Reading data file 'C:\Users\Linyong Mao\Documents\DNA-seq\cucumber reseq\sv rep sv table dchip.txt'...

Found 17633 lines

Found 126 arrays

Line 17600

Read data for 17632 probe sets and 126 arrays; 0 missing values

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| SV lineNumber | G1 | G10 | G11 | G12 | G13 | G14 |
| 2 | 0 | 0 | 0 | 0 | 0 | 0 |
| 3 | 0 | 0 | 0 | 0 | 0 | 0 |
| 4 | 0 | 0 | 0 | 0 | 0 | 0 |
| 5 | 0 | 0 | 1 | 0 | 0 | 0 |
| 6 | 0 | 1 | 0 | 0 | 0 | 0 |
| 7 | 0 | 1 | 0 | 0 | 0 | 0 |

Reading gene information file 'C:\Users\Linyong Mao\**Documents**\sv rep sv table gene info.txt'...

Gene 17632

Read gene information for 17632 genes

Found 0 FirstOfFunction terms

Found 4 SV type terms

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| SV lineNumber | Identifier | FirstOfLocuslink | FirstOfName | FirstOfFunction | SV type | Description |
| 2 | INSERTION |  |  |  | INSERTION |  |
| 3 | DELETION |  |  |  | DELETION | |
| 18 | LARGE\_DUPLI |  |  |  | LARGE\_DUPLI | |
| 19 | INSERTION |  |  |  | INSERTION | |
| 20 | INSERTION |  |  |  | INSERTION | |
| 21 | LARGE\_DUPLI |  |  |  | LARGE\_DUPLI | |
| 22 | INSERTION |  |  |  | INSERTION | |
| 23 | LARGE\_DUPLI |  |  |  | LARGE\_DUPLI | |

Reading sample information file 'C:\Users\Linyong Mao\Documents\sv rep sv table sample info.txt'...

|  |  |  |
| --- | --- | --- |
| Array name | Sample name | group |
| G8\_L5 | G8\_L5 | Indian |
| 86 | 86 | Indian |
| 69 | 69 | Xishuangbanna |
| 65 | 65 | Xishuangbanna |
| 6 | 6 | Eurasian |
| 9 | 9 | Eurasian |

Reading gene or SNP list file 'C:\Users\Linyong Mao\Documents\DNA-seq\cucumber reseq\sv rep sv table dchip del genes only.txt'...

Found 9169 genes or SNPs

Begin clustering...

{Get external data

Reading data file 'C:\Users\Linyong Mao\Documents\temp\metabolite Xiaojing\coloncancer-cellline-sieve-cleaned.txt'...

Found 167 lines

Found 24 arrays

Line 100

Read data for 166 probe sets and 24 arrays; 0 missing values

Reading sample information file 'C:\Users\Linyong Mao\Documents\sampleInfo xiaojing.txt'...

Read 1 sample information columns (besides the first two columns) for 24 arrays

Treat all the 24 arrays as 24 samples and 1 sample groups

|  |  |  |
| --- | --- | --- |
| Array name | Sample name | cell line |
| II\_4\_12C\_1 | II\_4\_12C\_1 | II\_4 |
| II\_4\_12C\_2 | II\_4\_12C\_2 | II\_4 |
| II\_4\_12C\_3 | II\_4\_12C\_3 | II\_4 |
| II\_5\_12C\_1 | II\_5\_12C\_1 | II\_5 |
| II\_5\_12C\_2 | II\_5\_12C\_2 | II\_5 |
| II\_5\_12C\_3 | II\_5\_12C\_3 | II\_5 |
| II\_6\_12C\_1 | II\_6\_12C\_1 | II\_6 |
| II\_6\_12C\_2 | II\_6\_12C\_2 | II\_6 |
| II\_6\_12C\_3 | II\_6\_12C\_3 | II\_6 |
| …… |  |  |

Finished}

{ANOVA or correlation filtering

Obtain factor information...

Use sample information column 'cell line'

24 of 24 samples have information on 'cell line'

ANOVA filtering by p-value 1.000000

Use array list file ''

Use standardize separators: Yes

Gene 0

166 genes passing ANOVA filtering at 1.000000 level (166 compared, expected false positive: 166), saved in 'C:\Users\Linyong Mao\Documents\dChip\_anova\_filtering.xls'

}