

# Comparaciones estadísticas

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## 1 Introducción y Objetivo

## 2 Paquetes y datos

### 2.1 Metadata original

Para asegurar que examinamos todas las opciones, examinamos las variables originales.

Los datos a comparar son los resultados obtenidos de los análisis previos de deconvolución:

- GSE22155 (<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi>) con dos plataformas: GPL6102 y GPL6947.
- GSE35640 (<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE35640>)
- GSE61992 (<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE61992>)
- GSE91061 (<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE91061>)
- TCGA-SKCM (<https://portal.gdc.cancer.gov/projects/TCGA-SKCM>)

De manera excepcional, tenemos GSE120575 (<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE120575>), que consiste en un dataset scRNA-seq en el que han analizado muestras tumorales y controles.

```
setwd("~/Desktop/ELENA_UOC/TFM")
GSE22155_GPL6102 <- read_csv("Deconvolution_analysis/Quantiseq_analyses/quantiseqr_GSE22155_GPL6102.csv")
GSE22155_GPL6947 <- read_csv("Deconvolution_analysis/Quantiseq_analyses/quantiseqr_GSE22155_GPL6947.csv")
GSE35640 <- read_csv("Deconvolution_analysis/Quantiseq_analyses/quantiseqr_GSE35640.csv")
GSE61992 <- read_csv("Deconvolution_analysis/Quantiseq_analyses/quantiseqr_GSE61992.csv")
```

```
#GSE91061 <- read_csv("Deconvolution_analysis/Quantiseq_analyses/quantiseq_GSE91061.csv")
GSE91061 <- read_delim("Deconvolution_analysis/Quantiseq_analyses/quantiseqr_GSE91061.csv",
  delim = ",")
tcga_skcm <- read_csv("Deconvolution_analysis/Quantiseq_analyses/quantiseq_tcga_skcm.csv")
TCGA_SKCM_clinical_data <- readxl::read_excel("Datasets/TCGA_SKCM_clinical_data.xlsx")
```

## 2.2 Metadata harmonizada

Para poder estudiar si podemos comparar

- Cohorte GSE22155 y plataforma GPL6947:
- Cohorte GSE22155 y plataforma GPL6102:
- Cohorte GSE35640:
- Cohorte GSE61992:
- Cohorte GSE91061:
- Cohorte TCGA-SKCM:

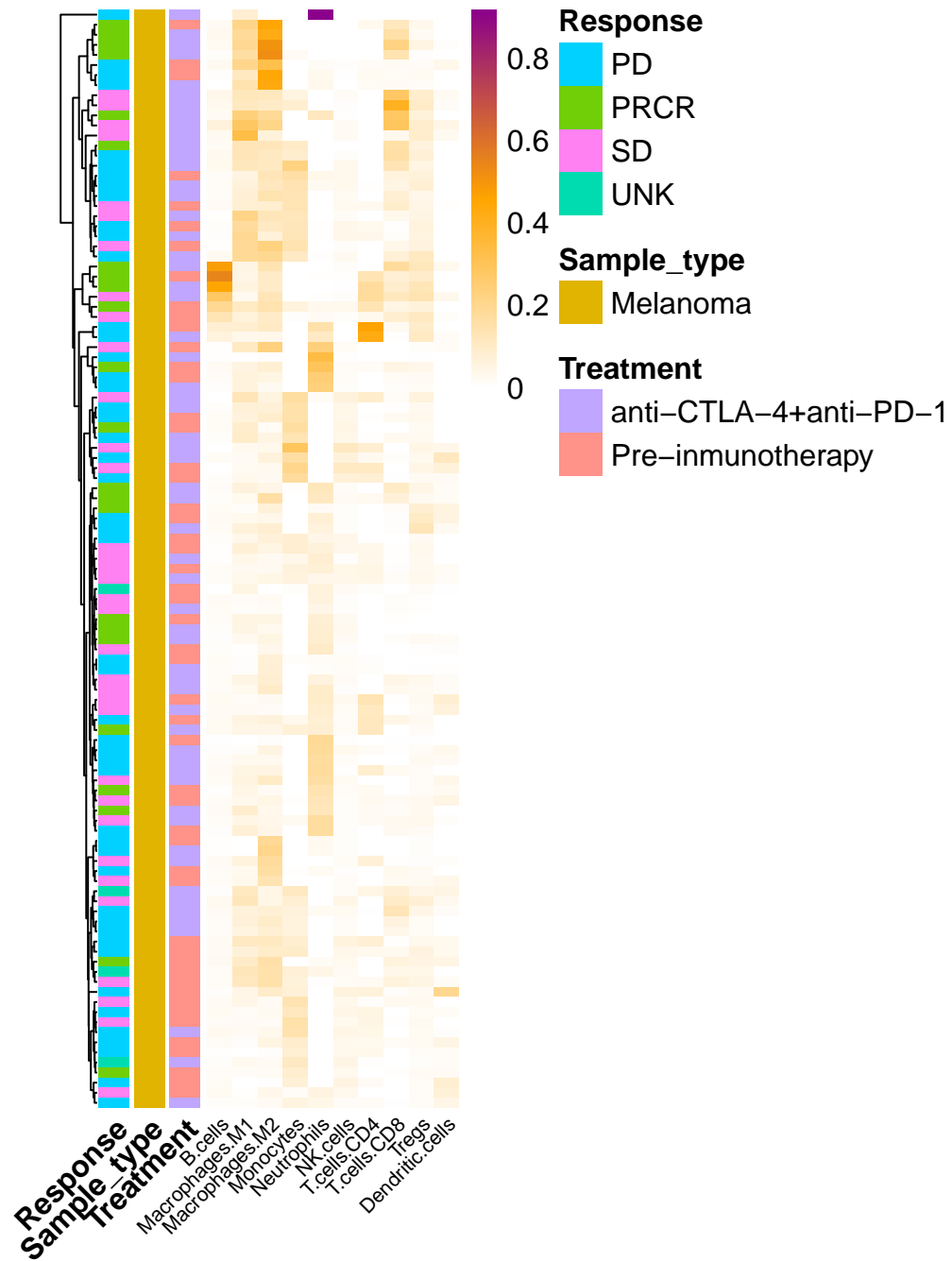
## 3 Heatmaps

- Packages:

### 3.1 GSE91061

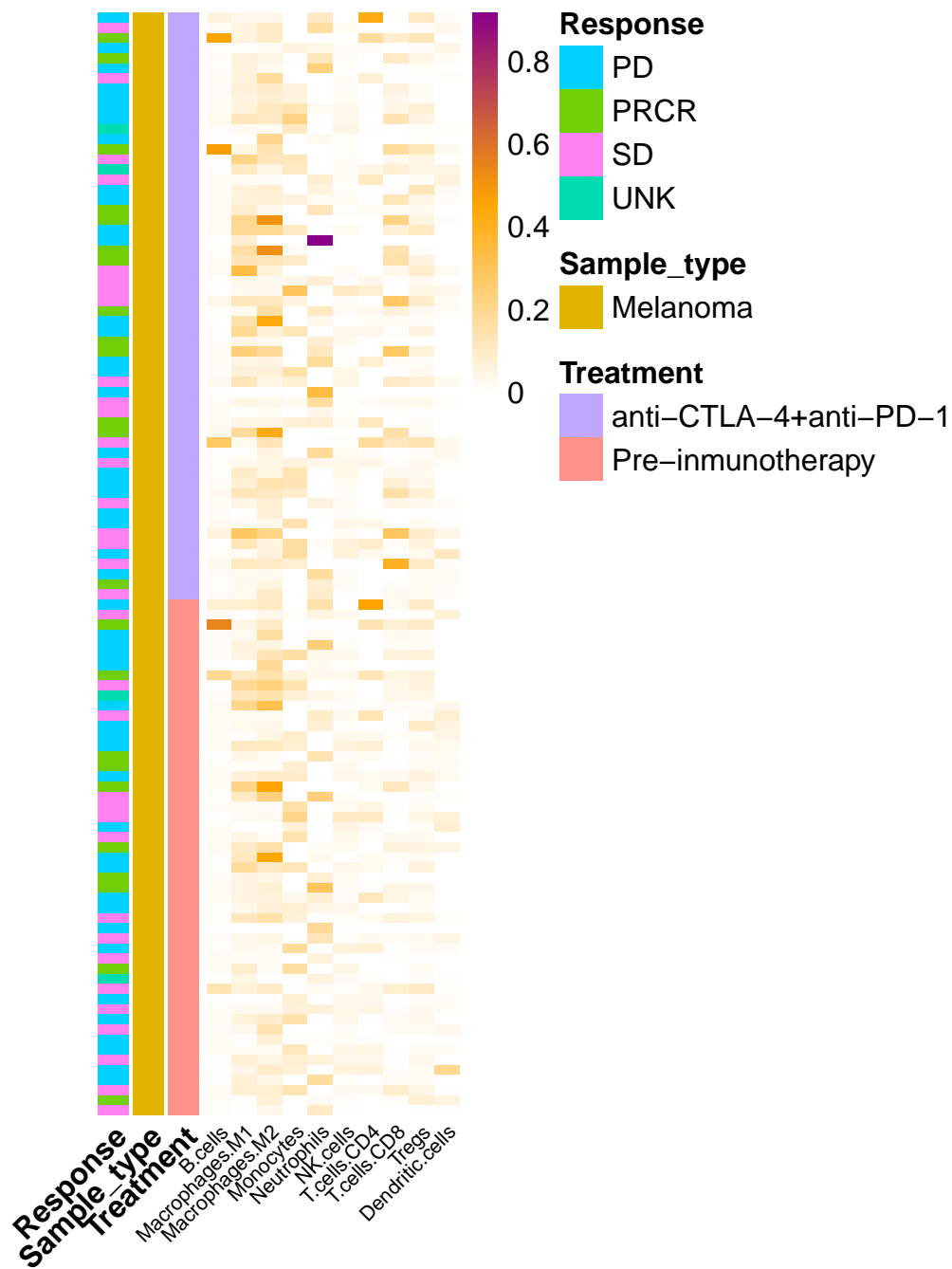
```
## [1] TRUE
## [1] 0
## [1] 0
```

## Deconvolution analysis GSE91061, clustered



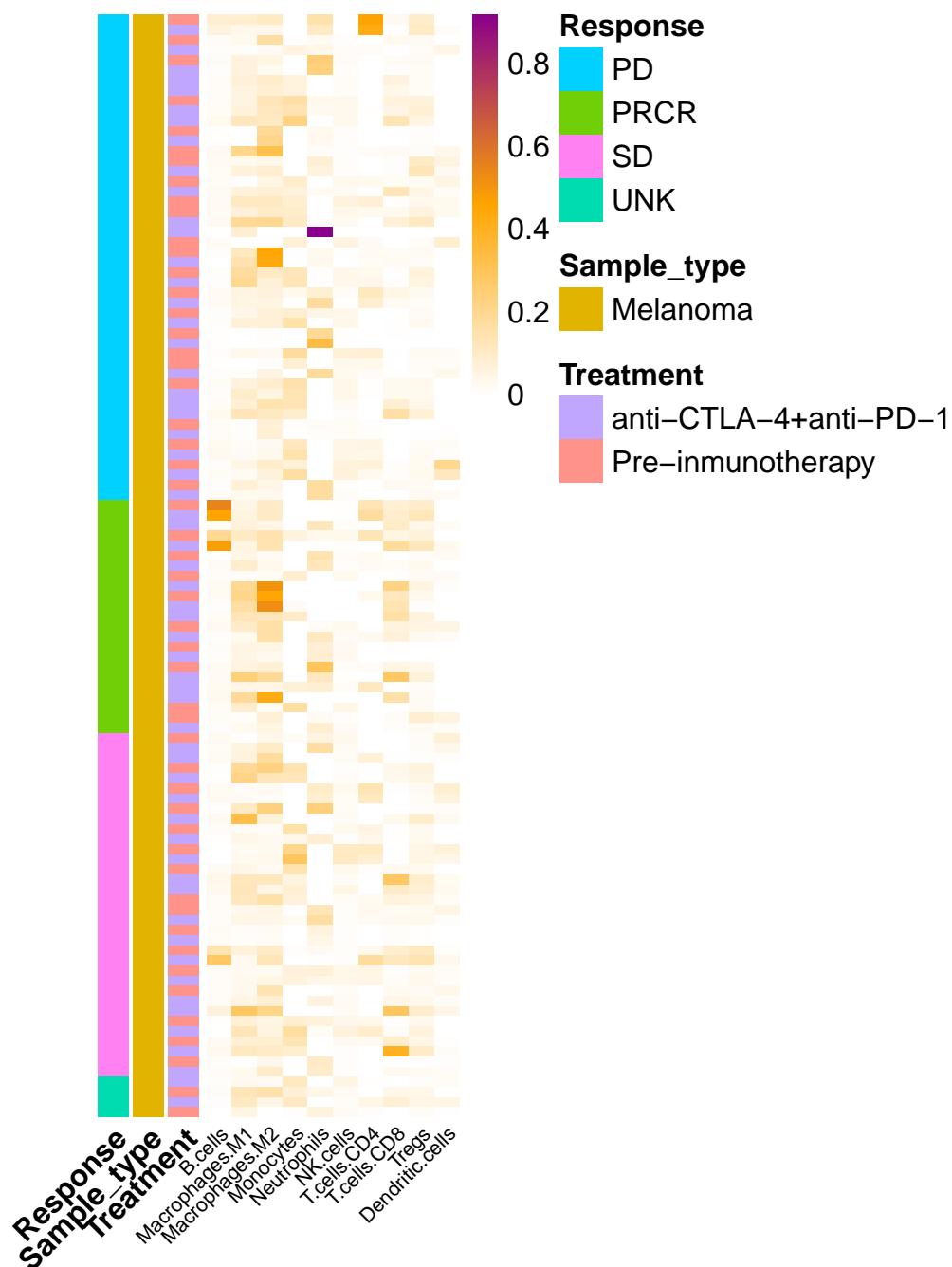
# Deconvolution analysis GSE91061

Ordered by treatment



## Deconvolution analysis GSE91061

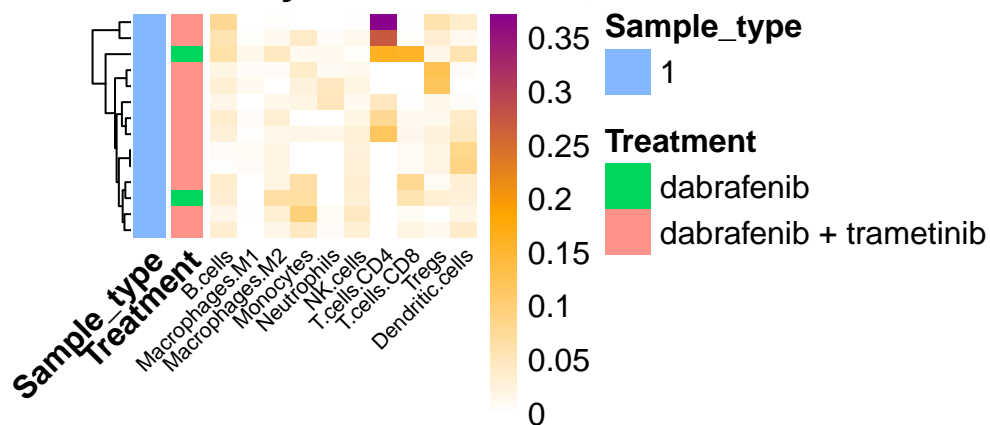
Ordered by response



### 3.2 GSE61992

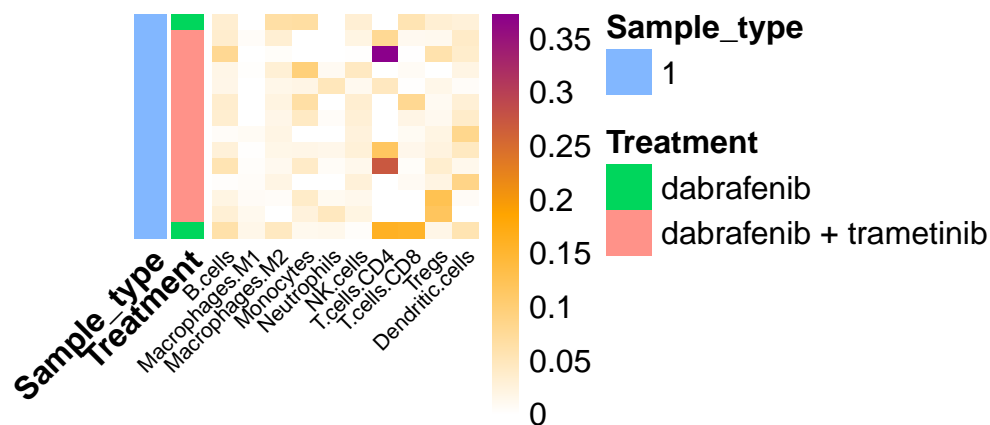
```
## [1] TRUE
## [1] 0
## [1] 0
```

## Deconvolution analysis GSE61992, clustered



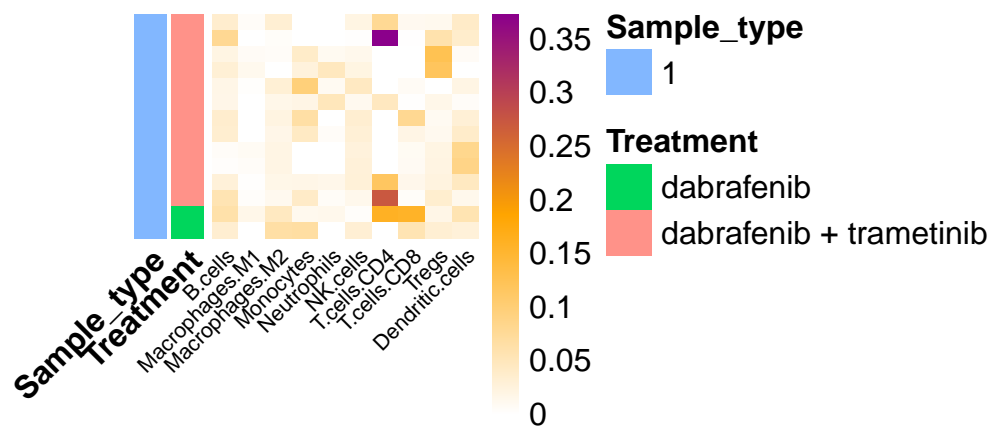
## Deconvolution analysis GSE61992

### Ordered by treatment



## Deconvolution analysis GSE61992

### Ordered by response



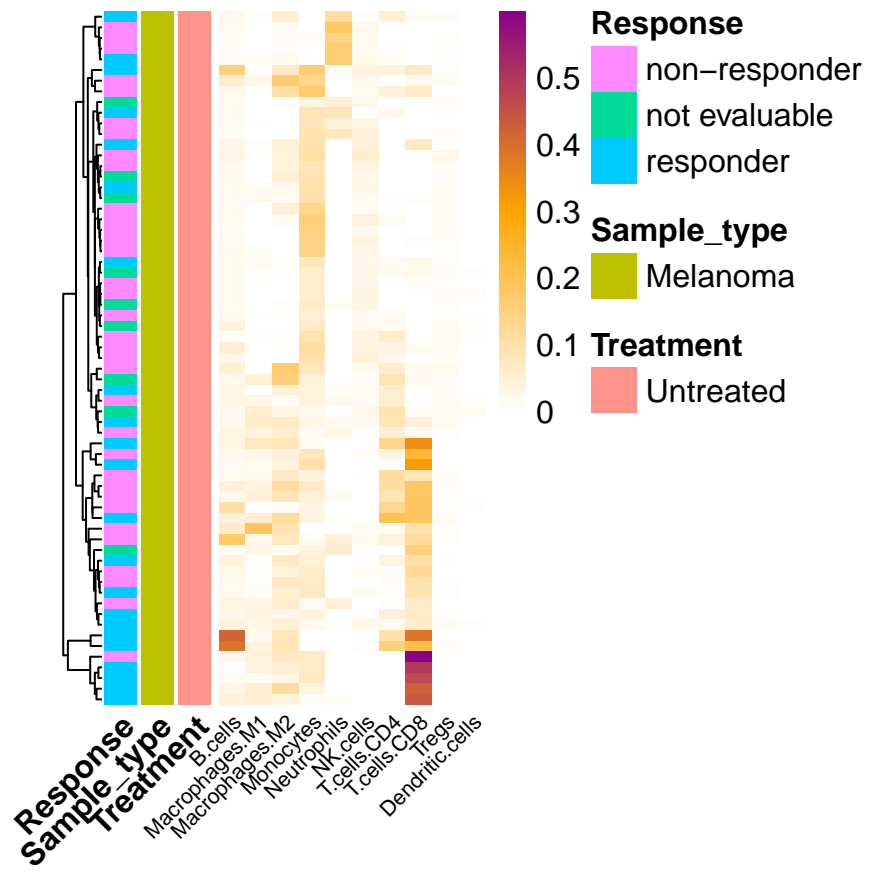
## 3.3 GSE35640

## [1] TRUE

```
## [1] 0
```

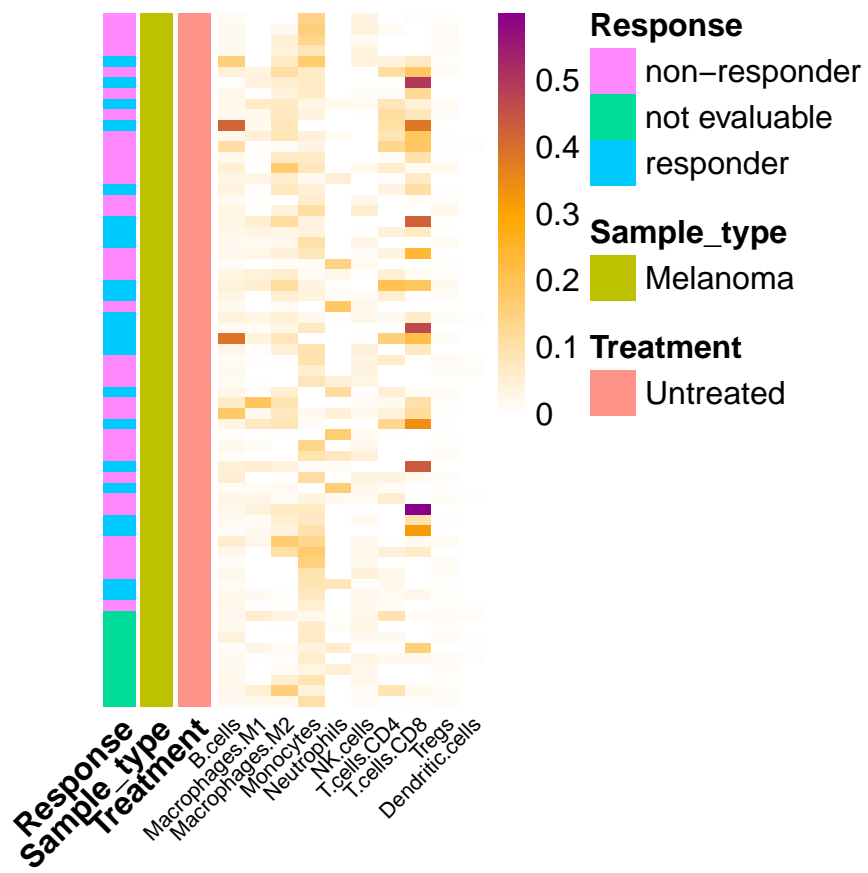
```
## [1] 0
```

## Deconvolution analysis GSE35640, clustered



# Deconvolution analysis GSE35640

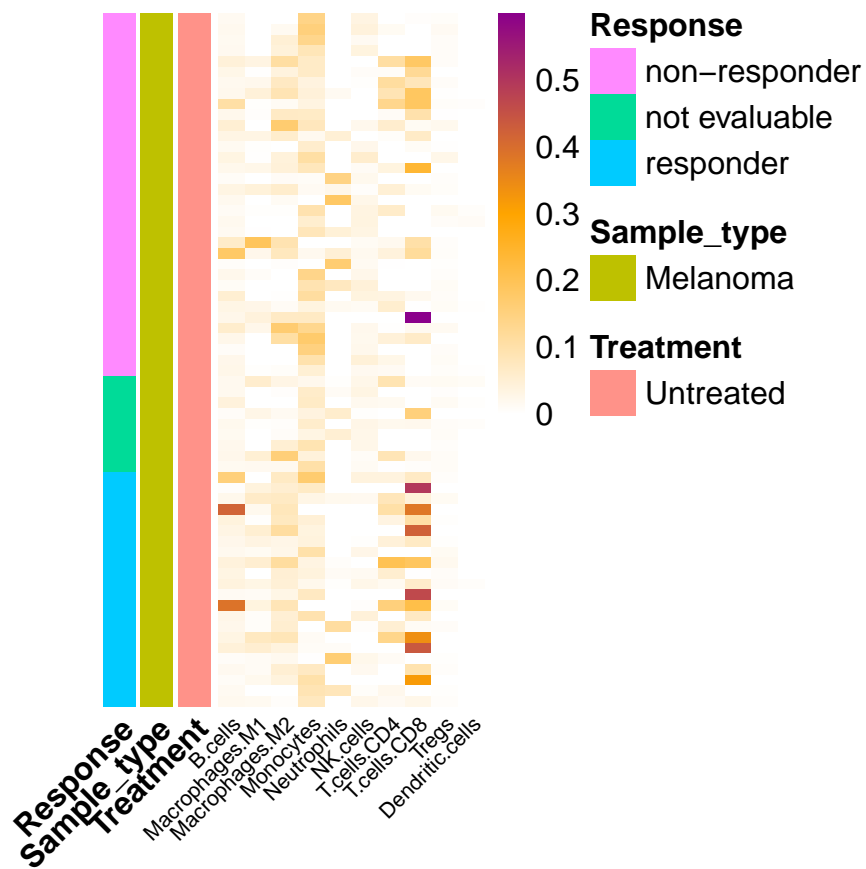
Ordered by treatment





## Deconvolution analysis GSE35640

Ordered by response



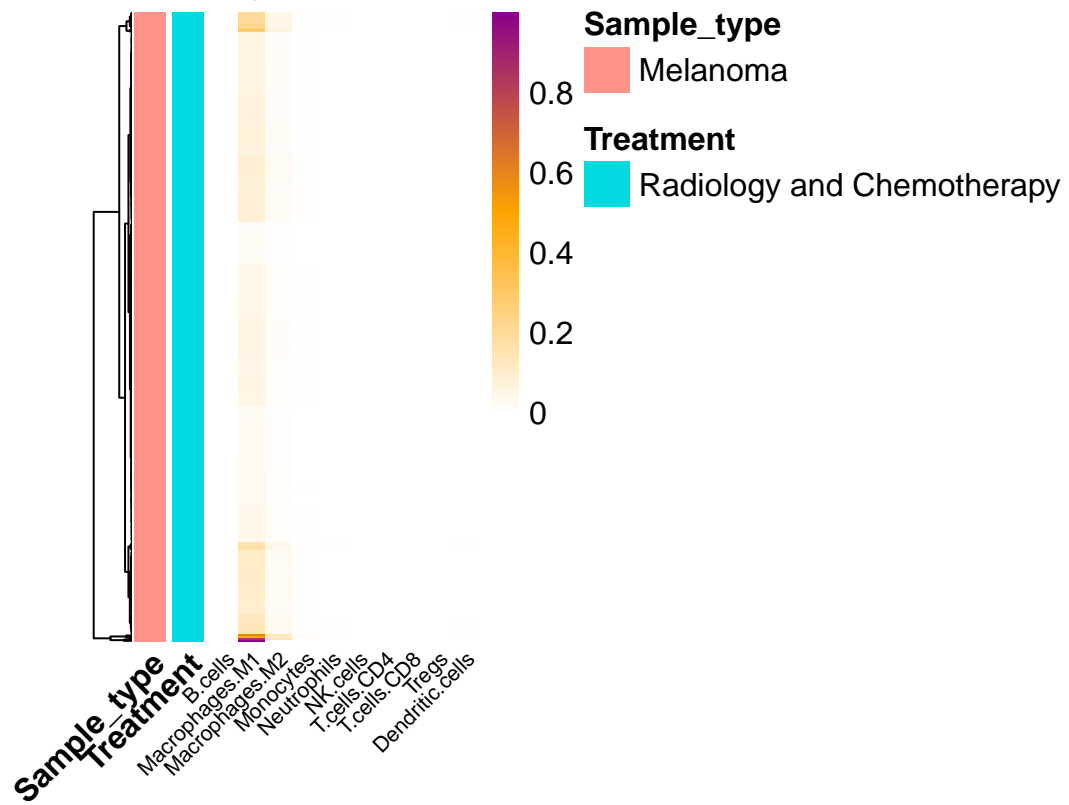
### 3.4 tcga\_skcm

## [1] TRUE

## [1] 0

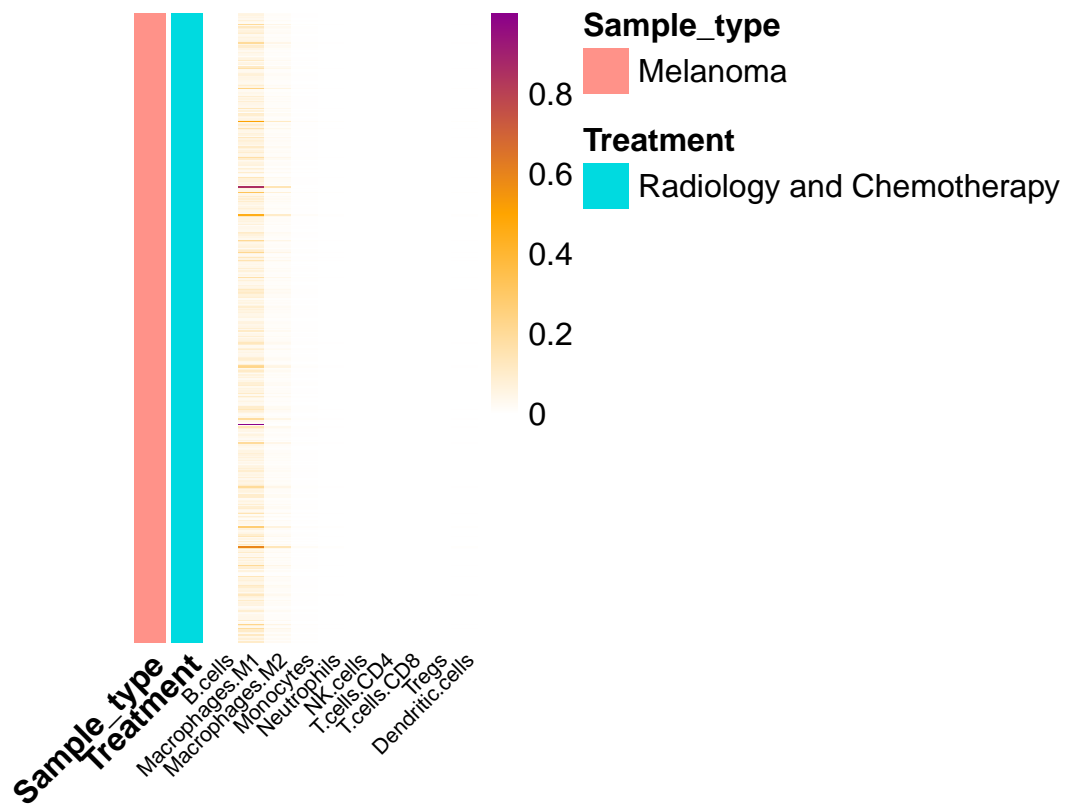
## [1] 0

## Deconvolution analysis TCGA-SKCM, clustered



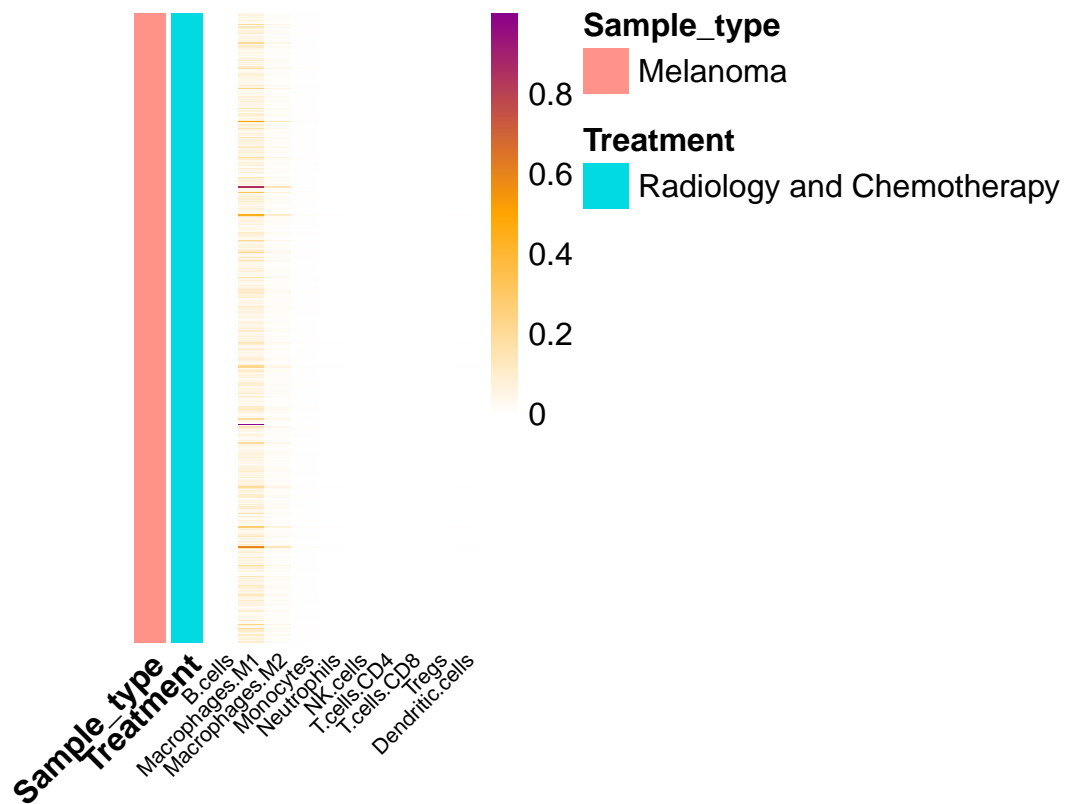
# Deconvolution analysis TCGA-SKCM

Ordered by treatment



## Deconvolution analysis TCGA-SKCM

Ordered by response



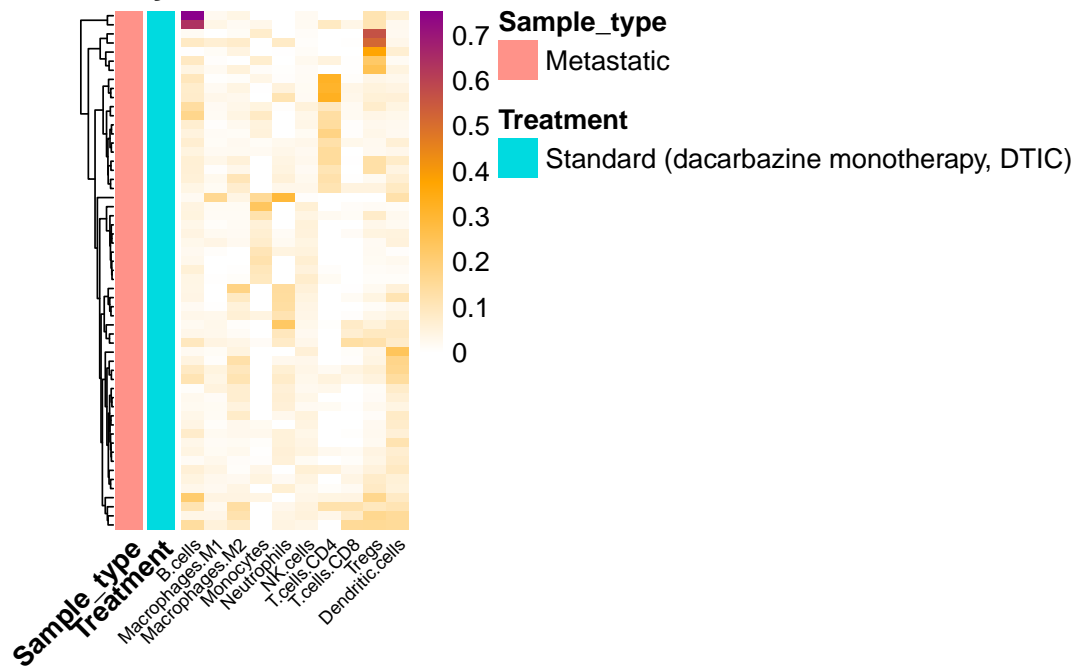
### 3.5 GSE22155-GPL6102

## [1] TRUE

## [1] 0

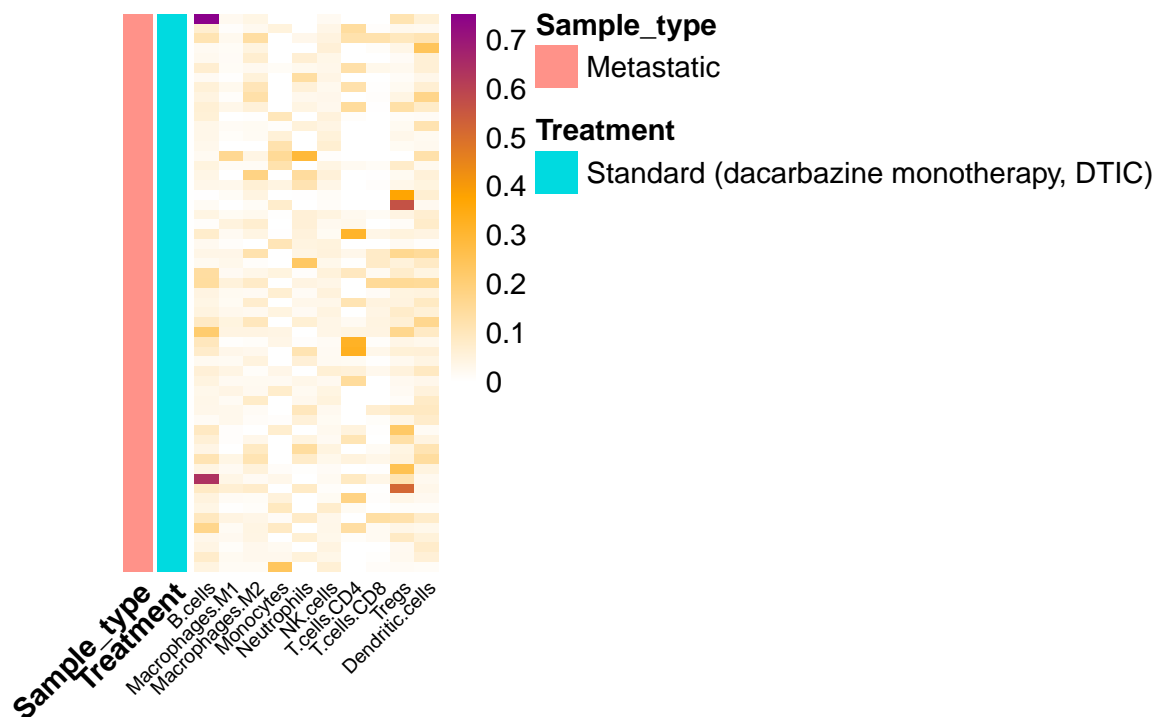
## [1] 0

## Deconvolution analysis GSE22155–GPL6102, clustered



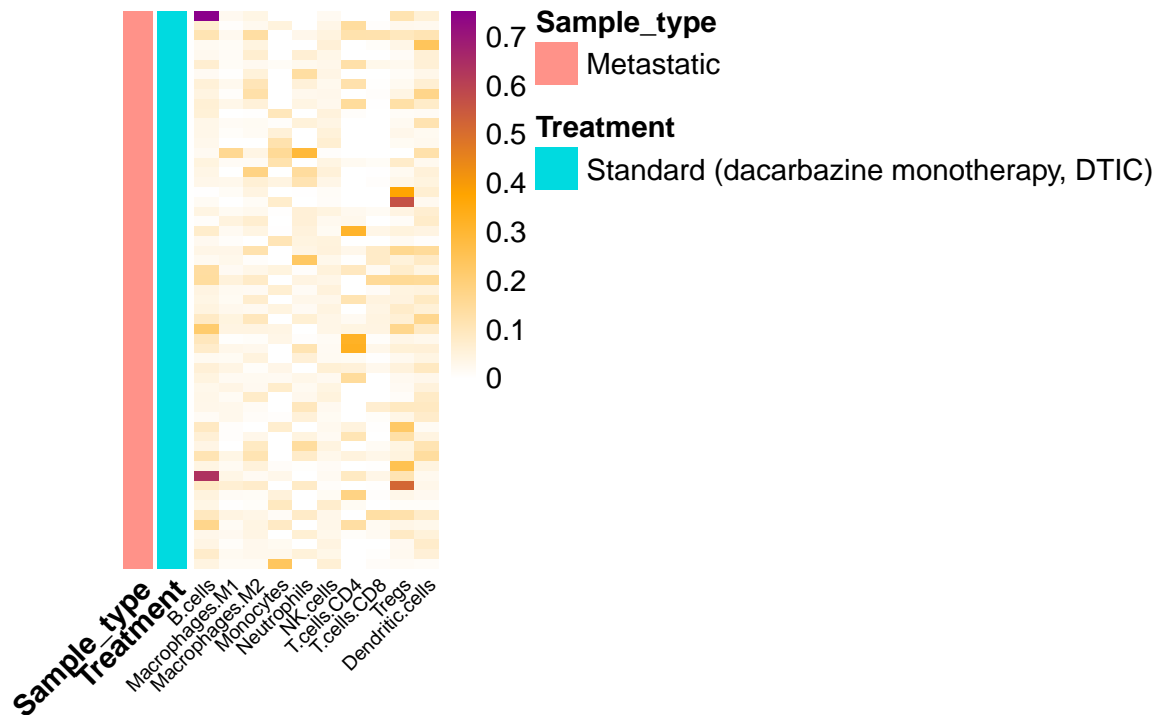
## Deconvolution analysis GSE22155–GPL6102

Ordered by treatment



## Deconvolution analysis GSE22155–GPL6102

Ordered by response



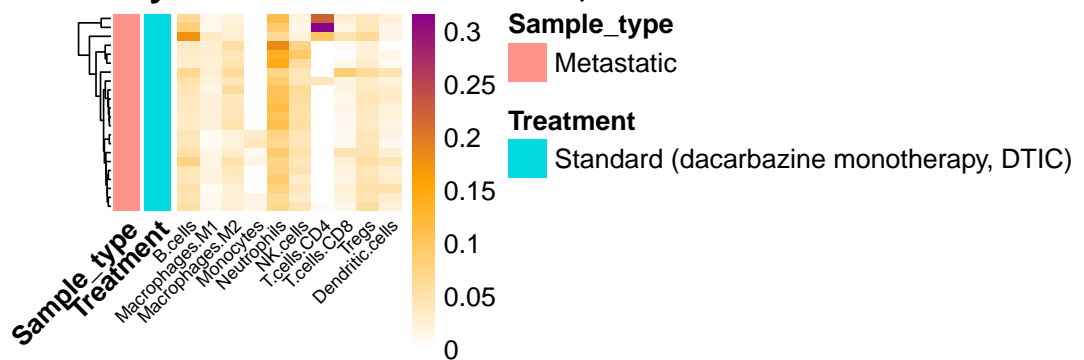
### 3.6 GSE22155-GPL6947

## [1] TRUE

## [1] 0

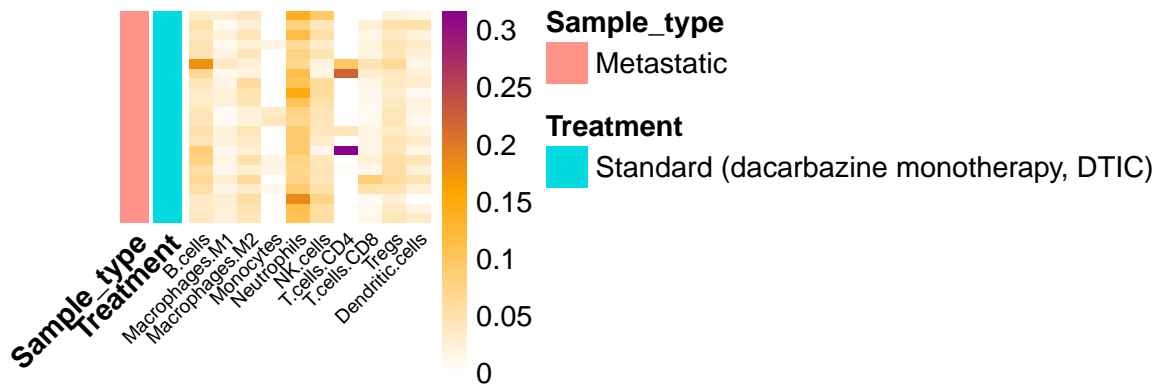
## [1] 0

### Deconvolution analysis GSE22155–GPL6947, clustered



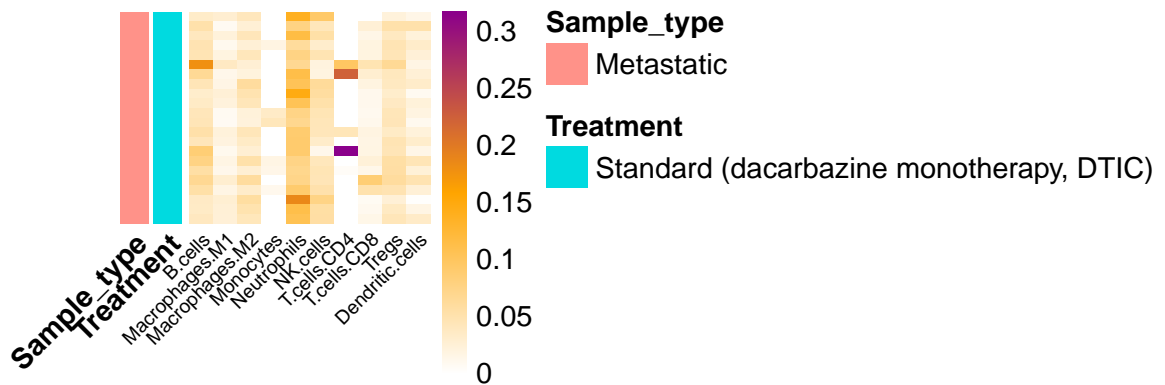
## Deconvolution analysis GSE22155–GPL6947

Ordered by treatment



## Deconvolution analysis GSE22155–GPL6947

Ordered by response



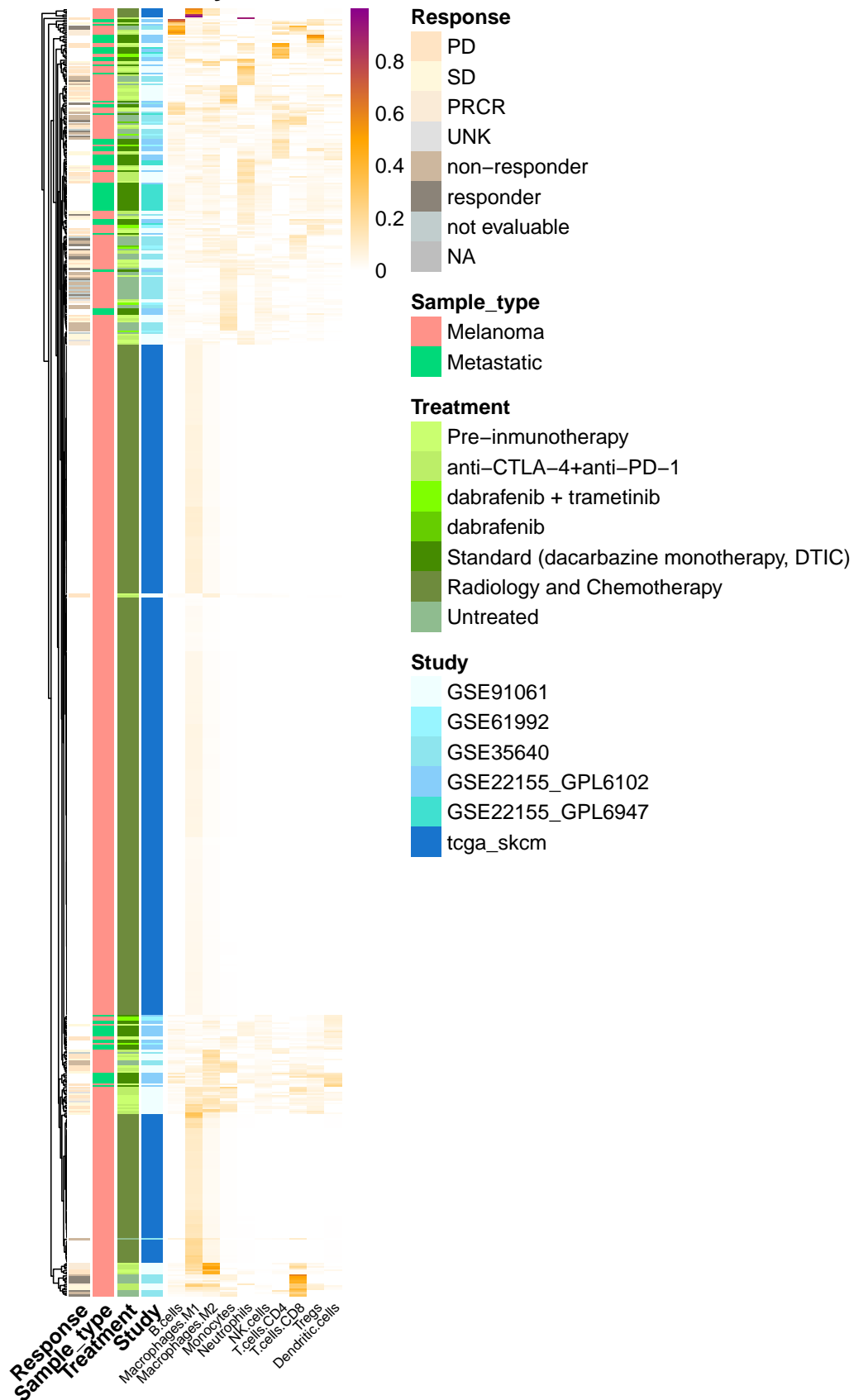
### 3.7 All

```
## [1] TRUE
```

```
## [1] 0
```

```
## [1] 0
```

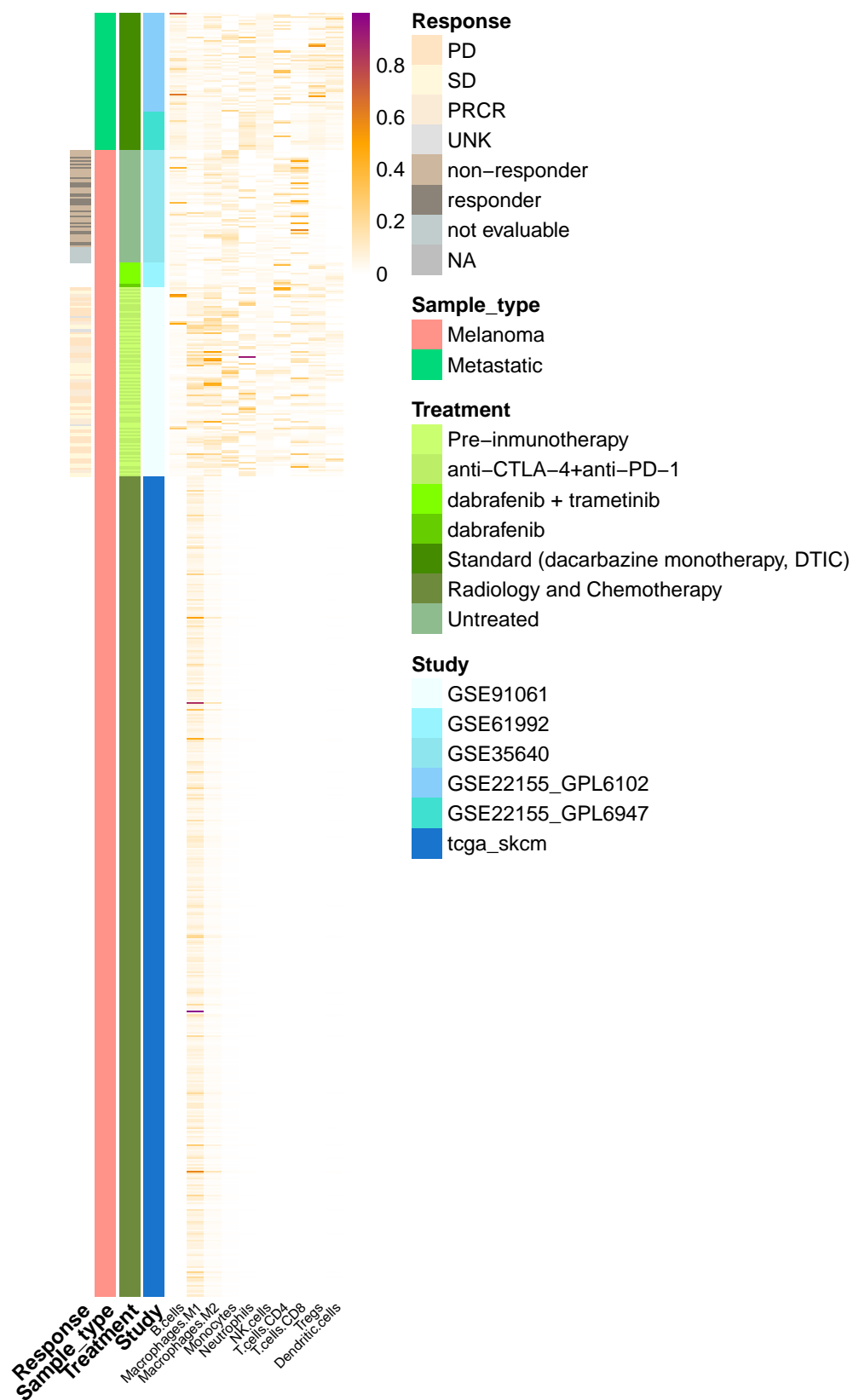
# Deconvolution analysis all studies, clustered





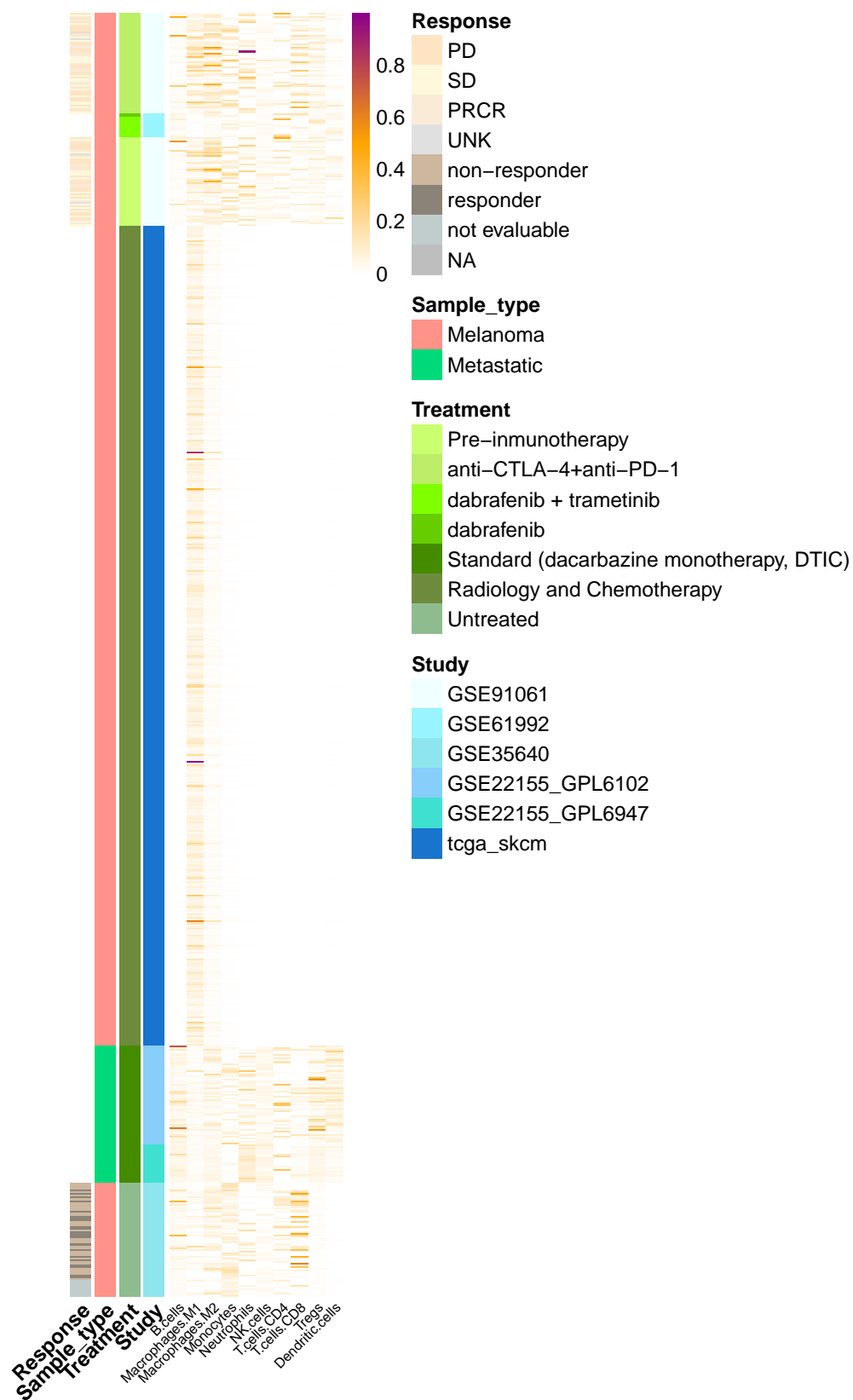
## Deconvolution analysis all studies

Ordered by study



## Deconvolution analysis all studies

Ordered by treatment



## Deconvolution analysis all studies

Ordered by response

