|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Genomic regions**  **MLP vs. C (no: 1183)** | **Length** | **Fold Enrichment** | **False discovery rate** | **E-value** | **No. of Tags** |
| **Mean** | 804.29 | 8.59 | 4.90 | 178.01 | 108.18 |
| **Median** | 729.5 | 7.79 | 4.94 | 126.75 | 75 |
| **Max** | 5062 | 117.59 | 5 | 3100 | 3617 |
| **Min** | 237 | 2.46 | 0 | 121.79 | 18 |
| **St Dev** | 384.61 | 5.83 | 0.42 | 315.62 | 148.74 |
| **Q. 0%** | 237.00 | 2.46 | 0.00 | 121.79 | 18 |
| **Q. 25%** | 572.75 | 6.36 | 4.93 | 123.94 | 44 |
| **Q. 50%** | 729.50 | 7.79 | 4.94 | 126.75 | 75 |
| **Q. 75%** | 952.00 | 9.60 | 4.97 | 129.36 | 128 |
| **Q. 100%** | 5062.0 | 117.59 | 5.00 | 3100 | 3617 |

Q. = quantile

St Dev = standard **deviation** (square root of variance)

E-value = -10log10(P-value)

**Repeats**

L1\_Rn 70

dust 42

trf 29

L1\_Rat1 16

B3 13

(other) 773

NA,s 240

**Stable ID (Ensemble ID)**

9 regions 3:1 (3 labels have been assigned 3 regions each)

122 regions 2:1 (61 labels have been assigned 2 regions each)

1052 regions 1:1 (1052 labels have been assigned to 1 region each)

1183 regions (number of hyper-methylated regions found in PvC FDR5% Liver, P1)

**Distance**

Min 7

1st q. 14,400

Median 39,903

Mean 83,065

3rd q. 96,948

Max 1,409,917

**Genomic Annotation**

**Intronic**: 474 regions

**Upstream**: 361 regions

**Downstream**: 320 regions

**Other** (5’/3’/UTR, exons): 28 regions

|  |  |  |  |
| --- | --- | --- | --- |
| UCSC LiftOver: MLP vs. C |  | species | # regions MBD-Seq FDR5% |
| Rat2Human/Mouse |  | RAT (RN4) | 1183 |
|  |  | MM9 | 901 |
|  |  | HG19 | 713 |
|  |  |  |  |