
13 KOs in module vs all remaining 6745 KOs



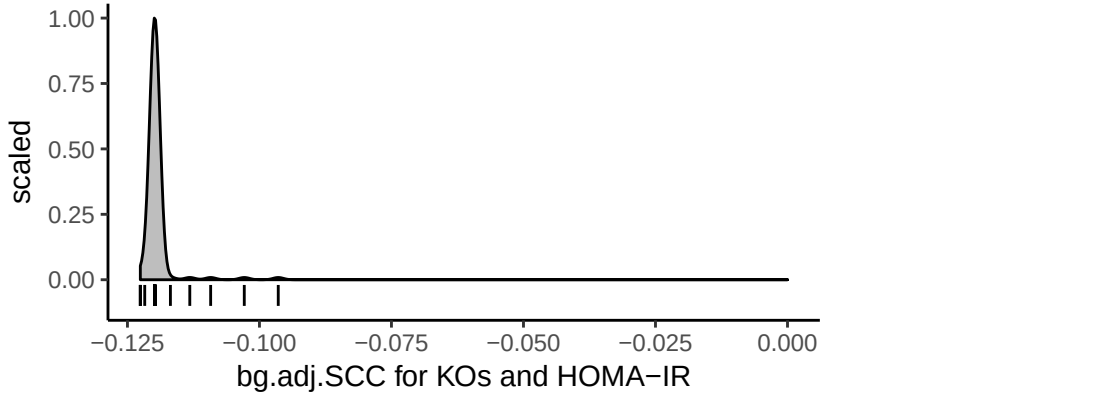
b

KEGG module: M00563
Methanogenesis
SCC for leave−1−MGS−out
Number of MGSs = 125



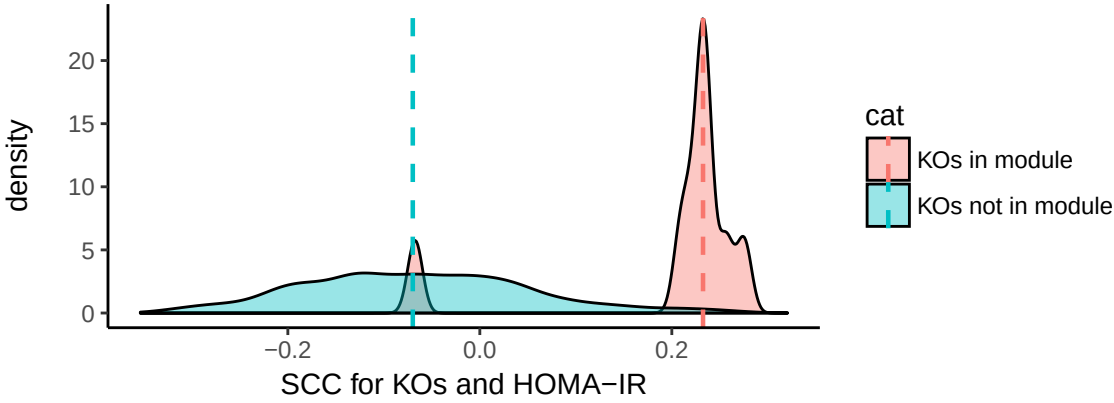
c

KEGG module: M00563
Methanogenesis
bg.adj.SCC for leave−1−MGS−out
Number of MGSs = 125



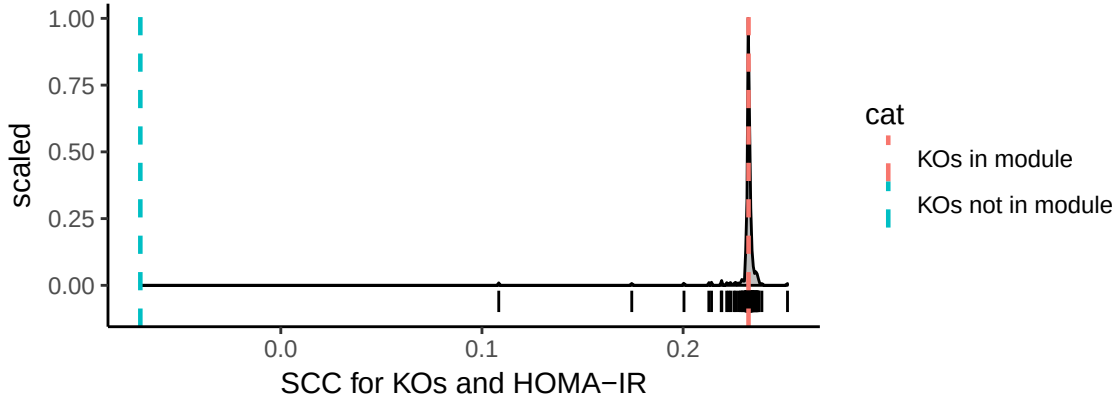
a

KEGG module: M00060
Lipopolysaccharide biosynthesis
10 KOs in module vs all remaining 6748 KOs



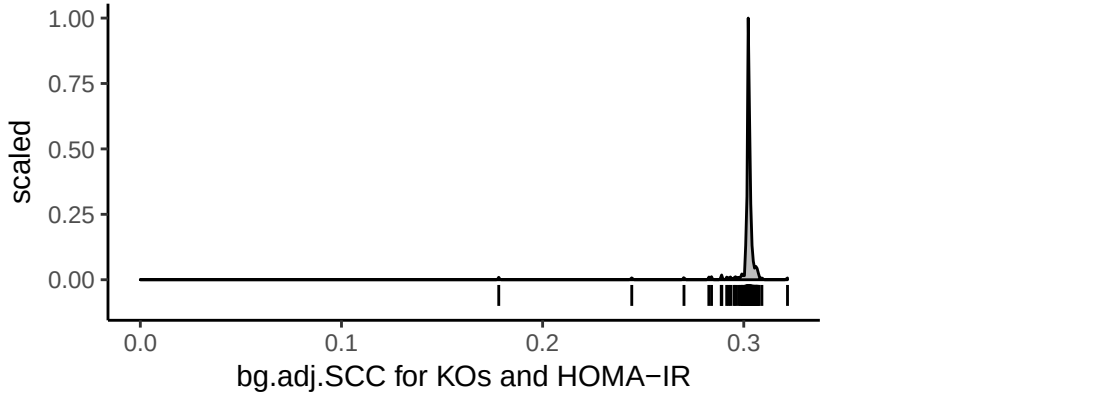
b

KEGG module: M00060
Lipopolysaccharide biosynthesis
SCC for leave−1−MGS−out
Number of MGSs = 237



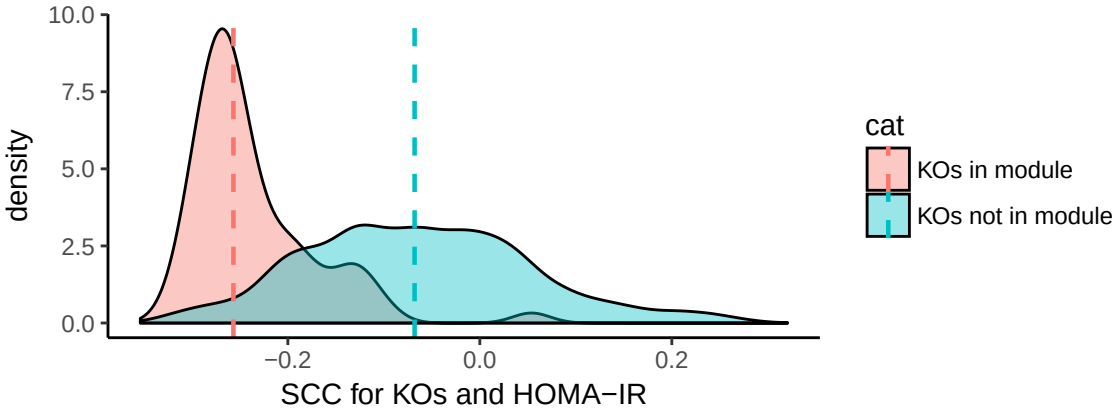
c

KEGG module: M00060
Lipopolysaccharide biosynthesis
bg.adj.SCC for leave−1−MGS−out
Number of MGSs = 237



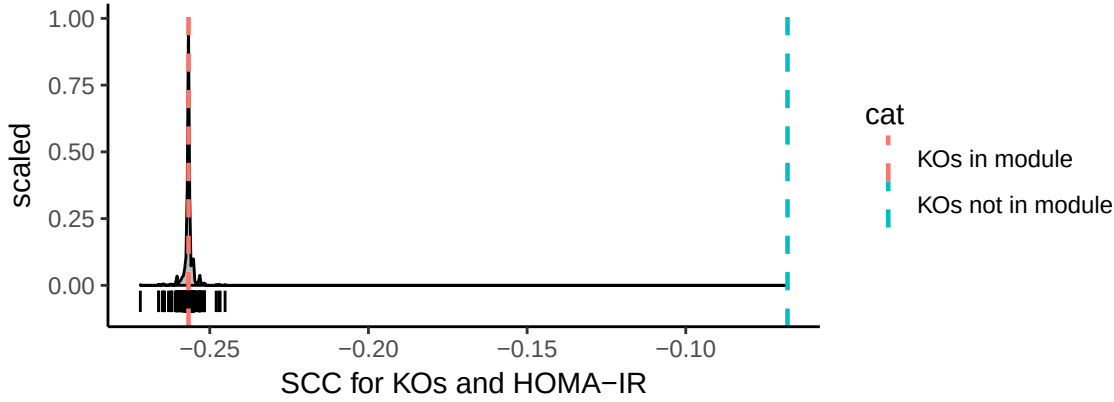
a

KEGG module: M00179
Ribosome
67 KOs in module vs all remaining 6691 KOs



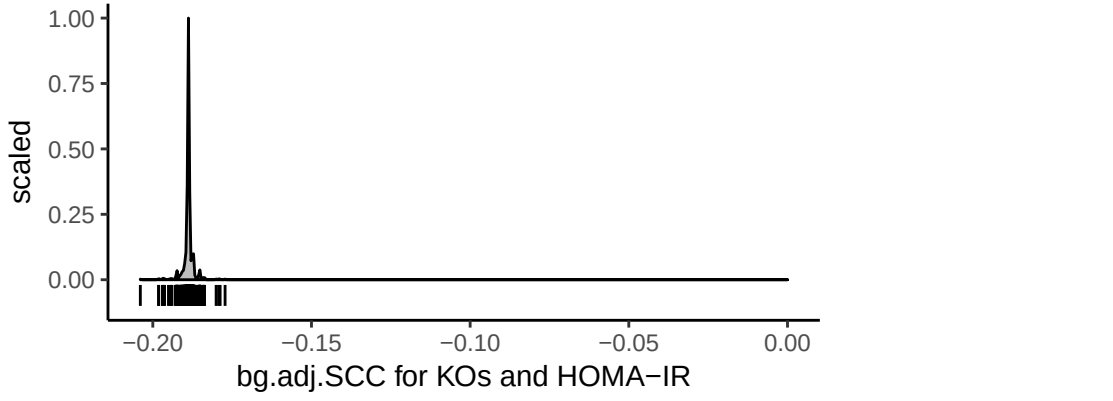
b

KEGG module: M00179
Ribosome
SCC for leave−1−MGS−out
Number of MGSs = 711



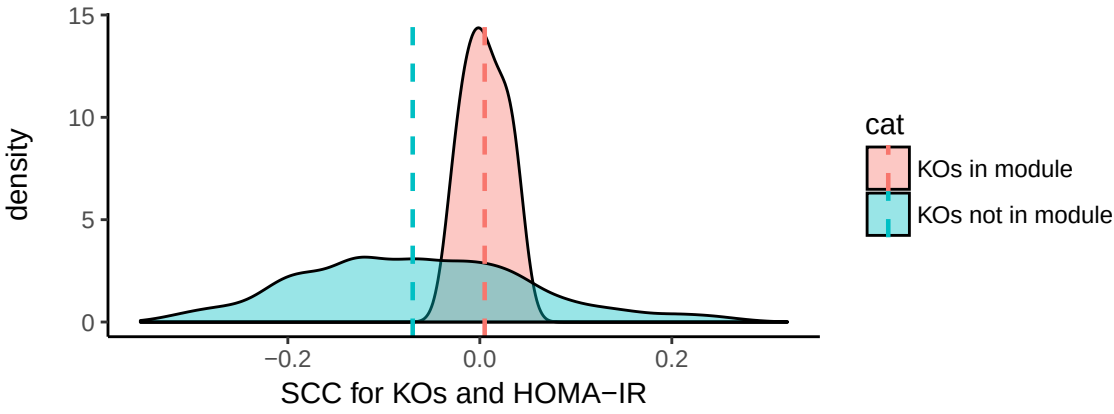
c

KEGG module: M00179
Ribosome
bg.adj.SCC for leave−1−MGS−out
Number of MGSs = 711



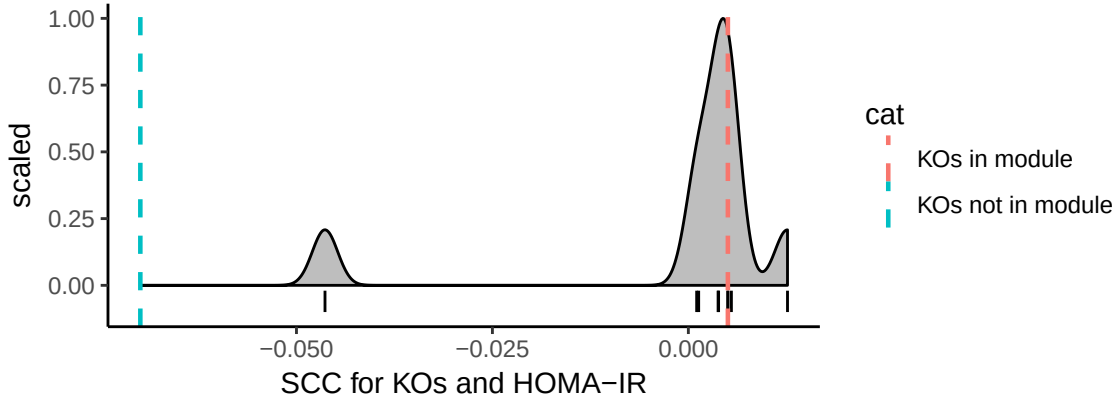
a

KEGG module: M00332
Type III secretion system
15 KOs in module vs all remaining 6743 KOs



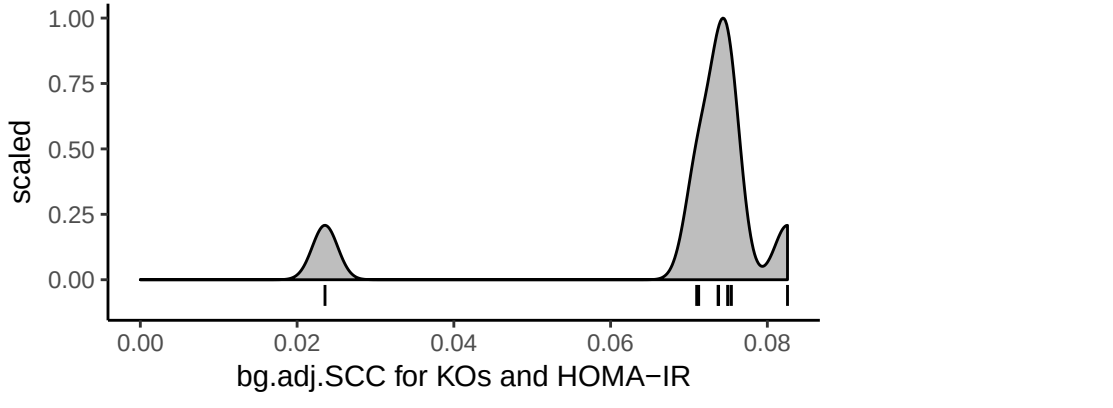
b

KEGG module: M00332
Type III secretion system
SCC for leave−1−MGS−out
Number of MGSs = 9



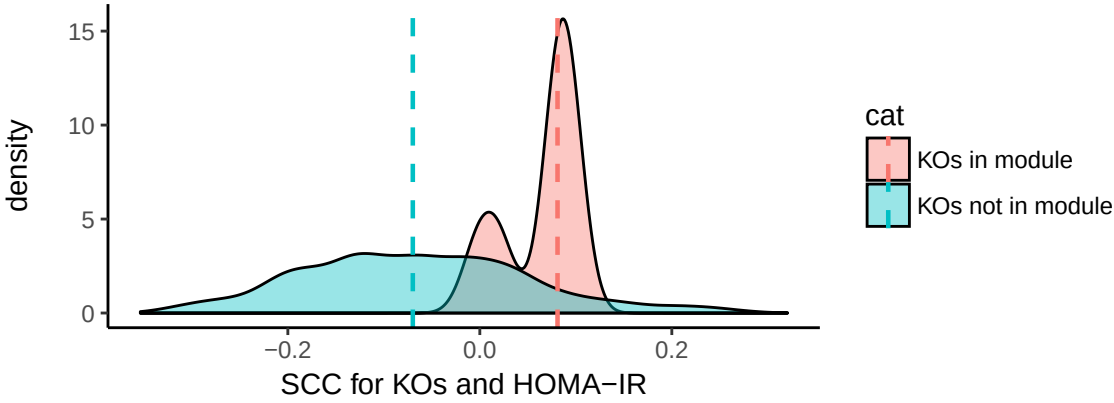
c

KEGG module: M00332
Type III secretion system
bg.adj.SCC for leave−1−MGS−out
Number of MGSs = 9



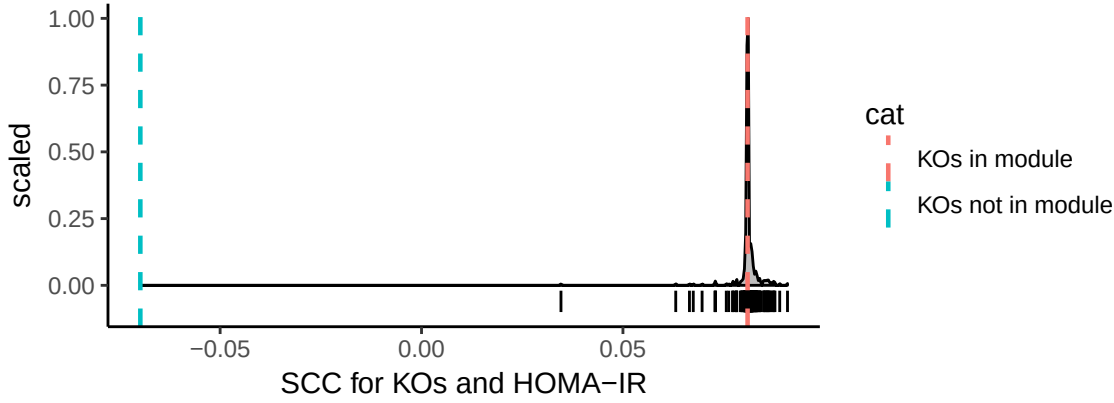
a

KEGG module: M00122
Cobalamin biosynthesis
9 KOs in module vs all remaining 6749 KOs



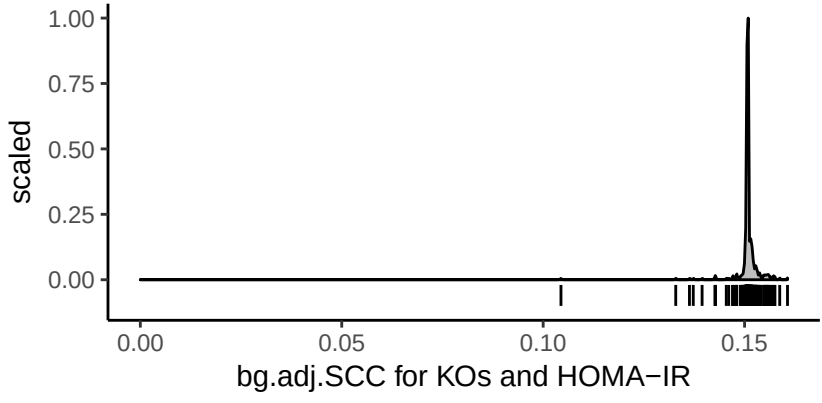
b

KEGG module: M00122
Cobalamin biosynthesis
SCC for leave−1−MGS−out
Number of MGSs = 396



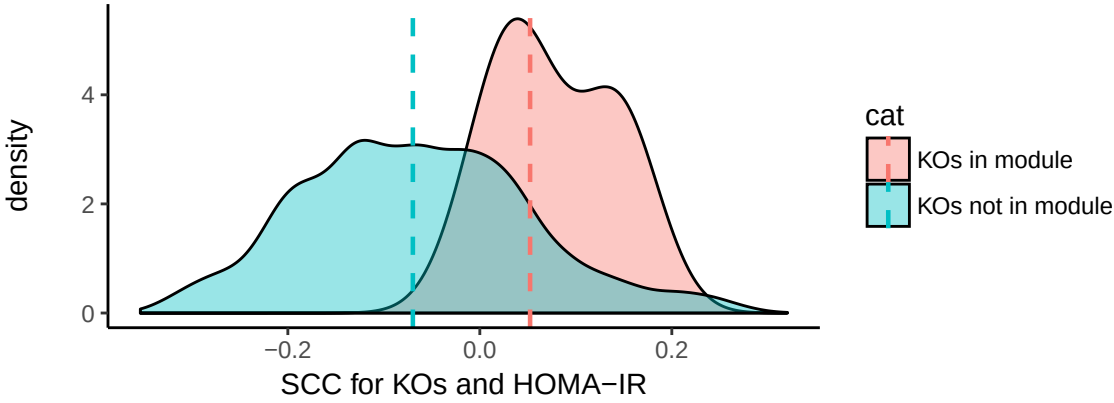
c

KEGG module: M00122
Cobalamin biosynthesis
bg.adj.SCC for leave−1−MGS−out
Number of MGSs = 396



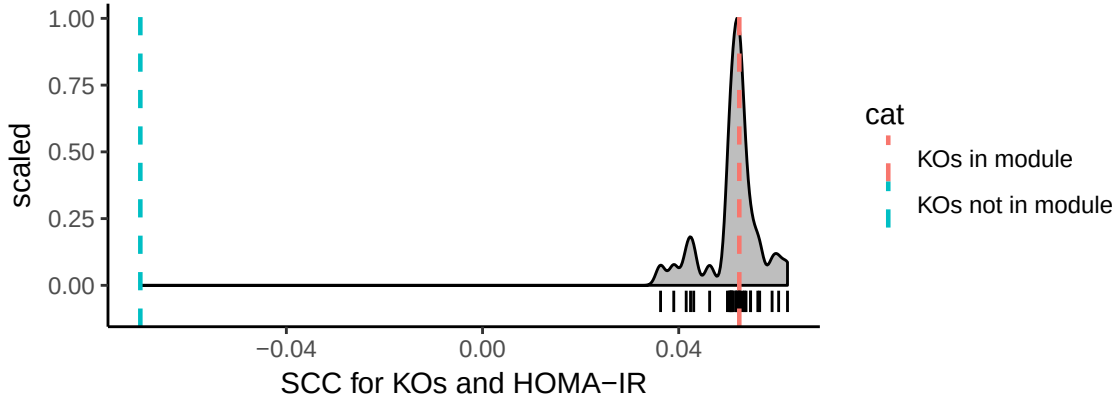
a

KEGG module: M00440
Nickel transport system
5 KOs in module vs all remaining 6753 KOs



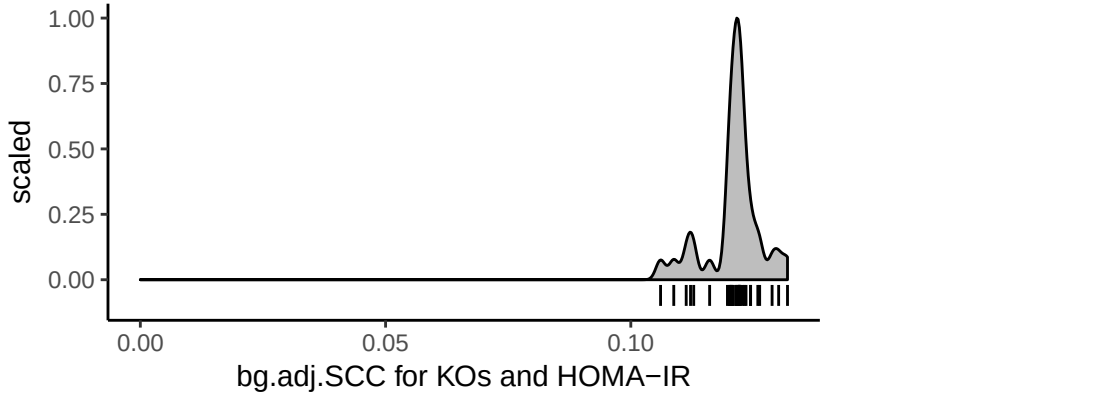
b

KEGG module: M00440
Nickel transport system
SCC for leave−1−MGS−out
Number of MGSs = 34



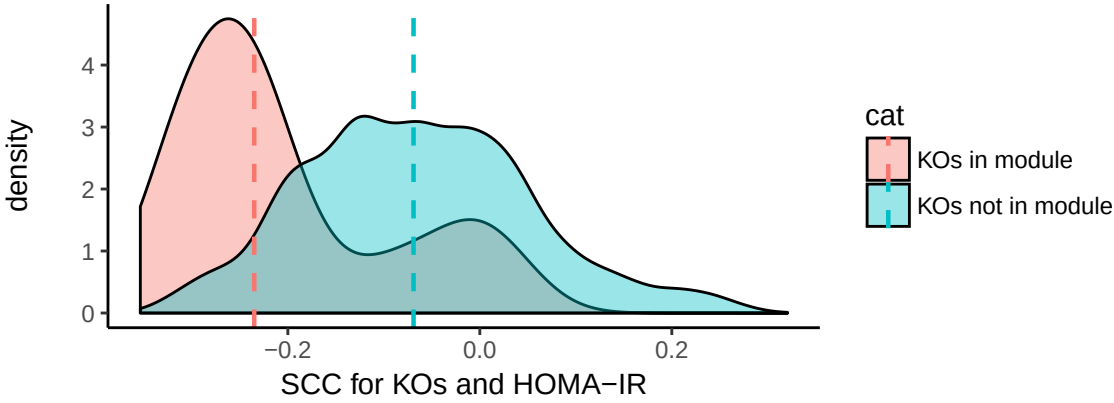
c

KEGG module: M00440
Nickel transport system
bg.adj.SCC for leave−1−MGS−out
Number of MGSs = 34



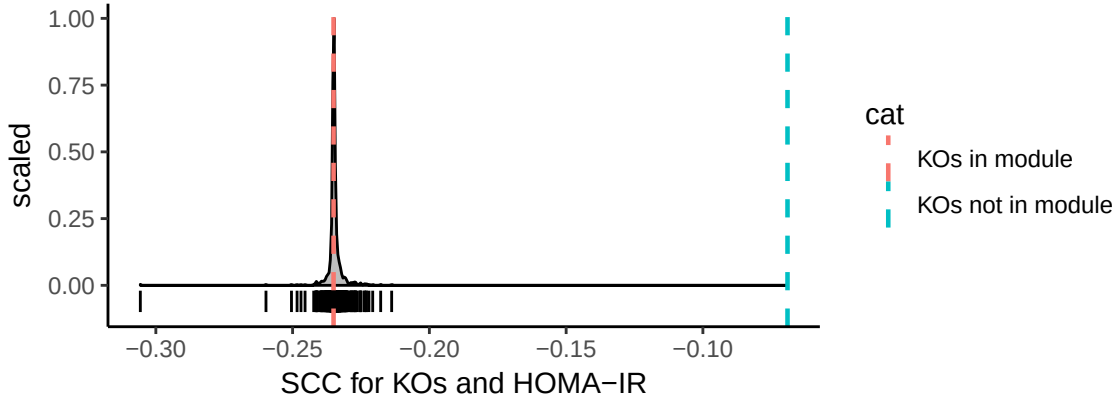
a

KEGG module: M00360
Aminoacyl−tRNA biosynthesis
31 KOs in module vs all remaining 6727 KOs



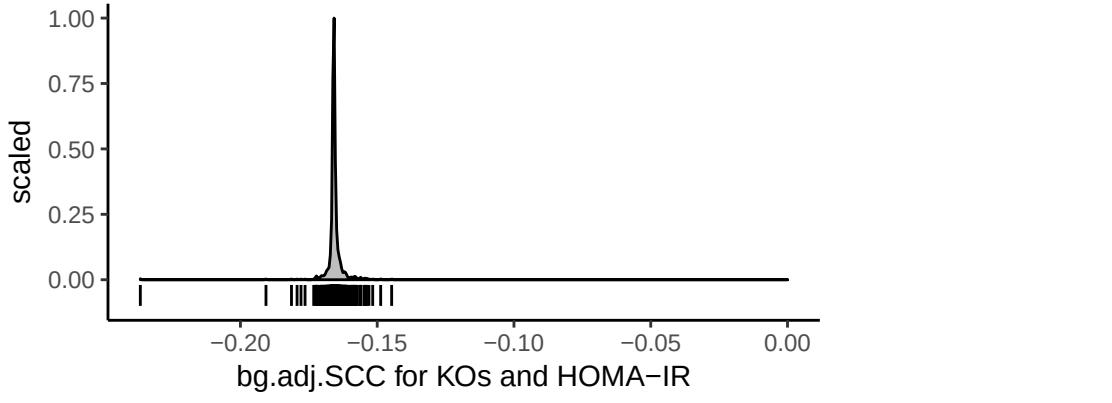
b

KEGG module: M00360
Aminoacyl−tRNA biosynthesis
SCC for leave−1−MGS−out
Number of MGSs = 787



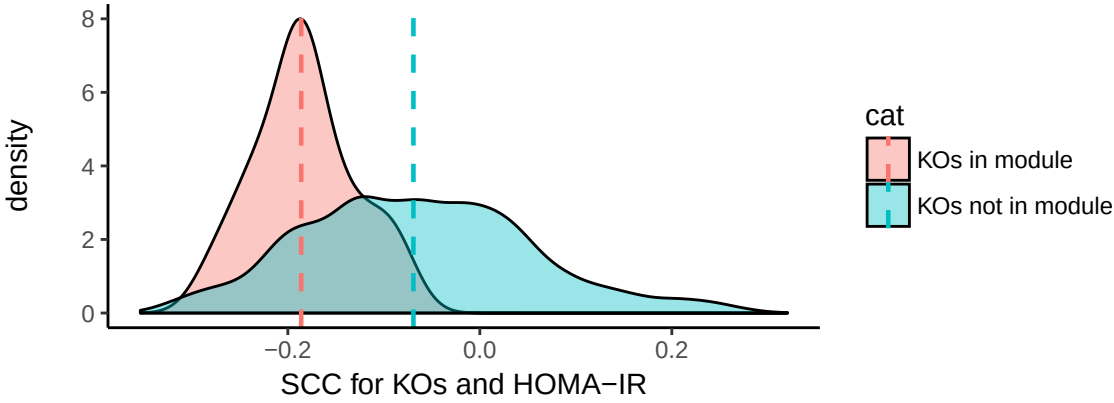
c

KEGG module: M00360
Aminoacyl−tRNA biosynthesis
bg.adj.SCC for leave−1−MGS−out
Number of MGSs = 787



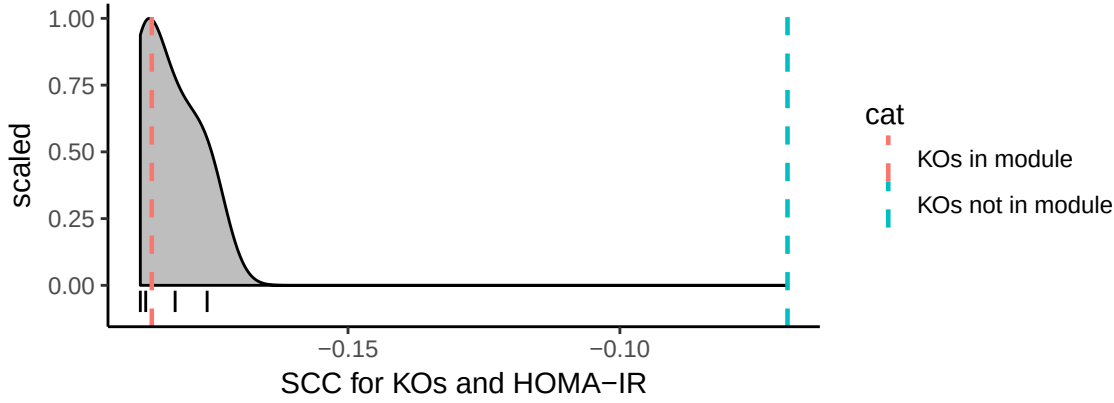
a

KEGG module: M00184
RNA polymerase
16 KOs in module vs all remaining 6742 KOs



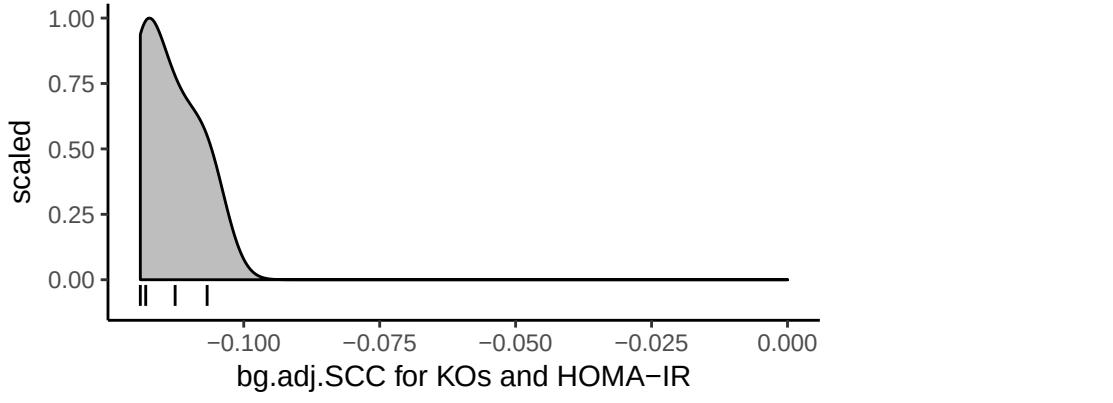
b

KEGG module: M00184
RNA polymerase
SCC for leave−1−MGS−out
Number of MGSs = 4



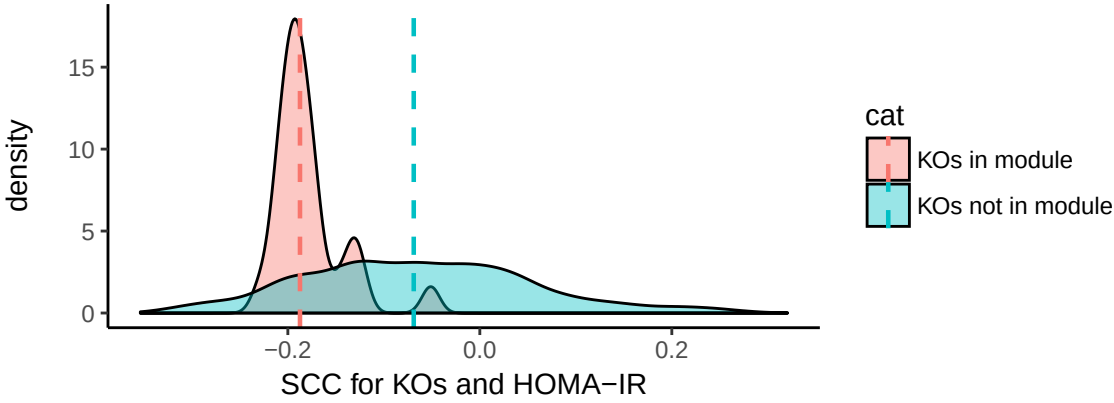
c

KEGG module: M00184
RNA polymerase
bg.adj.SCC for leave−1−MGS−out
Number of MGSs = 4



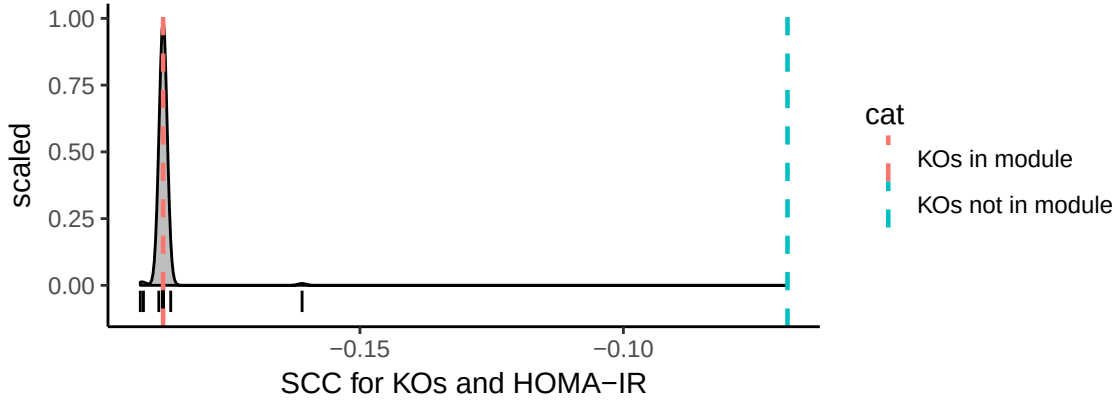
a

KEGG module: M00567
Methanogenesis
27 KOs in module vs all remaining 6731 KOs



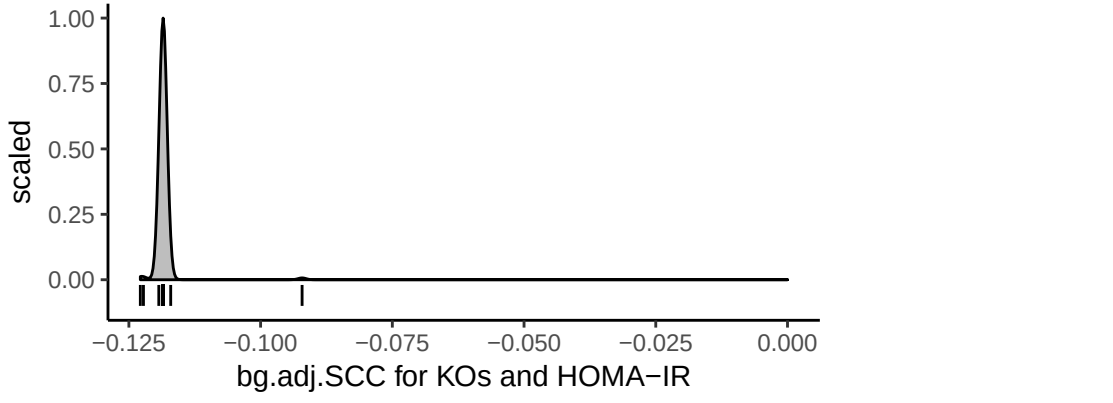
b

KEGG module: M00567
Methanogenesis
SCC for leave−1−MGS−out
Number of MGSs = 145



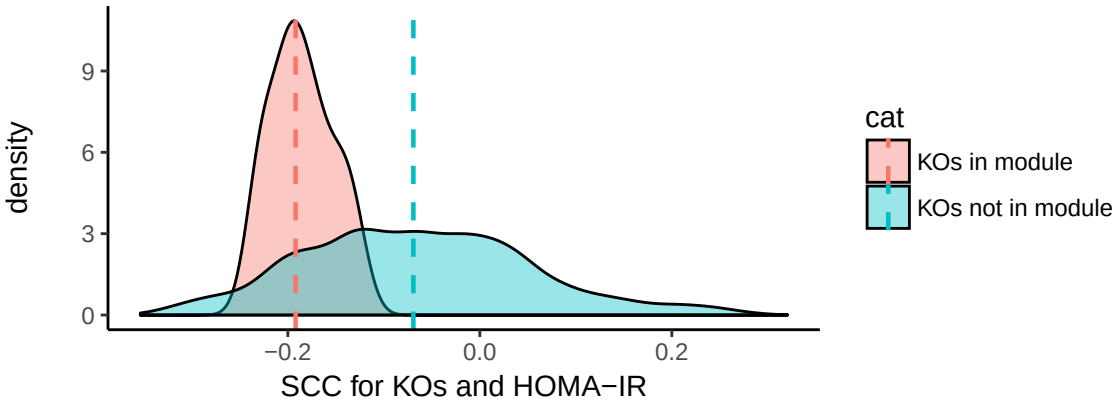
c

KEGG module: M00567
Methanogenesis
bg.adj.SCC for leave−1−MGS−out
Number of MGSs = 145



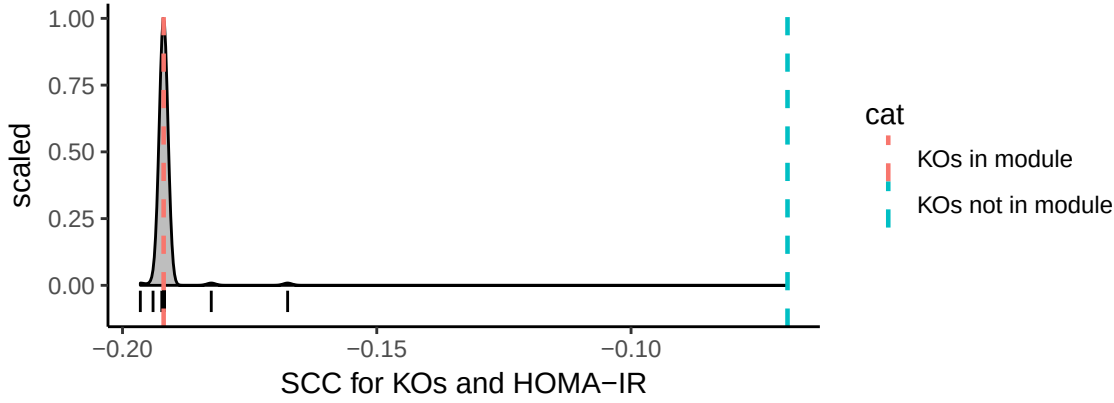
a

KEGG module: M00356
Methanogenesis
9 KOs in module vs all remaining 6749 KOs



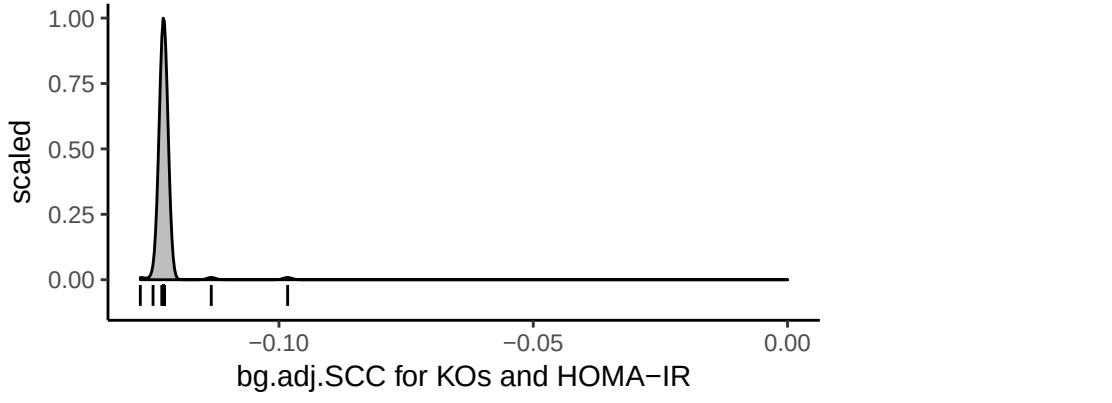
b

KEGG module: M00356
Methanogenesis
SCC for leave−1−MGS−out
Number of MGSs = 121



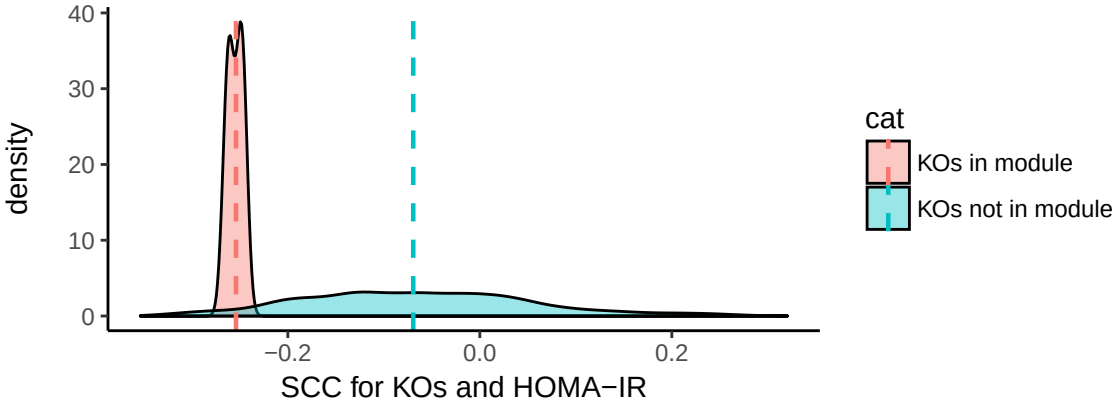
c

KEGG module: M00356
Methanogenesis
bg.adj.SCC for leave−1−MGS−out
Number of MGSs = 121



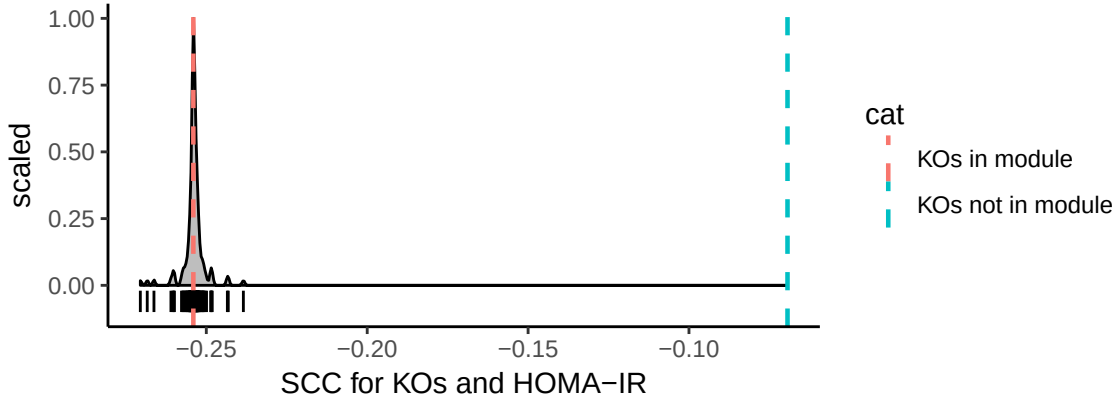
a

KEGG module: M00310
Pyruvate:ferredoxin oxidoreductase
4 KOs in module vs all remaining 6754 KOs



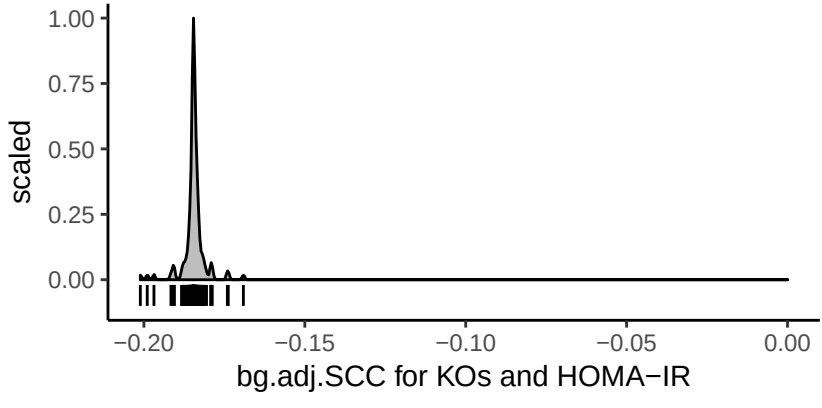
b

KEGG module: M00310
Pyruvate:ferredoxin oxidoreductase
SCC for leave−1−MGS−out
Number of MGSs = 129



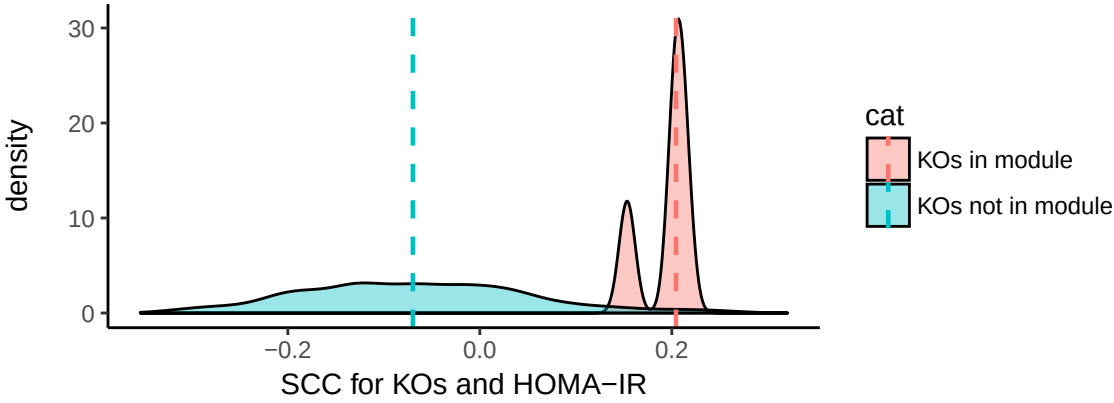
c

KEGG module: M00310
Pyruvate:ferredoxin oxidoreductase
bg.adj.SCC for leave−1−MGS−out
Number of MGSs = 129



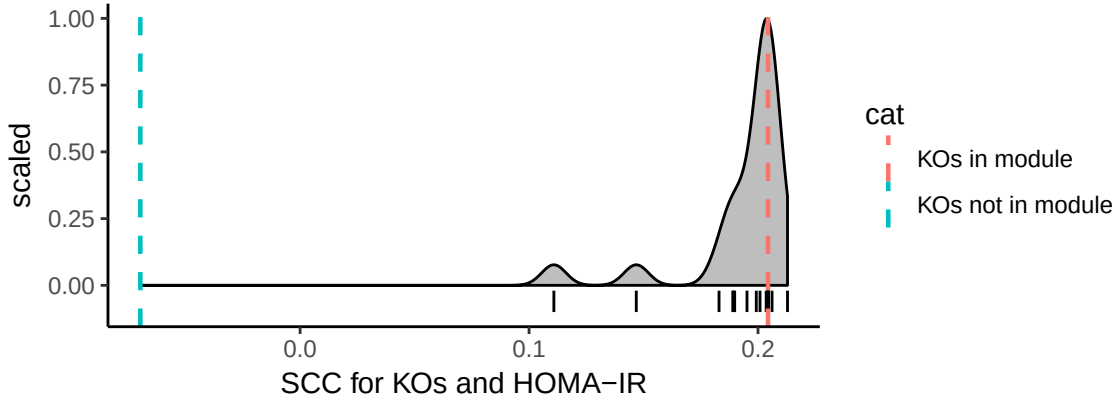
a

KEGG module: M00230
Glutamate/aspartate transport system
4 KOs in module vs all remaining 6754 KOs



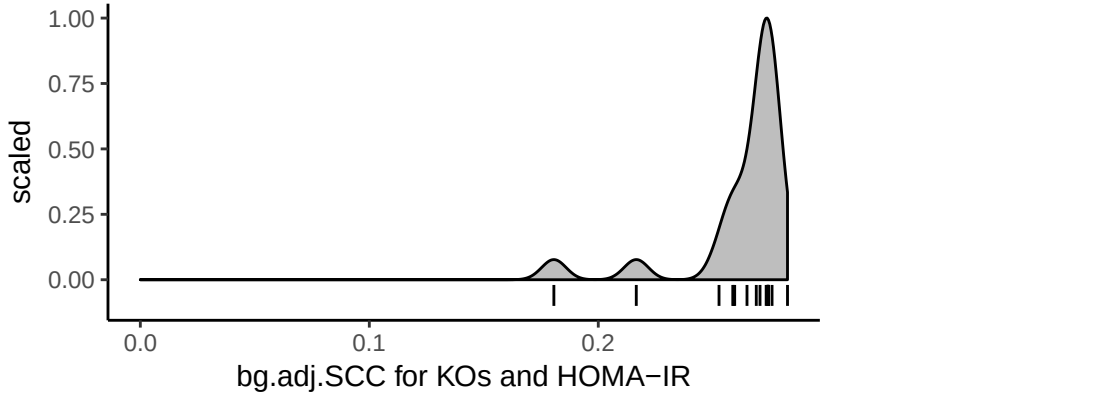
b

KEGG module: M00230
Glutamate/aspartate transport system
SCC for leave−1−MGS−out
Number of MGSs = 21



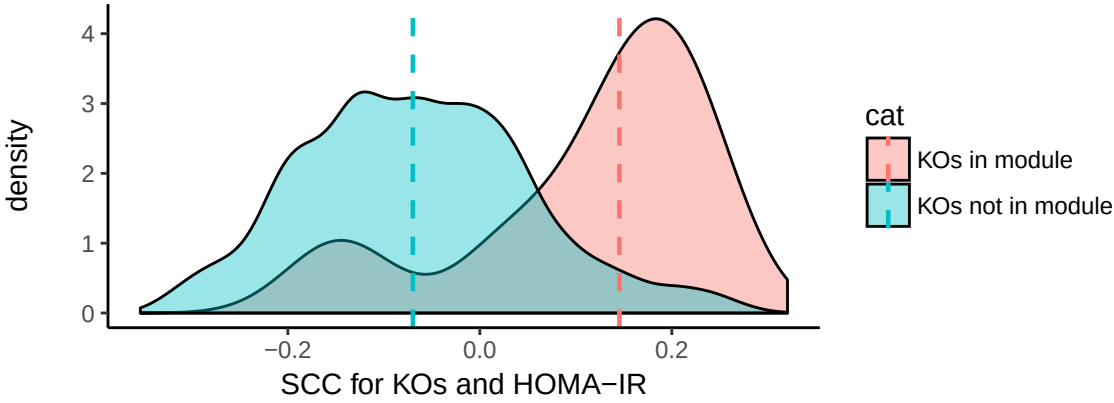
c

KEGG module: M00230
Glutamate/aspartate transport system
bg.adj.SCC for leave−1−MGS−out
Number of MGSs = 21



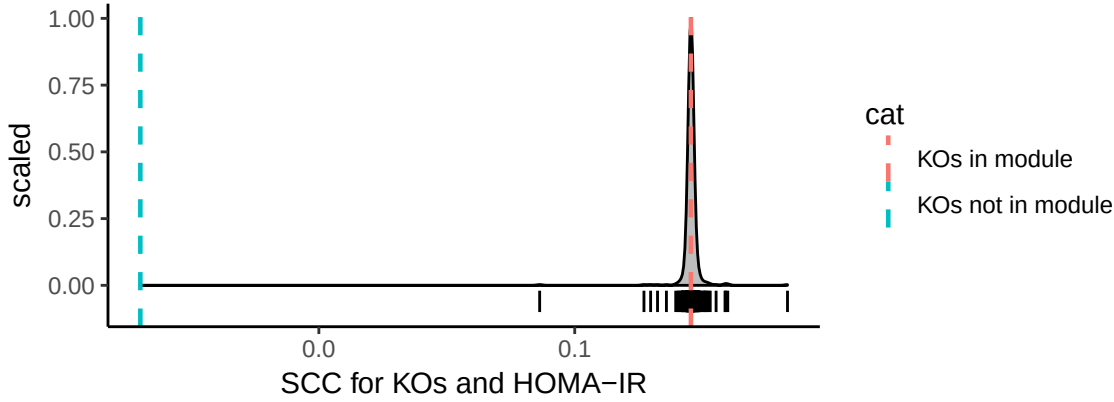
a

KEGG module: M00127
Thiamine biosynthesis
8 KOs in module vs all remaining 6750 KOs



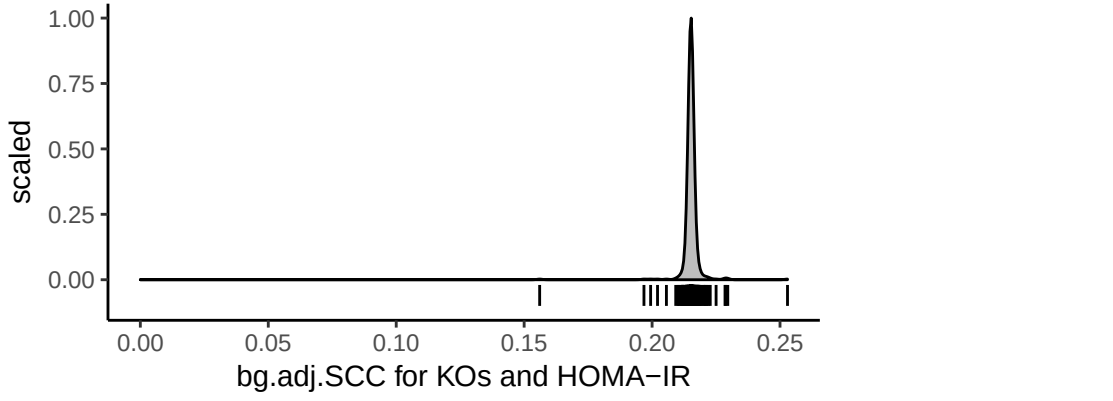
b

KEGG module: M00127
Thiamine biosynthesis
SCC for leave−1−MGS−out
Number of MGSs = 484



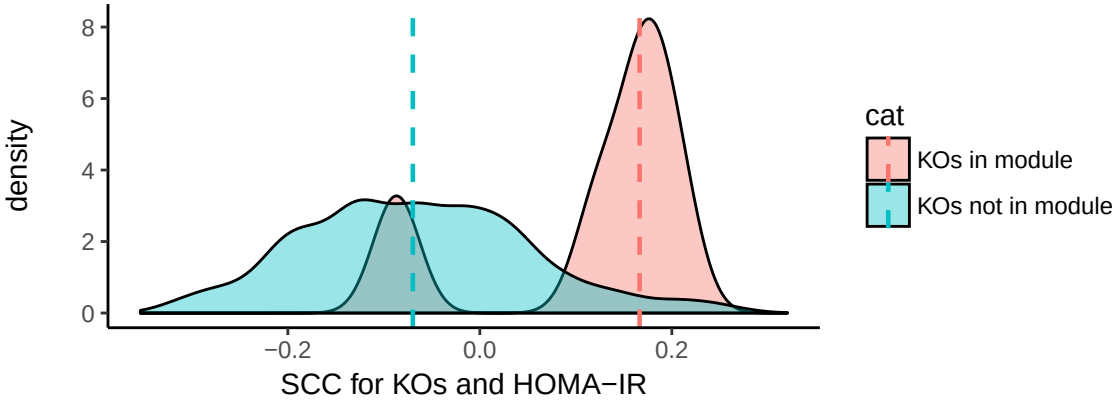
c

KEGG module: M00127
Thiamine biosynthesis
bg.adj.SCC for leave−1−MGS−out
Number of MGSs = 484



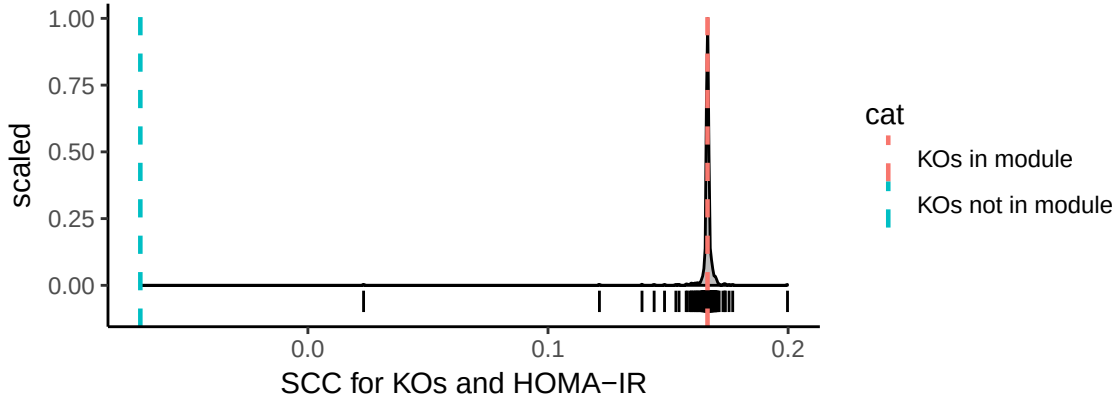
a

KEGG module: M00023
Tryptophan biosynthesis
14 KOs in module vs all remaining 6744 KOs



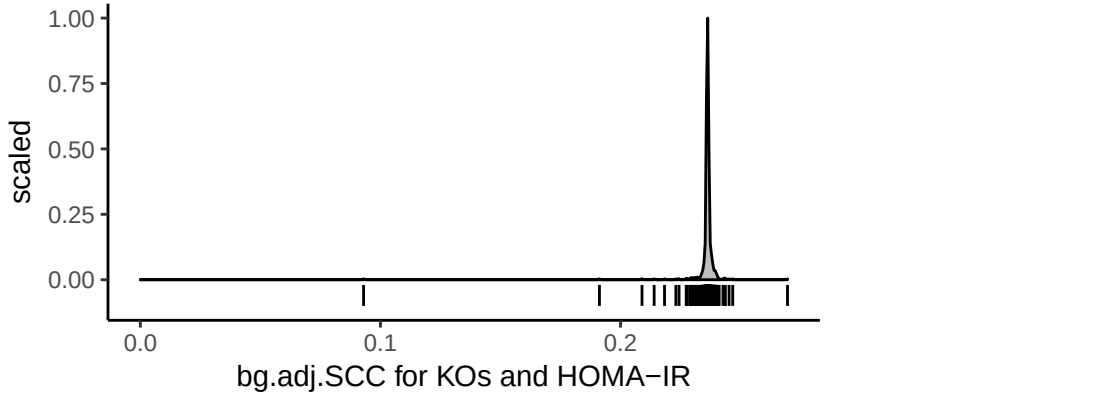
b

KEGG module: M00023
Tryptophan biosynthesis
SCC for leave−1−MGS−out
Number of MGSs = 487



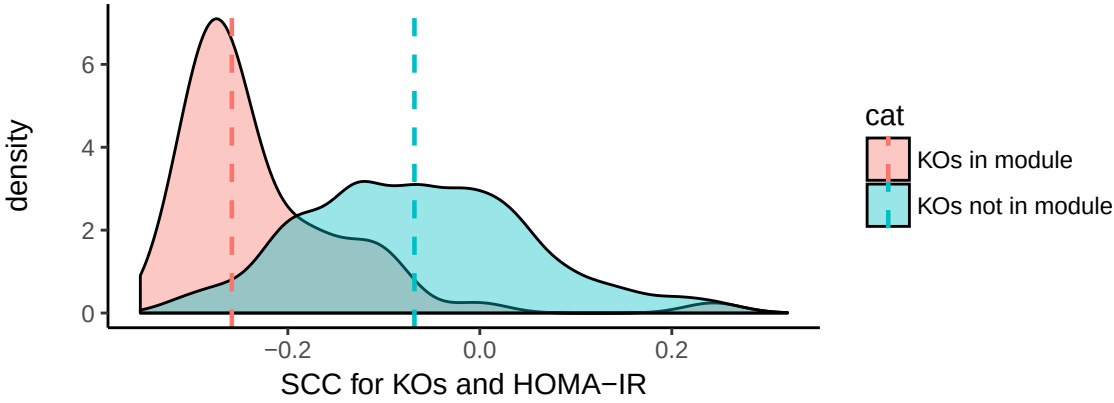
c

KEGG module: M00023
Tryptophan biosynthesis
bg.adj.SCC for leave−1−MGS−out
Number of MGSs = 487



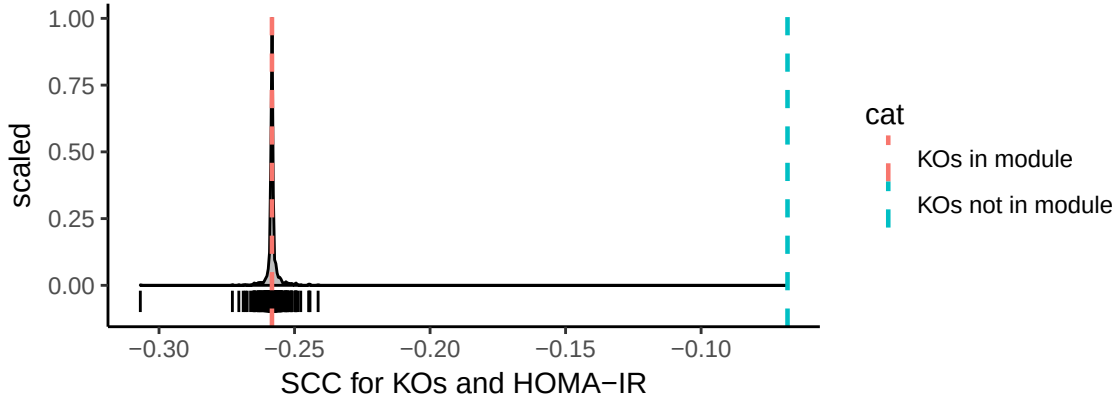
a

KEGG module: M00178
Ribosome
55 KOs in module vs all remaining 6703 KOs



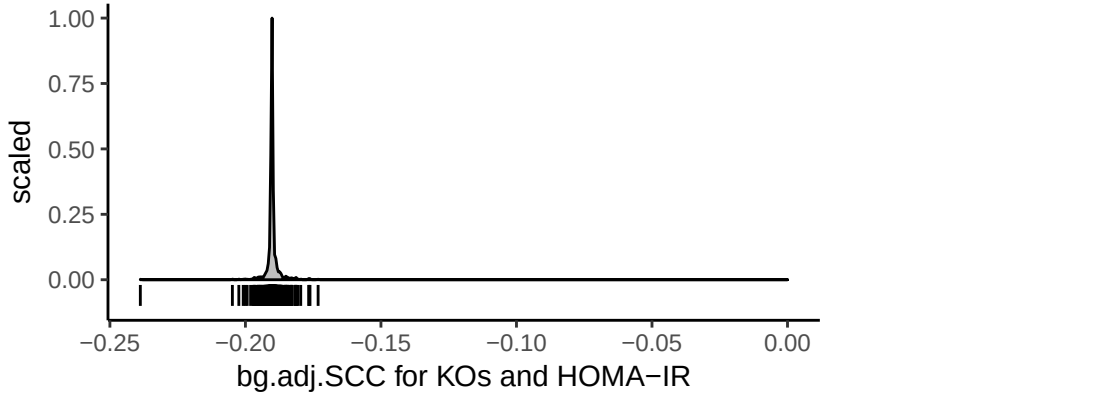
b

KEGG module: M00178
Ribosome
SCC for leave−1−MGS−out
Number of MGSs = 767



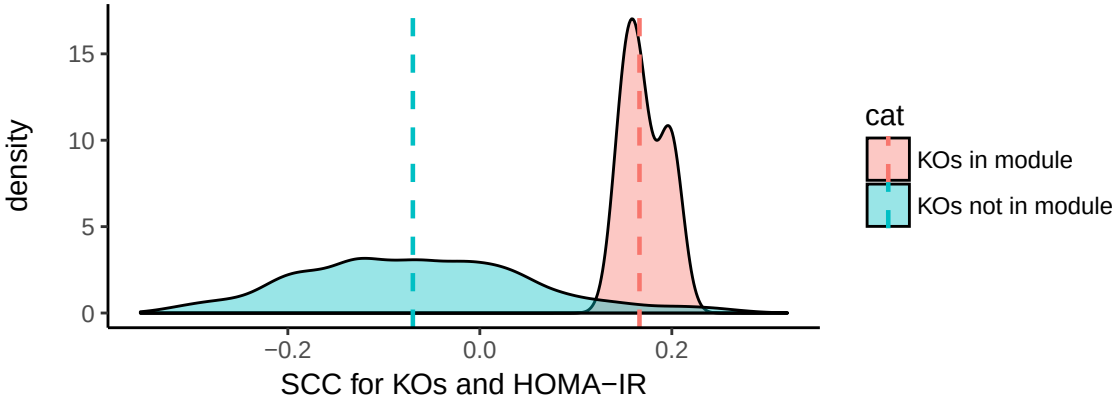
c

KEGG module: M00178
Ribosome
bg.adj.SCC for leave−1−MGS−out
Number of MGSs = 767



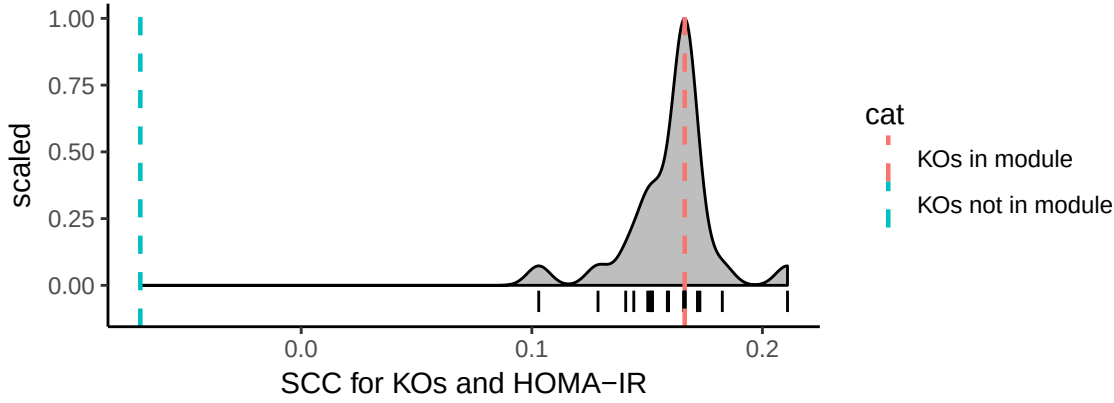
a

KEGG module: M00259
Heme transport system
3 KOs in module vs all remaining 6755 KOs



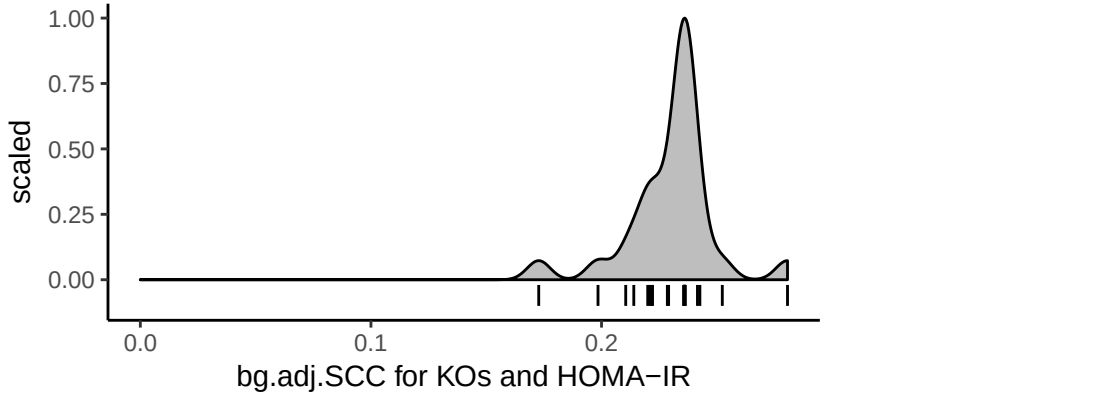
b

KEGG module: M00259
Heme transport system
SCC for leave−1−MGS−out
Number of MGSs = 26



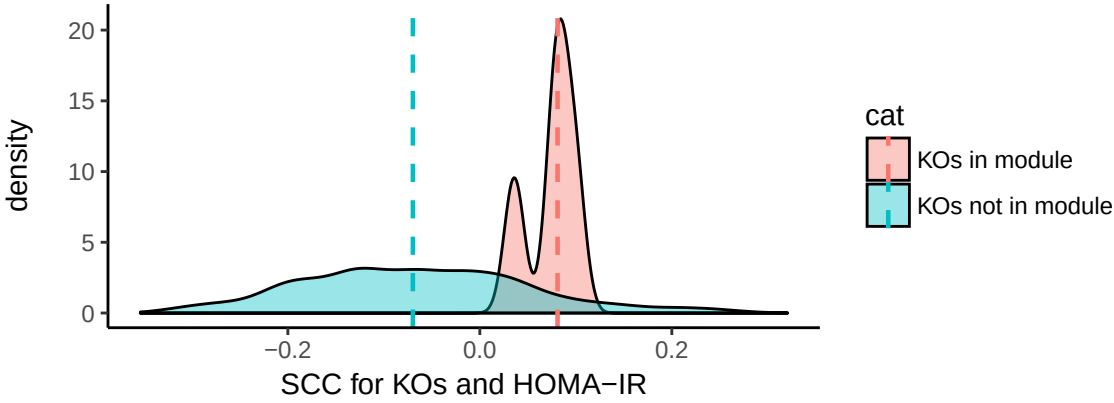
c

KEGG module: M00259
Heme transport system
bg.adj.SCC for leave−1−MGS−out
Number of MGSs = 26



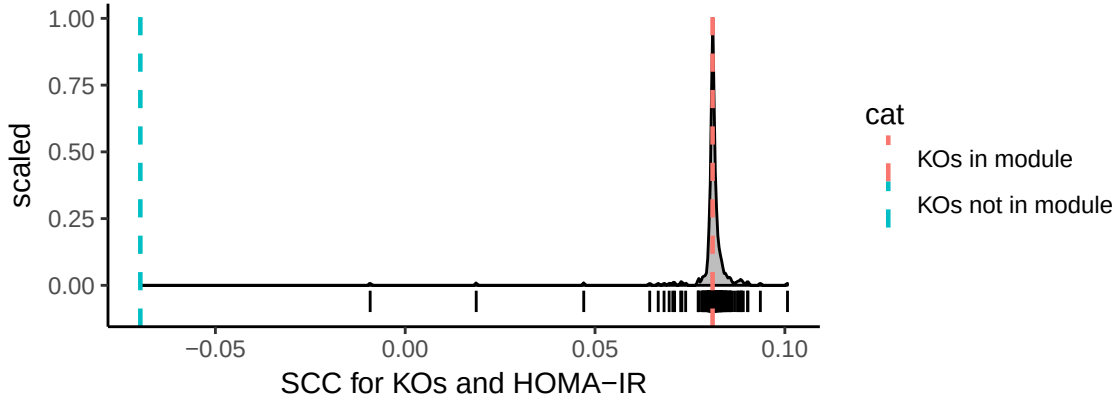
a

KEGG module: M00311
2−oxoglutarate:ferredoxin oxidoreductase
4 KOs in module vs all remaining 6754 KOs



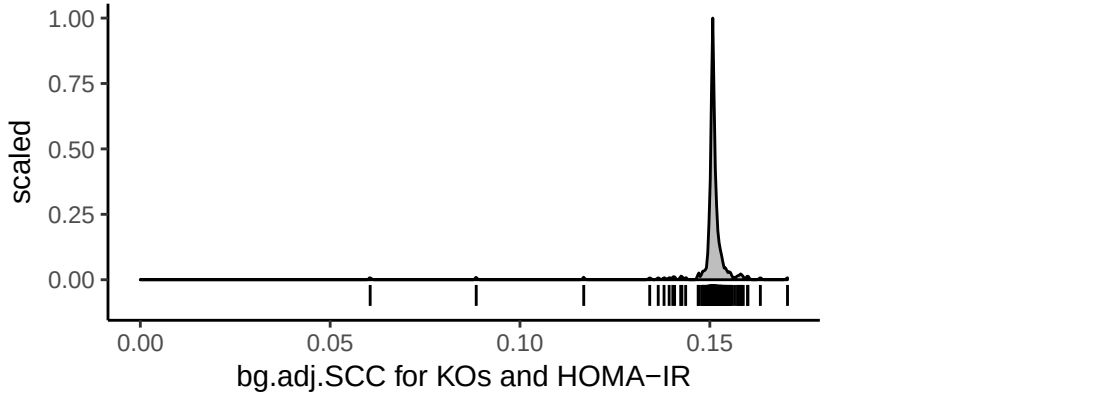
b

KEGG module: M00311
2−oxoglutarate:ferredoxin oxidoreductase
SCC for leave−1−MGS−out
Number of MGSs = 296



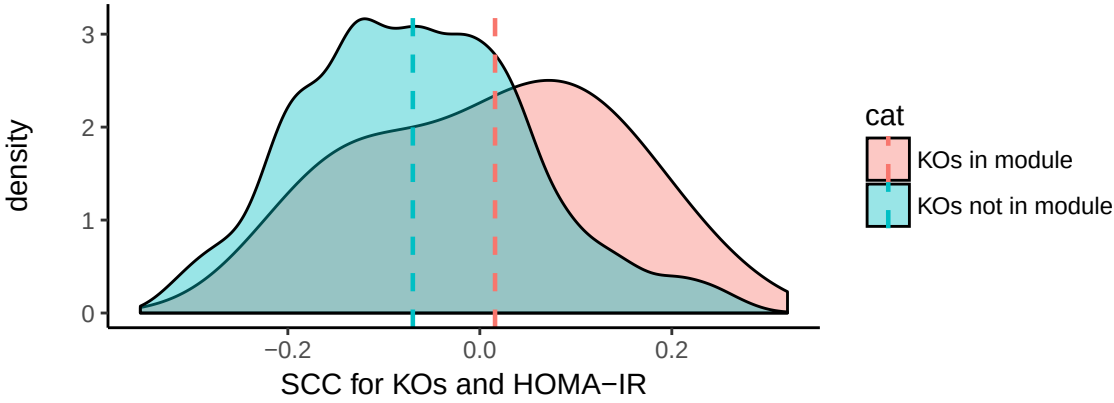
c

KEGG module: M00311
2−oxoglutarate:ferredoxin oxidoreductase
bg.adj.SCC for leave−1−MGS−out
Number of MGSs = 296



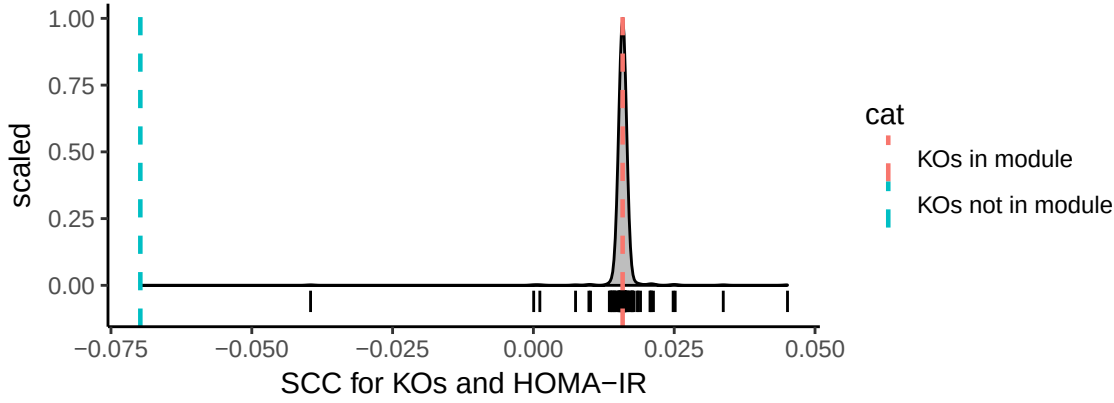
a

KEGG module: M00048
Inosine monophosphate biosynthesis
20 KOs in module vs all remaining 6738 KOs



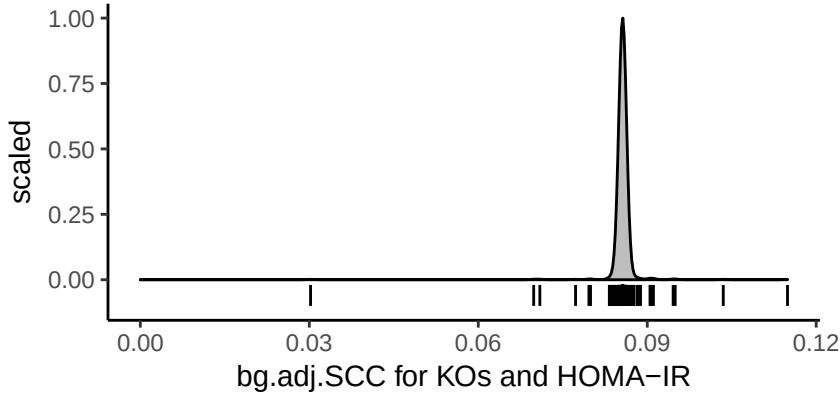
b

KEGG module: M00048
Inosine monophosphate biosynthesis
SCC for leave−1−MGS−out
Number of MGSs = 688



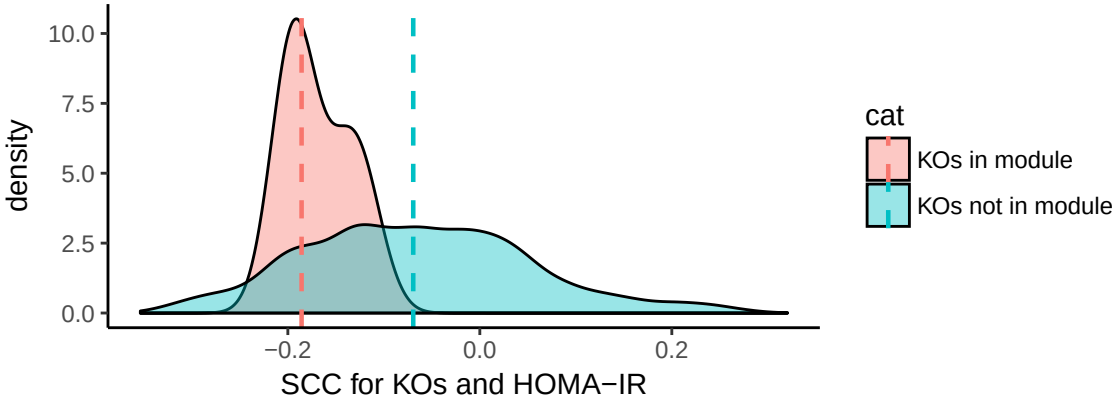
c

KEGG module: M00048
Inosine monophosphate biosynthesis
bg.adj.SCC for leave−1−MGS−out
Number of MGSs = 688



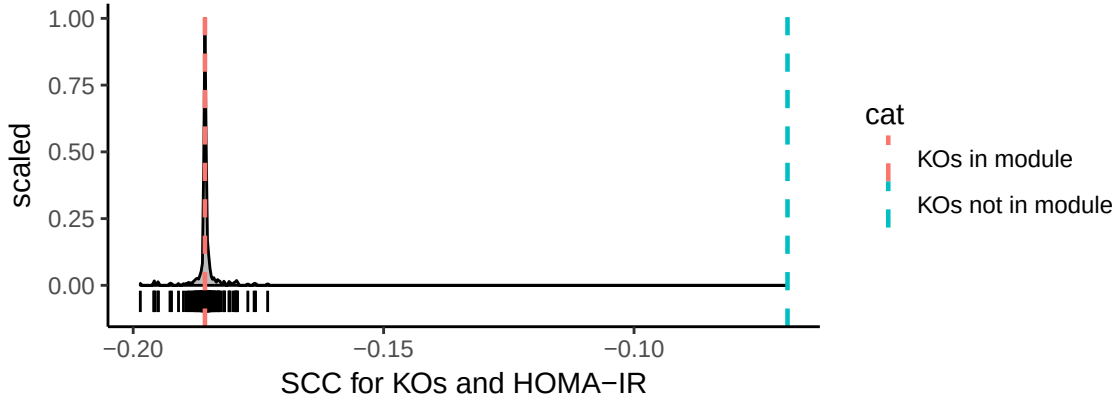
a

KEGG module: M00439
Oligopeptide transport system
5 KOs in module vs all remaining 6753 KOs



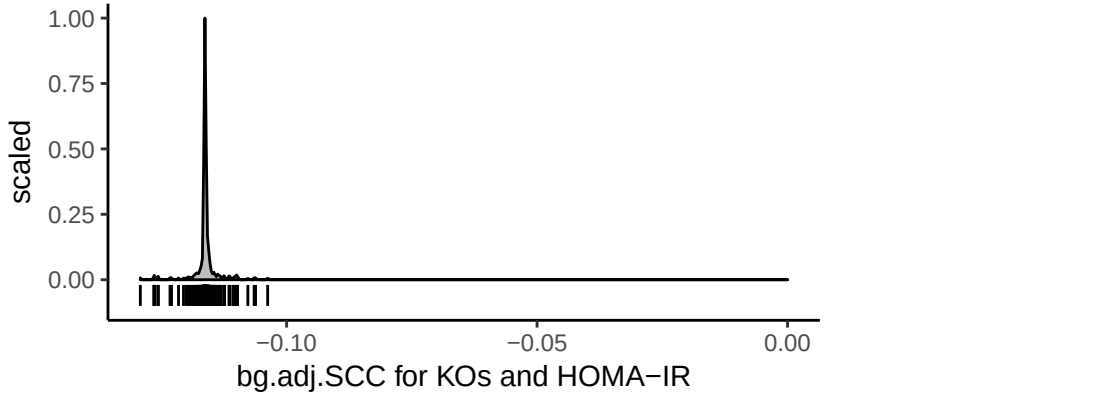
b

KEGG module: M00439
Oligopeptide transport system
SCC for leave−1−MGS−out
Number of MGSs = 307



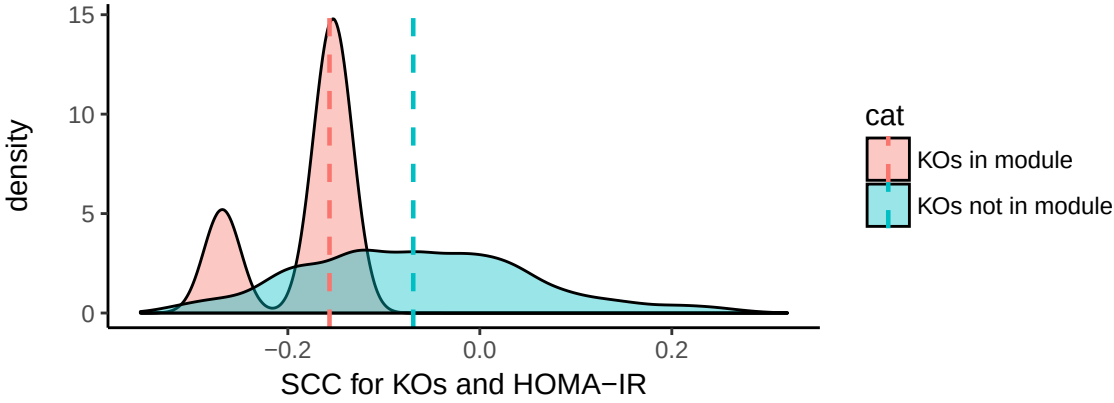
c

KEGG module: M00439
Oligopeptide transport system
bg.adj.SCC for leave−1−MGS−out
Number of MGSs = 307



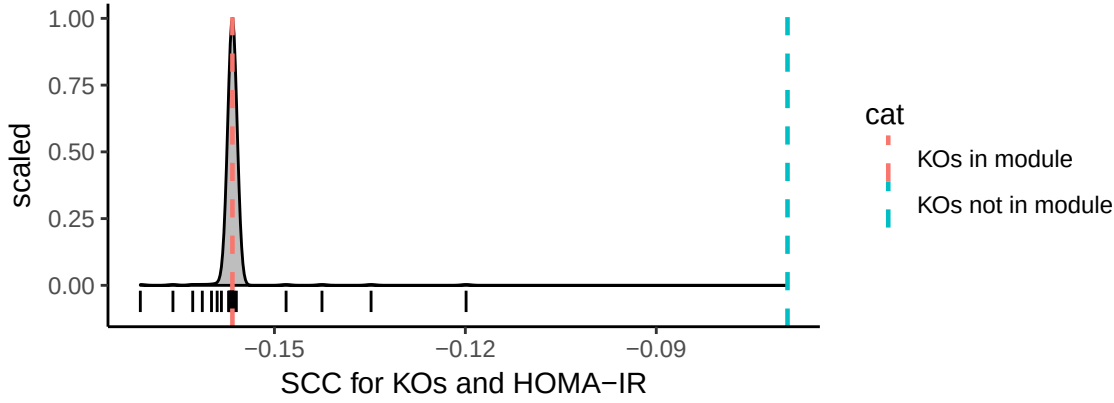
a

KEGG module: M00197
Putative fructooligosaccharide transport system
4 KOs in module vs all remaining 6754 KOs



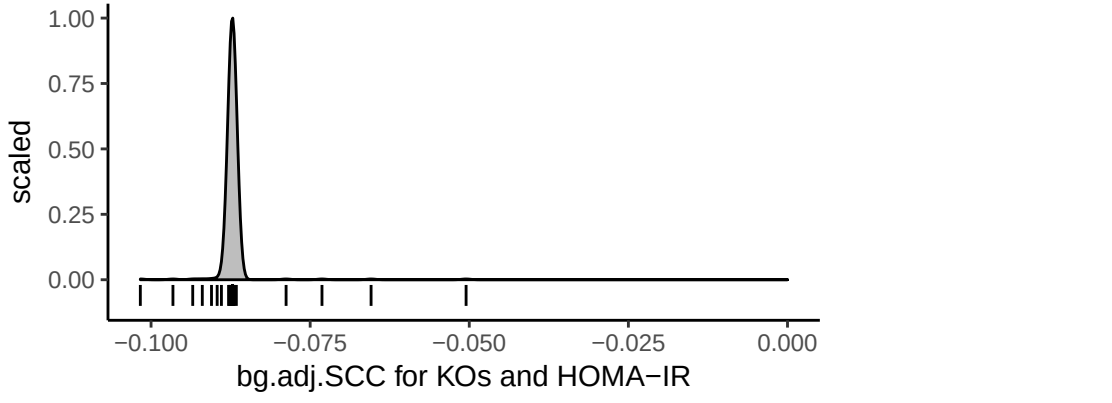
b

KEGG module: M00197
Putative fructooligosaccharide transport system
SCC for leave−1−MGS−out
Number of MGSs = 365



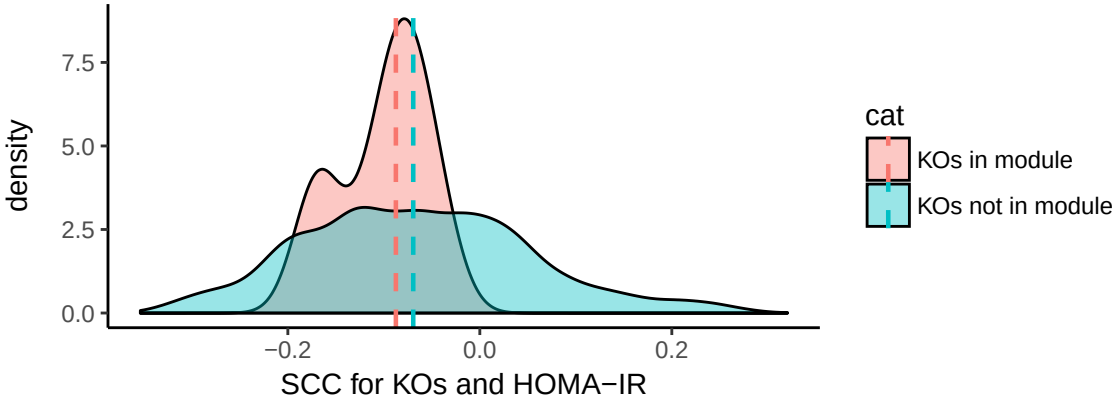
c

KEGG module: M00197
Putative fructooligosaccharide transport system
bg.adj.SCC for leave−1−MGS−out
Number of MGSs = 365



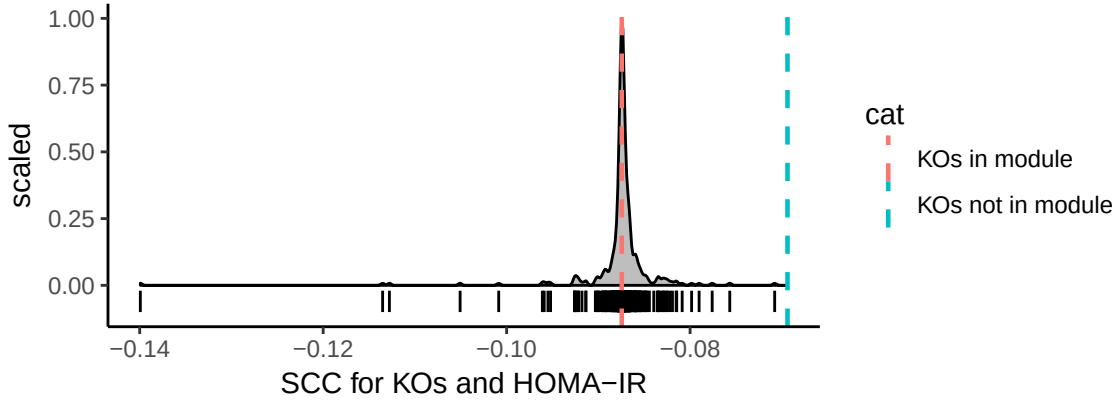
a

KEGG module: M00159
V−type ATPase
8 KOs in module vs all remaining 6750 KOs



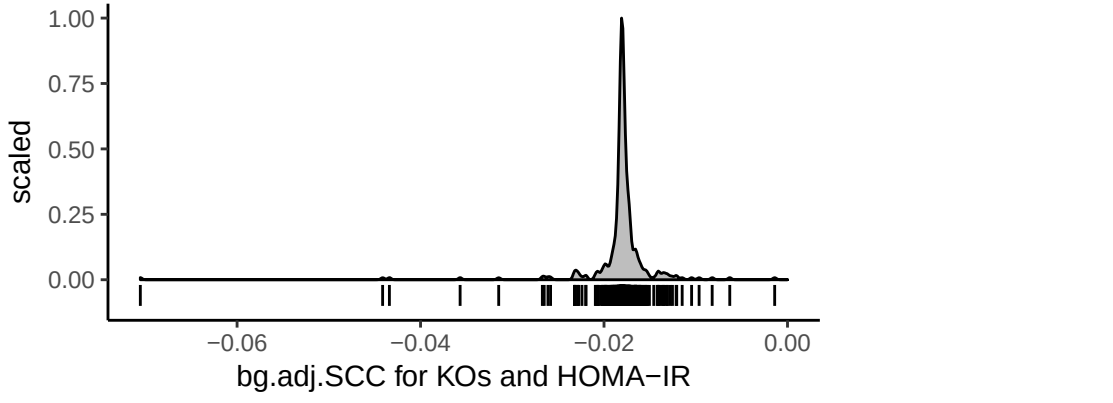
b

KEGG module: M00159
V−type ATPase
SCC for leave−1−MGS−out
Number of MGSs = 355



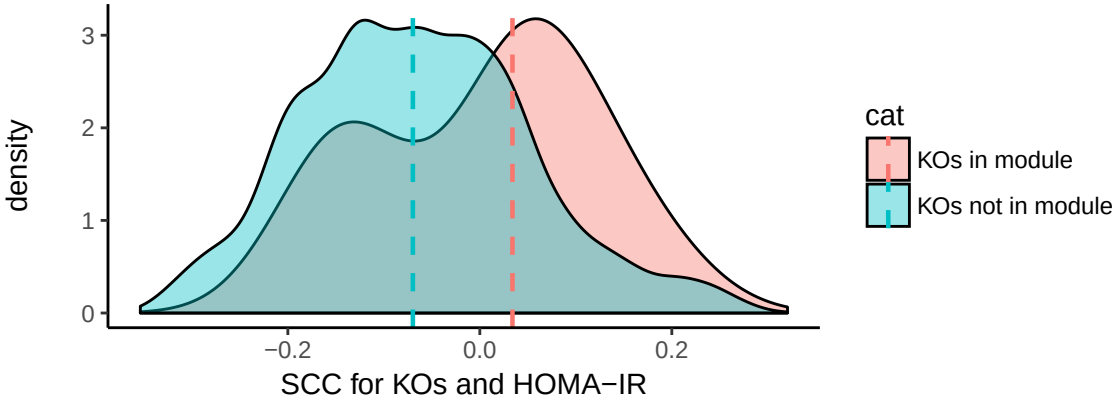
c

KEGG module: M00159
V−type ATPase
bg.adj.SCC for leave−1−MGS−out
Number of MGSs = 355



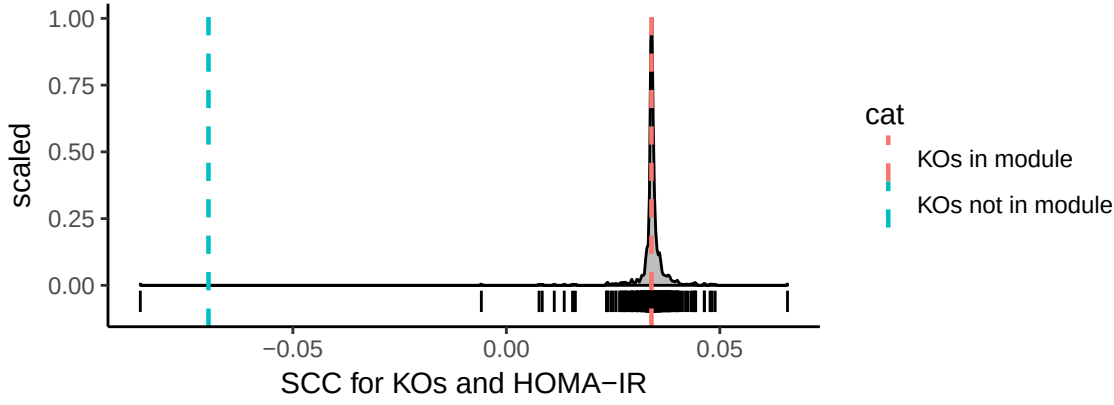
a

KEGG module: M00051
Uridine monophosphate biosynthesis
14 KOs in module vs all remaining 6744 KOs



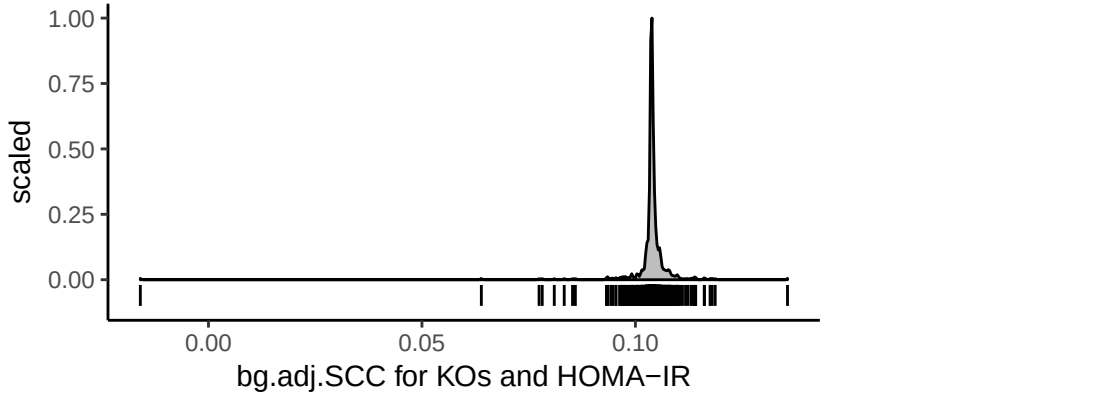
b

KEGG module: M00051
Uridine monophosphate biosynthesis
SCC for leave−1−MGS−out
Number of MGSs = 651



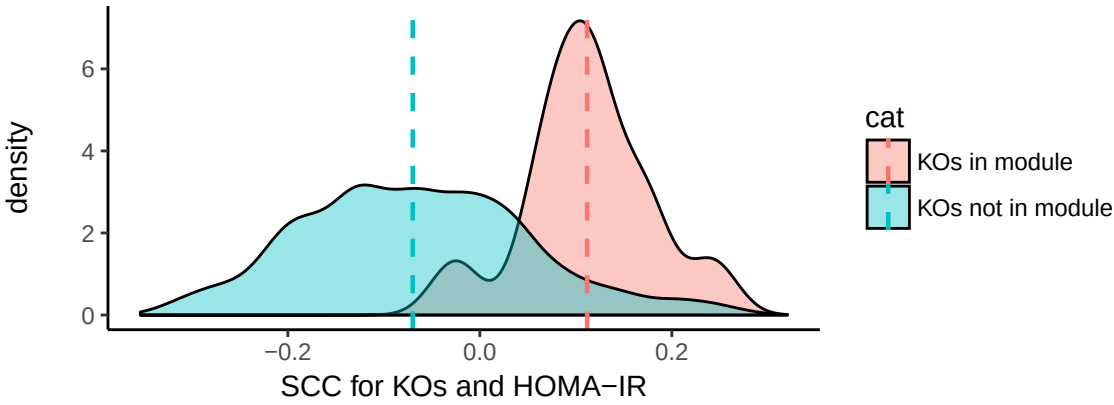
c

KEGG module: M00051
Uridine monophosphate biosynthesis
bg.adj.SCC for leave−1−MGS−out
Number of MGSs = 651



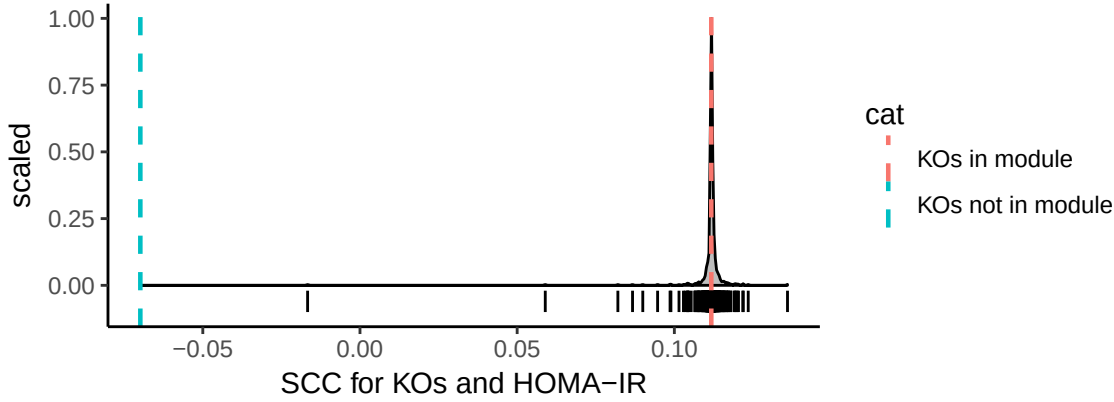
a

KEGG module: bcaa_biosyn
NA
13 KOs in module vs all remaining 6745 KOs



b

KEGG module: bcaa_biosyn
NA
SCC for leave−1−MGS−out
Number of MGSs = 646



c

KEGG module: bcaa_biosyn
NA
bg.adj.SCC for leave−1−MGS−out
Number of MGSs = 646