1 Introduction

This package provides a basic set of R functions for querying the Cancer Genomic Data Server (CGDS) hosted by the Computational Biology Center (cBio) at the Memorial Sloan-Kettering Cancer Center (MSKCC). This service is a part of the cBio Cancer Genomics Portal, http://www.cbioportal.org/.

In summary, the library can issue the following types of queries:

- `getCancerStudies()`: What cancer studies are hosted on the server? For example, TCGA glioblastoma or TCGA ovarian cancer.
- `getGeneticProfiles()`: What genetic profile types are available for cancer study X? For example, mRNA expression or copy number alterations.
- `getCaseLists()`: What case sets are available for cancer study X? For example, all samples or only samples corresponding to a given cancer subtype.
• **getProfileData()**: Retrieve slices of genomic data. For example, a client can retrieve all mutation data for PTEN and EGFR in TCGA glioblastoma.

• **getClinicalData()**: Retrieve clinical data (e.g., patient survival time and age) for a given cancer study and list of cases.

Each of these functions will be briefly described in the following sections. The last part of this document includes some concrete examples of how to access and plot the data.

The purpose of this document is to give the reader a quick overview of the cgdsr package. Please refer to the corresponding R manual pages for a more detailed explanation of arguments and output for each function.

## 2 The CGDS R interface

### 2.1 CGDS(): Create a CGDS connection object

Initially, we will establish a connection to the public CGDS server hosted by Memorial Sloan-Kettering Cancer Center. The function for creating a CGDS connection object requires the URL of the CGDS server service, in this case [http://www.cbioportal.org/](http://www.cbioportal.org/), as an argument.

```r
> library(cgdsr)
> # Create CGDS object
> mycgds = CGDS("http://www.cbioportal.org/")
```

The variable `mycgds` is now a CGDS connection object pointing at the URL for the public CGDS server. This connection object must be included as an argument to all subsequent interface calls. Optionally, we can now perform a set of simple tests of the data returned from the CGDS connection object using the `test` function:

```r
> # Test the CGDS endpoint URL using a few simple API tests
> test(mycgds)
```

```
getCancerStudies... OK
gCaseLists (1/2) ... OK
gCaseLists (2/2) ... OK
gGetGeneticProfiles (1/2) ... OK
gGetGeneticProfiles (2/2) ... OK
gGetClinicalData (1/1) ... OK
gGetProfileData (1/6) ... OK
gGetProfileData (2/6) ... OK
gGetProfileData (3/6) ... OK
gGetProfileData (4/6) ... OK
gGetProfileData (5/6) ... OK
gGetProfileData (6/6) ... OK
```
2.2 `getCancerStudies()` : Retrieve a set of available cancer studies

Having created a CGDS connection object, we can now retrieve a data frame with available cancer studies using the `getCancerStudies` function:

```r
> # Get list of cancer studies at server
> getCancerStudies(mycgds)[,c(1,2)]

cancer_study_id
1 paac_jhu_2014
2 laml_tcga_pub
3 laml_tcga
4 acyc_fmi_2014
5 acyc_mda_2015
6 acyc_mskcc_2013
7 acyc_sanger_2013
8 acpc_mskcc_2015
9 acc_tcga
10 blca_mskcc_solit_2014
11 blca_mskcc_solit_2012
12 blca_plasmacytoid_mskcc_2016
13 blca_bgi
14 blca_dfarber_mskcc_2014
15 blca_tcga_pub
16 blca_tcga
17 lgg_tcga
18 brca_metabric
19 brca_bccrc
20 brca_broad
21 brca_sanger
22 brca_tcga_pub2015
23 brca_tcga_pub
24 brca_tcga
25 brca_bccrc_xenograft_2014
26 cellline_ccle_broad
27 cesc_tcga
28 chol_nccs_2013
29 chol_nus_2012
30 chol_tcga
31 lcll_broad_2013
32 cll_iuopa_2015
33 ccrc_utokyo_2013
34 coadread_dfcic_2016
35 coadread_genentech
36 coadread_tcga_pub
37 coadread_tcga
38 coadread_mskcc
39 ctcl_columbia_2015
40 cscc_dfarber_2015
41 desm_broad_2015
```
dlbc_broad_2012
esca_broad
esca_tcga
escc_icgc
escc_ucla_2014
es_iocurie_2014
gbc_shanghai_2014
egc_tmucih_2015
prad_cpcg_2017
gbm_tcga_pub2013

gbm_tcga_pub

gbm_tcga
hnsc_broad
hnsc_jhu
hnsc_tcga_pub

liad_inserm_fr_2014
all_stjude_2013
all_stjude_2015
panet_shanghai_2013

chol_jhu_2013
kich_tcga_pub
kich_tcga
kirc_bgci

kirc_tcga_pub

kirc_tcga
kirc_tcga
kirp_tcga
lihc_amc_prv
lihc_amc_prv
lihc_riken

lihc_tcga

lgg_ucsf_2014

luad_broad
luad_mskcc_2015

luad_tcga
luad_tcga

luad_tsp

lusc_tcga_pub
lusc_tcga

lusc_tcga

dlbc_tcga

mpnst_mskcc

plmeso_nyu_2015

mcl_idibips_2013

mbl_broad_2012

mbl_icgc

mbl_pcgp

skcm_broad_dfarber

lgggbm_tcga_pub

meso_tcga

prad_su2c_2015

mm_broad
ccrc_irc_2014
brca_igr_2015
mds_tokyo_2011
celline_nci60
npc_nusingapore
nbl_amc_2012
nbl_ucologne_2015
nepc_wcm_2016
hnsc_mdanderson_2013
ov_tcga_pub
ov_tcga
nsclc_tcga_broad_2016
paad_icgc
paad_qcmg_uq_2016
paad_tcga
paad_utsw_2015
panet_jhu_2011
thca_tcga_pub
es_dfarber_broad_2014
pcpg_tcga
thyroid_mskcc_2016
pcnsl_mayo_2015
prad_broad_2013
prad_broad
prad_fhcrc
prad_mskcc
prad_tcga_pub
prad_tcga
prad_mskcc_2014
prad_mskcc_cheny1_organoids_2014
prad_mich
hnc_mskcc_2016
nccrc_genentech_2014
rms_nih_2014
sarc_mskcc
sarc_tcga
skcm_broad
skcm_tcga
skcm_yale
scco_mskcc
sclc_clcgp
sclc_jhu
sclc_ucologne_2015
stad_pfizer_uhongkong
stad_tcga_pub
stad_tcga
stad_utokyo
stad_uhongkong
stes_tcga_pub
tgct_tcga
name
tet_nci_2014
thym_tcga
urcc_mskcc_2016
ucsb_jhu_2014
ucsb_tcga
ucec_tcga_pub
ucec_tcga
uvm_tcga

Acinar Cell Carcinoma of the Pancreas (Johns Hopkins, J Pathol 2014)
Acute Myeloid Leukemia (TCGA, NEJM 2013)
Acute Myeloid Leukemia (TCGA, Provisional)
Adenoid Cystic Carcinoma (FMI, Am J Surg Pathl. 2014)
Adenoid Cystic Carcinoma (MDA, Clin Cancer Res 2015)
Adenoid Cystic Carcinoma (MSKCC, Nat Genet 2013)
Adenoid Cystic Carcinoma (Sanger/MDA, JCI 2013)
Adenoid Cystic Carcinoma of the Breast (MSKCC, J Pathol. 2015)
Adrenocortical Carcinoma (TCGA, Provisional)
Bladder Cancer (MSKCC, Eur Urol 2014)
Bladder Cancer (MSKCC, JCO 2013)
Bladder Cancer, Plasmacytoid Variant (MSKCC, Nat Genet 2016)
Bladder Urothelial Carcinoma (BGI, Nat Genet 2013)
Bladder Urothelial Carcinoma (Dana Farber & MSKCC, Cancer Discov 2014)
Bladder Urothelial Carcinoma (TCGA, Nature 2014)
Bladder Urothelial Carcinoma (TCGA, Provisional)
Brain Lower Grade Glioma (TCGA, Provisional)
Breast Invasive Carcinoma (British Columbia, Nature 2012)
Breast Invasive Carcinoma (Broad, Nature 2012)
Breast Invasive Carcinoma (Sanger, Nature 2012)
Breast Invasive Carcinoma (TCGA, Cell 2015)
Breast Invasive Carcinoma (TCGA, Nature 2012)
Breast Invasive Carcinoma (TCGA, Provisional)
Breast cancer patient xenografts (British Columbia, Nature 2014)
Cancer Cell Line Encyclopedia (Novartis/Broad, Nature 2012)
Cervical Squamous Cell Carcinoma and Endocervical Adenocarcinoma (TCGA, Provisional)
Cholangiocarcinoma (National Cancer Centre of Singapore, Nat Genet 2013)
Cholangiocarcinoma (National University of Singapore, Nat Genet 2012)
Cholangiocarcinoma (TCGA, Provisional)
Chronic Lymphocytic Leukemia (Broad, Cell 2013)
Chronic Lymphocytic Leukemia (IUOPA, Nature 2015)
Clear Cell Renal Cell Carcinoma (U Tokyo, Nat Genet 2013)
Colorectal Adenocarcinoma (DPCI, Cell Reports 2016)
Colorectal Adenocarcinoma (Genentech, Nature 2012)
Colorectal Adenocarcinoma (TCGA, Nature 2012)
Colorectal Adenocarcinoma (TCGA, Provisional)
Colorectal Adenocarcinoma Triplet (MSKCC, Genome Biol 2014)
Cutaneous T Cell Lymphoma (Columbia U, Nat Genet 2015)
Cutaneous squamous cell carcinoma (DPCI, Clin Cancer Res 2015)
Desmoplastic Melanoma (Broad Institute, Nat Genet 2015)
Diffuse Large B-Cell Lymphoma (Broad, PNAS 2012)
Esophageal Adenocarcinoma (Broad, Nat Genet 2013)
Esophageal Carcinoma (TCGA, Provisional)
Esophageal Squamous Cell Carcinoma (TCGA, Nature 2014)
Esophageal Squamous Cell Carcinoma (UCLA, Nat Genet 2014)
Ewing Sarcoma (Institut Curie, Cancer Discov 2014)
Gallbladder Carcinoma (Shanghai, Nat Genet 2014)
Gastric Adenocarcinoma (TMUCIH, PNAS 2015)
Genomic Hallmarks of Prostate Adenocarcinoma (CPC-GENE, Nature 2017)
Glioblastoma (TCGA, Cell 2013)
Glioblastoma (TCGA, Nature 2008)
Glioblastoma Multiforme (TCGA, Provisional)
Head and Neck Squamous Cell Carcinoma (Broad, Science 2011)
Head and Neck Squamous Cell Carcinoma (Johns Hopkins, Science 2011)
Head and Neck Squamous Cell Carcinoma (TCGA, Nature 2015)
Head and Neck Squamous Cell Carcinoma (TCGA, Provisional)
Hepatocellular Adenoma (Inserm, Cancer Cell 2014)
Hypodiploid Acute Lymphoid Leukemia (St Jude, Nat Genet 2013)
Infant MLL-Rearranged Acute Lymphoblastic Leukemia (St Jude, Nat Genet 2015)
Insulinoma (Shanghai, Nat Commun 2013)
Intrahepatic Cholangiocarcinoma (Johns Hopkins University, Nat Genet 2013)
Kidney Chromophobe (TCGA, Cancer Cell 2014)
Kidney Chromophobe (TCGA, Provisional)
Kidney Renal Clear Cell Carcinoma (BSI, Nat Genet 2012)
Kidney Renal Clear Cell Carcinoma (TCGA, Nature 2013)
Kidney Renal Clear Cell Carcinoma (TCGA, Provisional)
Kidney Renal Papillary Cell Carcinoma (TCGA, Provisional)
Liver Hepatocellular Carcinoma (AMC, Hepatology 2014)
Liver Hepatocellular Carcinoma (RIKEN, Nat Genet 2012)
Liver Hepatocellular Carcinoma (TCGA, Provisional)
Low-Grade Gliomas (UCSF, Science 2014)
Lung Adenocarcinoma (Broad, Cell 2012)
Lung Adenocarcinoma (MSKCC, 2015)
Lung Adenocarcinoma (TCGA, Nature 2014)
Lung Adenocarcinoma (TCGA, Provisional)
Lung Adenocarcinoma (TSP, Nature 2008)
Lung Squamous Cell Carcinoma (TCGA, Nature 2012)
Lung Squamous Cell Carcinoma (TCGA, Provisional)
Lymphoid Neoplasm Diffuse Large B-cell Lymphoma (TCGA, Provisional)
Malignant Peripheral Nerve Sheath Tumor (MSKCC, Nat Genet 2014)
Malignant Pleural Mesothelioma (NYU, Cancer Res 2015)
Mantle Cell Lymphoma (IDIBIPS, PNAS 2013)
Medulloblastoma (Broad, Nature 2012)
Medulloblastoma (ICGC, Nature 2012)
Medulloblastoma (PCGP, Nature 2012)
Melanoma (Broad/Dana Farber, Nature 2012)
Merged Cohort of LGG and GBM (TCGA, Cell 2016)
Mesothelioma (TCGA, Provisional)
Metastatic Prostate Cancer, SU2C/PCF Dream Team (Robinson et al., Cell 2015)

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Multiple Myeloma (Broad, Cancer Cell 2014)

Multiregion Sequencing of Clear Cell Renal Cell Carcinoma (IRC, Nat Genet 2014).

Mutational profiles of metastatic breast cancer (France, 2016)

Myelodysplasia (Tokyo, Nature 2011)

NCI-60 Cell Lines (NCI, Cancer Res. 2012)

Nasopharyngeal Carcinoma (Singapore, Nat Genet 2014)

Neuroblastoma (AMC Amsterdam, Nature 2012)

Neuroblastoma (Broad, Nat Genet 2013)

Neuroendocrine Prostate Cancer (Trento/Cornell/Broad 2016)

Oral Squamous Cell Carcinoma (MD Anderson, Cancer Discov 2013)

Ovarian Serous Cystadenocarcinoma (TCGA, Nature 2011)

Ovarian Serous Cystadenocarcinoma (TCGA, Provisional)

Pan-Lung Cancer (TCGA, Nat Genet 2016)

Pancreatic Adenocarcinoma (IGCC, Nature 2012)

Pancreatic Adenocarcinoma (QCMG, Nature 2016)

Pancreatic Neuroendocrine Tumors (Johns Hopkins University, Science 2011)

Papillary Thyroid Carcinoma (TCGA, Cell 2014)

Pediatric Ewing Sarcoma (DFCI, Cancer Discov 2014)

Pheochromocytoma and Paraganglioma (TCGA, Provisional)

Poorly-Differentiated and Anaplastic Thyroid Cancers (MSKCC, JCI 2016)

Primary Central Nervous System Lymphoma (Mayo Clinic, Clin Cancer Res 2015)

Prostate Adenocarcinoma (Broad/Cornell, Cell 2013)

Prostate Adenocarcinoma (Broad/Cornell, Nat Genet 2012)

Prostate Adenocarcinoma (Fred Hutchinson CRC, Nat Med 2016)

Prostate Adenocarcinoma (MSKCC, Cancer Cell 2010)

Prostate Adenocarcinoma (TCGA, Cell 2015)

Prostate Adenocarcinoma (TGCA, Provisional)

Prostate Adenocarcinoma CNA study (MSKCC, PNAS 2014)

Prostate Adenocarcinoma Organoids (MSKCC, Cell 2014)

Prostate Adenocarcinoma, Metastatic (Michigan, Nature 2012)

Recurrent and Metastatic Head & Neck Cancer (JAMA Oncology, 2016)

Renal Non-Clear Cell Carcinoma (Genentech, Nat Genet 2014)

Rhabdomyosarcoma (NIH, Cancer Discov 2014)

Sarcoma (MSKCC/Broad, Nat Genet 2010)

Sarcoma (TCGA, Provisional)

Skin Cutaneous Melanoma (Broad, Cell 2012)

Skin Cutaneous Melanoma (TCGA, Provisional)

Skin Cutaneous Melanoma (Yale, Nat Genet 2012)

Small Cell Carcinoma of the Ovary (MSKCC, Nat Genet 2014)

Small Cell Lung Cancer (CLCGP, Nat Genet 2012)

Small Cell Lung Cancer (Johns Hopkins, Nat Genet 2012)

Small Cell Lung Cancer (U Cologne, Nature 2015)

Stomach Adenocarcinoma (Pfizer and UHK, Nat Genet 2014)

Stomach Adenocarcinoma (TCGA, Nature 2014)

Stomach Adenocarcinoma (TCGA, Provisional)

Stomach Adenocarcinoma (U Tokyo, Nat Genet 2014)

Stomach Adenocarcinoma (UHK, Nat Genet 2011)

TCGA data for Esophagus-Stomach Cancers (TCGA, Nature 2017)
141 Testicular Germ Cell Cancer (TCGA, Provisional)
142 Thymic Epithelial Tumors (NCI, Nat Genet 2014)
143 Thymoma (TCGA, Provisional)
144 Thyroid Carcinoma (TCGA, Provisional)
145 Unclassified Renal Cell Carcinoma (MSKCC 2016)
146 Uterine Carcinosarcoma (Johns Hopkins University, Nat Commun 2014)
147 Uterine Carcinosarcoma (TCGA, Provisional)
148 Uterine Corpus Endometrial Carcinoma (TCGA, Nature 2013)
149 Uterine Corpus Endometrial Carcinoma (TCGA, Provisional)
150 Uveal Melanoma (TCGA, Provisional)

Here we are only showing the first two columns, the cancer study ID and short name, of the result data frame. There is also a third column, a longer description of the cancer study. The cancer study ID must be used in subsequent interface calls to retrieve case lists and genetic data profiles (see below).

2.3 getGeneticProfiles() : Retrieve genetic data profiles for a specific cancer study

This function queries the CGDS API and returns the available genetic profiles, e.g. mutation or copy number profiles, stored about a specific cancer study. Below we list the current genetic profiles for the TCGA glioblastoma cancer study:

```r
> getGeneticProfiles(mycgds, 'gbm_tcga')[,c(1:2)]
genetic_profile_id   genetic_profile_name
1  gbm_tcga_rppa         Protein expression (RPPA)
2  gbm_tcga_rppa_Zscores Protein expression Z-scores (RPPA)
3  gbm_tcga_gistic       Putative copy-number alterations from GISTIC
4  gbm_tcga_mrna_U133    mRNA expression (U133 microarray only)
5  gbm_tcga_mrna_U133_Zscores mRNA Expression z-Scores (U133 microarray only)
6  gbm_tcga_mrna_median_Zscores mRNA Expression z-Scores (microarray)
7  gbm_tcga_rna_seq_v2_mrna mRNA expression (RNA Seq V2 RSEM)
8  gbm_tcga_rna_seq_v2_mrna_median_Zscores mRNA Expression z-Scores (RNA Seq V2 RSEM)
9  gbm_tcga_linear_CNA    Relative linear copy-number values
10 gbm_tcga_methylation_hm27
11 gbm_tcga_methylation_hm450
12 gbm_tcga_mutations
13 gbm_tcga_mrna
```

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Here we are only listing the first two columns, genetic profile ID and short name, of the resulting data frame. Please refer to the R manual pages for a more extended specification of the arguments and output.

2.4 `getCaseLists()` : Retrieve case lists for a specific cancer study

This function queries the CGDS API and returns available case lists for a specific cancer study. For example, within a particular study, only some cases may have sequence data, and another subset of cases may have been sequenced and treated with a specific therapeutic protocol. Multiple case lists may be associated with each cancer study, and this method enables you to retrieve meta-data regarding all of these case lists. Below we list the current case lists for the TCGA glioblastoma cancer study:

```r
> getCaseLists(mycgds, 'gbm_tcga')[,c(1:2)]

    case_list_id case_list_name
 1  gbm_tcga_3way_complete     All Complete Tumors
 2  gbm_tcga_all                All Tumors
 3  gbm_tcga_sequenced          Sequenced Tumors
 4  gbm_tcga_cna                Tumor Samples with CNA data
 5  gbm_tcga_methylation_hm27   Tumor Samples with methylation data (HM27)
 6  gbm_tcga_methylation_hm450  Tumor Samples with methylation data (HM450)
 7  gbm_tcga_rna_seq_v2_mrna    Tumor Samples with mRNA data (RNA Seq V2)
 8  gbm_tcga_rna_mrna_U133      Tumor Samples with mRNA data (U133 microarray only)
 9  gbm_tcga_rppa               Tumor Samples with RPPA data
10  gbm_tcga_cnaseq            Tumor Samples with sequencing and CNA data
```

Here we are only listing the first two columns, case list ID and short name, of the resulting data frame. Please refer to the R manual pages for a more extended specification of the arguments and output.
2.5 getProfileData() : Retrieve genomic profile data for genes and genetic profiles

The function queries the CGDS API and returns data based on gene(s), genetic profile(s), and a case list. The function only allows specifying a list of genes and a single genetic profile, or oppositely a single gene and a list of genetic profiles. Importantly, the format of the output data frame depends on if a single or a list of genes was specified in the arguments. Below we are retrieving mRNA expression and copy number alteration genetic profiles for the NF1 gene in all samples of the TCGA glioblastoma cancer study:

```r
> getProfileData(mycgds, "NF1", c("gbm_tcga_gistic","gbm_tcga_mrna"), "gbm_tcga_all")[c(1:5),]
gbm_tcga_gistic gbm_tcga_mrna
TCGA.02.0001.01 -1 NaN
TCGA.02.0003.01 0 NaN
TCGA.02.0006.01 0 NaN
TCGA.02.0007.01 0 NaN
TCGA.02.0009.01 0 NaN
```

We are here only showing the first five rows of the data frame. In the next example, we are retrieving mRNA expression data for the MDM2 and MDM4 genes:

```r
> getProfileData(mycgds, c("MDM2","MDM4"), "gbm_tcga_mrna", "gbm_tcga_all")[c(1:5),]
MDM2 MDM4
TCGA.02.0001.01 NaN NaN
TCGA.02.0003.01 NaN NaN
TCGA.02.0006.01 NaN NaN
TCGA.02.0007.01 NaN NaN
TCGA.02.0009.01 NaN NaN
```

We are again only showing the first five rows of the data frame.

2.6 getClinicalData() : Retrieve clinical data for a list of cases

The function queries the CGDS API and returns available clinical data (e.g. patient survival time and age) for a given case list. Results are returned in a data frame with a row for each case and a column for each clinical attribute. The available clinical attributes are:

- **overall_survival_months**: Overall survival, in months.
- **overall_survival_status**: Overall survival status, usually indicated as "LIVING" or "DECEASED".
- **disease_free_survival_months**: Disease free survival, in months.
- **disease_free_survival_status**: Disease free survival status, usually indicated as "DiseaseFree" or "Recurred/Progressed".
• **age_at_diagnosis**: Age at diagnosis.

Below we retrieve clinical data for the TCGA ovarian cancer dataset (only first five cases/rows are shown):

```r
c > getClinicalData(mycgds, "ova_all")[,1:5]
data frame with 0 columns and 5 rows
```

### 3 Examples

#### 3.1 Example 1: Association of NF1 copy number alteration and mRNA expression in glioblastoma

As a simple example, we will generate a plot of the association between copy number alteration (CNA) status and mRNA expression change for the NF1 tumor suppressor gene in glioblastoma. This plot is very similar to Figure 2b in the TCGA research network paper on glioblastoma (McLendon et al. 2008). The mRNA expression of NF1 has been median adjusted on the gene level (by globally subtracting the median expression level of NF1 across all samples).

```r
df = getProfileData(mycgds, "NF1", c("gbm_tcga_gistic","gbm_tcga_mrna"), "gbm_tcga_all")
df = getProfileData(mycgds, "NF1", c("gbm_tcga_gistic","gbm_tcga_mrna"), "gbm_tcga_all")
df = getProfileData(mycgds, "NF1", c("gbm_tcga_gistic","gbm_tcga_mrna"), "gbm_tcga_all")
```

```r
df = getProfileData(mycgds, "NF1", c("gbm_tcga_gistic","gbm_tcga_mrna"), "gbm_tcga_all")
```

```r
df = getProfileData(mycgds, "NF1", c("gbm_tcga_gistic","gbm_tcga_mrna"), "gbm_tcga_all")
```

```r
df = getProfileData(mycgds, "NF1", c("gbm_tcga_gistic","gbm_tcga_mrna"), "gbm_tcga_all")
```

```r
df = getProfileData(mycgds, "NF1", c("gbm_tcga_gistic","gbm_tcga_mrna"), "gbm_tcga_all")
```

```r
df = getProfileData(mycgds, "NF1", c("gbm_tcga_gistic","gbm_tcga_mrna"), "gbm_tcga_all")
```

```r
df = getProfileData(mycgds, "NF1", c("gbm_tcga_gistic","gbm_tcga_mrna"), "gbm_tcga_all")
```

```r
df = getProfileData(mycgds, "NF1", c("gbm_tcga_gistic","gbm_tcga_mrna"), "gbm_tcga_all")
```

```r
df = getProfileData(mycgds, "NF1", c("gbm_tcga_gistic","gbm_tcga_mrna"), "gbm_tcga_all")
```

```r
df = getProfileData(mycgds, "NF1", c("gbm_tcga_gistic","gbm_tcga_mrna"), "gbm_tcga_all")
```

```r
df = getProfileData(mycgds, "NF1", c("gbm_tcga_gistic","gbm_tcga_mrna"), "gbm_tcga_all")
```

```r
df = getProfileData(mycgds, "NF1", c("gbm_tcga_gistic","gbm_tcga_mrna"), "gbm_tcga_all")
```

```r
df = getProfileData(mycgds, "NF1", c("gbm_tcga_gistic","gbm_tcga_mrna"), "gbm_tcga_all")
```

```r
df = getProfileData(mycgds, "NF1", c("gbm_tcga_gistic","gbm_tcga_mrna"), "gbm_tcga_all")
```

```r
df = getProfileData(mycgds, "NF1", c("gbm_tcga_gistic","gbm_tcga_mrna"), "gbm_tcga_all")
```

```r
df = getProfileData(mycgds, "NF1", c("gbm_tcga_gistic","gbm_tcga_mrna"), "gbm_tcga_all")
```

```r
df = getProfileData(mycgds, "NF1", c("gbm_tcga_gistic","gbm_tcga_mrna"), "gbm_tcga_all")
```

```r
df = getProfileData(mycgds, "NF1", c("gbm_tcga_gistic","gbm_tcga_mrna"), "gbm_tcga_all")
```

```r
df = getProfileData(mycgds, "NF1", c("gbm_tcga_gistic","gbm_tcga_mrna"), "gbm_tcga_all")
```

```r
df = getProfileData(mycgds, "NF1", c("gbm_tcga_gistic","gbm_tcga_mrna"), "gbm_tcga_all")
```

```r
df = getProfileData(mycgds, "NF1", c("gbm_tcga_gistic","gbm_tcga_mrna"), "gbm_tcga_all")
```

```r
df = getProfileData(mycgds, "NF1", c("gbm_tcga_gistic","gbm_tcga_mrna"), "gbm_tcga_all")
```

```r
df = getProfileData(mycgds, "NF1", c("gbm_tcga_gistic","gbm_tcga_mrna"), "gbm_tcga_all")
```

```r
df = getProfileData(mycgds, "NF1", c("gbm_tcga_gistic","gbm_tcga_mrna"), "gbm_tcga_all")
```

```r
df = getProfileData(mycgds, "NF1", c("gbm_tcga_gistic","gbm_tcga_mrna"), "gbm_tcga_all")
```

```r
df = getProfileData(mycgds, "NF1", c("gbm_tcga_gistic","gbm_tcga_mrna"), "gbm_tcga_all")
```

```r
df = getProfileData(mycgds, "NF1", c("gbm_tcga_gistic","gbm_tcga_mrna"), "gbm_tcga_all")
```

```r
df = getProfileData(mycgds, "NF1", c("gbm_tcga_gistic","gbm_tcga_mrna"), "gbm_tcga_all")
```

```r
df = getProfileData(mycgds, "NF1", c("gbm_tcga_gistic","gbm_tcga_mrna"), "gbm_tcga_all")
```

```r
df = getProfileData(mycgds, "NF1", c("gbm_tcga_gistic","gbm_tcga_mrna"), "gbm_tcga_all")
```

```r
df = getProfileData(mycgds, "NF1", c("gbm_tcga_gistic","gbm_tcga_mrna"), "gbm_tcga_all")
```

```r
df = getProfileData(mycgds, "NF1", c("gbm_tcga_gistic","gbm_tcga_mrna"), "gbm_tcga_all")
```

```r
df = getProfileData(mycgds, "NF1", c("gbm_tcga_gistic","gbm_tcga_mrna"), "gbm_tcga_all")
```

```r
df = getProfileData(mycgds, "NF1", c("gbm_tcga_gistic","gbm_tcga_mrna"), "gbm_tcga_all")
```

```r
df = getProfileData(mycgds, "NF1", c("gbm_tcga_gistic","gbm_tcga_mrna"), "gbm_tcga_all")
```
Alternatively, the generic cgdsr plot() function can be used to generate a similar plot:

```r
> plot(mycgds, "gbm_tcga", "NF1", c("gbm_tcga_gistic","gbm_tcga_mrna"), "gbm_tcga_all", skin = 'disc_cont')
[1] TRUE
```
3.2 Example 2: MDM2 and MDM4 mRNA expression levels in glioblastoma

In this example, we evaluate the relationship of MDM2 and MDM4 expression levels in glioblastoma. mRNA expression levels of MDM2 and MDM4 have been median adjusted on the gene level (by globally subtracting the median expression level of the individual gene across all samples).

```r
> df = getProfileData(mycgds, c("MDM2","MDM4"), "gbm_tcga_mrna", "gbm_tcga_all")
> head(df)

   MDM2 MDM4
TCGA.02.0001.01 NaN NaN
TCGA.02.0003.01 NaN NaN
TCGA.02.0006.01 NaN NaN
TCGA.02.0007.01 NaN NaN
TCGA.02.0009.01 NaN NaN
TCGA.02.0010.01 NaN NaN

> plot(df, main="MDM2 and MDM4 mRNA expression", xlab="MDM2 mRNA expression", ylab="MDM4 mRNA expression")
```
Alternatively, the generic `cgdsr plot()` function can be used to generate a similar plot:

```r
> plot(mycgds, "gbm_tcga", c("MDM2","MDM4"), "gbm_tcga_mrna" ,"gbm_tcga_all")
[1] TRUE
```
3.3 Example 3: Comparing expression of PTEN in primary and metastatic prostate cancer tumors

In this example we plot the mRNA expression levels of PTEN in primary and metastatic prostate cancer tumors.

> df.pri = getProfileData(mycgds, "PTEN", "prad_mskcc_mrna", "prad_mskcc_primary")
> head(df.pri)

<p>| | | | | |</p>
<table>
<thead>
<tr>
<th></th>
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</thead>
<tbody>
<tr>
<td>PTEN</td>
<td>PCA0001</td>
<td>9.467183</td>
<td>PCA0002</td>
<td>9.041528</td>
</tr>
<tr>
<td></td>
<td>PCA0003</td>
<td>8.511305</td>
<td>PCA0004</td>
<td>NaN</td>
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<tr>
<td></td>
<td>PCA0005</td>
<td>9.413217</td>
<td>PCA0006</td>
<td>NaN</td>
</tr>
</tbody>
</table>

> df.met = getProfileData(mycgds, "PTEN", "prad_mskcc_mrna", "prad_mskcc_mets")
> head(df.met)

<p>| | | | | |</p>
<table>
<thead>
<tr>
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<tbody>
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<td>PCA0186</td>
<td>NaN</td>
<td>PCA0187</td>
<td>8.756132</td>
</tr>
</tbody>
</table>
> boxplot(list(t(df.pri),t(df.met)), main="PTEN expression in primary and metastatic tumors", names=c('primary','metastatic'), outpch = NA)
> stripchart(list(t(df.pri),t(df.met)), vertical=T, add=T, method="jitter", pch=1,col='red')