

# iLINCS API R Notebook

```
#Loading packages
#Setting default width option
```

## Display Signature Libraries

```
apiUrl <- "http://www.ilincs.org/api/SignatureLibraries"
req <- GET(apiUrl)
json <- httr::content(req, as = "text")
ilincs_libraries <- fromJSON(json)
ilincs_libraries[,c("libraryID", "libraryName")]
```

##	libraryID	libraryName
## 1	LIB_1	Disease related signatures
## 2	LIB_10	Cancer therapeutics response signatures
## 3	LIB_11	LINCS gene overexpression signatures
## 4	LIB_12	DrugMatrix signatures
## 5	LIB_13	Transcriptional signatures from EBI Expression Atlas
## 6	LIB_14	Pharmacogenomics transcriptional signatures
## 7	LIB_2	Connectivity Map signatures
## 8	LIB_3	ENCODE transcription factor binding signatures
## 9	LIB_5	LINCS chemical perturbagen signatures
## 10	LIB_6	LINCS consensus gene (CGS) knockdown signatures
## 11	LIB_8	LINCS RNA-Seq signatures
## 12	LIB_9	LINCS targeted proteomics signatures

## Searching for MTOR CRIPR genetic loss of function (CGS) perturbation signatures in the MCF7 cell line

```
term <- "MTOR"
ilincs_libId <- "LIB_6"
apiUrl <- paste("http://www.ilincs.org/api/SignatureMeta/findTermWithSynonyms?term=", term, "&library=", i
req <- GET(apiUrl)

mtorCgs <- fromJSON(httr::content(req, type = "text"))$data
```

```
## No encoding supplied: defaulting to UTF-8.
```

```
mtorCgsMcf7 <- mtorCgs[intersect(grep("MCF7", mtorCgs$cellline), grep("trt_xpr.cgs", mtorCgs$pert_type)), ]
mtorCgsMcf7[, c("cellline", "time", "treatment", "signatureid", "pert_type")]
```

##	cellline	time	treatment	signatureid	pert_type
## 26	MCF7.101	96 h	MTOR	LINCSKD_33763	trt_xpr.cgs
## 27	MCF7.311	96 h	MTOR	LINCSKD_33816	trt_xpr.cgs

# Finding and summarizing connected CGSes to the first MTOR CRISPR CGS (LINCSKD\_33763)

## Finding connected CGSes

```
ilincs_signatureId <- mtorCgsMcf7$signatureid[1]

apiUrl <- paste("http://www.ilincs.org/api/SignatureMeta/findConcordantSignatures?sigID=",ilincs_signatureId)
req <- GET(apiUrl)

connectedCgs<-fromJSON(httr::content(req,type="text"))

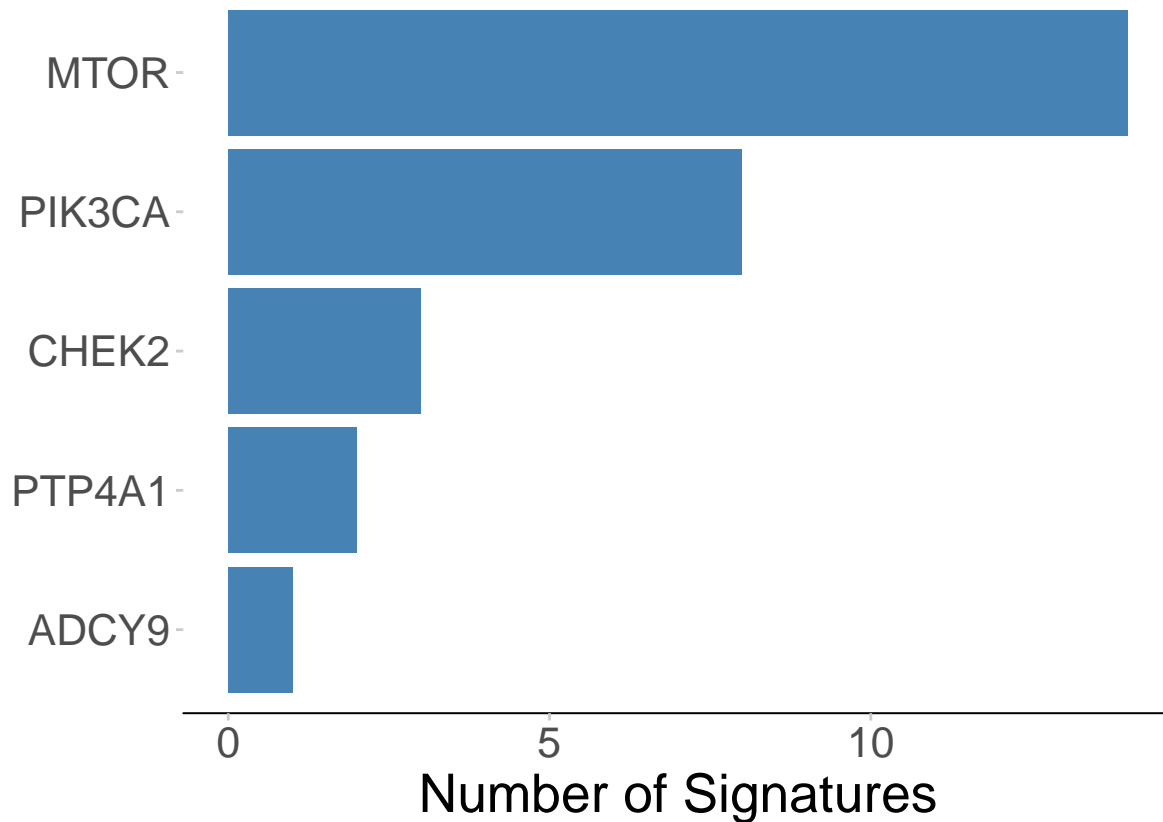
## No encoding supplied: defaulting to UTF-8.
head(connectedCgs[,c("signatureid","similarity","pValue","cellline","treatment")])

##      signatureid similarity      pValue cellline treatment
## 1 LINCSKD_33768  0.361049 4.719053e-36 MCF7.101    PIK3CA
## 2 LINCSKD_33816  0.356419 3.071392e-35 MCF7.311      MTOR
## 3 LINCSKD_33710  0.289951 5.716644e-25 HT29.311      MTOR
## 4 LINCSKD_33821  0.270321 2.072215e-22 MCF7.311    PIK3CA
## 5 LINCSKD_33445  0.260006 3.801609e-21 A375.311     MTOR
## 6 LINCSKD_33657  0.251621 3.687196e-20 HELA.311      MTOR
```

## Summary boxplot, Figure 2A in the manuscript

```
geneFreq <- sort(table(connectedCgs$treatment[1:100]),decreasing=TRUE)[5:1]
geneFreqDf<-data.frame(gene=factor(names(geneFreq),levels=names(geneFreq),ordered=T),geneFreq=as.vector(geneFreq))

tp100cgs<-ggplot(data=geneFreqDf,aes(x=gene,y=geneFreq)) +
  geom_bar(stat="identity",fill="steelblue") +
  coord_flip() + theme_bw() +
  theme(axis.ticks=element_line(color="grey80"),text=element_text(size=20),legend.key.size=unit(1,"cm"))
labs(x="",y="Number of Signatures")
print(tp100cgs)
```



## Finding and summarizing connected chemical perturbation (CP) signatures to MTOR CRISPR CGS (LINCSKD\_33763)

### Finding connected CPs

```
ilincs_libId<-"LIB_5"

apiUrl <- paste("http://www.ilincs.org/api/SignatureMeta/findConcordantSignatures?sigID=",ilincs_sigID)
req <- GET(apiUrl)

connectedCps<-fromJSON(httr::content(req,type="text"))

## No encoding supplied: defaulting to UTF-8.
head(connectedCps)
```

##	signatureid	similarity	significance	pValue	nGenes	factor	compound	concentration	cell
## 1	LINCSCP_137891	0.319918	29.1413	7.222069e-30	978	NA	Everolimus	0.04uM	
## 2	LINCSCP_141783	0.315187	28.4269	3.741927e-29	978	NA	SCHEMBL6851809	0.12uM	
## 3	LINCSCP_137889	0.314463	28.3185	4.802370e-29	978	NA	Everolimus	0.37uM	
## 4	LINCSCP_141782	0.300157	26.2408	5.744227e-27	978	NA	SCHEMBL6851809	0.37uM	
## 5	LINCSCP_38560	0.295942	25.6504	2.236856e-26	978	NA	Sirolimus	3.33uM	
## 6	LINCSCP_143289	0.293372	25.2952	5.067947e-26	978	NA	AZD2014	0.12uM	

```
##
##               lincsSigID is_exemplar GeneTargets
## 1             REP.A010_MCF7_24H:H06          NA FKBP1A|MTOR
## 2             REP.A021_MCF7_24H:E05          NA          MTOR
## 3             REP.A010_MCF7_24H:H04          NA FKBP1A|MTOR
```

```
## 4          REP.A021_MCF7_24H:E04          NA          MTOR
## 5 PCLB002_MCF7_24H:BRD-K84937637:3.33      0 FKBP1A|MTOR
## 6          REP.A025_MCF7_24H:H05          NA          MTOR
```

Summary boxplot, Figure 2B in the manuscript

```
top100GeneTargets<-unlist(strsplit.connectedCps$GeneTargets[1:100],split="\\|")
geneFreq <- sort(table(top100GeneTargets),decreasing=TRUE)[5:1]
geneFreqDf<-data.frame(gene=factor(names(geneFreq),levels=names(geneFreq),ordered=T),geneFreq=as.vector(geneFreq))

tp100cps<-ggplot(data=geneFreqDf,aes(x=gene,y=geneFreq)) +
  geom_bar(stat="identity",fill="steelblue") +
  coord_flip() + theme_bw() +
  theme(axis.ticks=element_line(color="grey80"),text=element_text(size=20),legend.key.size=unit(1,"cm"))
labs(x="",y="Number of Signatures")
tp100cps
```

