HW3 – Bioinformatics – 236523

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# Question 1

Part a

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| |  |  |  | | --- | --- | --- | | sample\_name | cell line | dex | | AE1148 | EBC1 | No treatment | | AE1149 | EBC1 | No treatment | | AE1150 | EBC1 | No treatment | | AE1151 | EBC1 | Crizotinib | | AE1152 | EBC1 | Crizotinib | | AE1153 | EBC1 | Crizotinib | | AE1154 | EBC1 | Interferon Î³ | | AE1155 | EBC1 | Interferon Î³ | | AE1156 | EBC1 | Interferon Î³ | | AE1157 | H1573 | No treatment | | AE1158 | H1573 | No treatment | | AE1159 | H1573 | No treatment | | AE1160 | H1573 | Interferon Î³ | | AE1161 | H1573 | Interferon Î³ | | AE1162 | H1573 | Interferon Î³ | | AE1163 | H1993 | No treatment | | AE1164 | H1993 | No treatment | | AE1165 | H1993 | No treatment | | AE1166 | H1993 | Interferon Î³ | | AE1167 | H1993 | Interferon Î³ | | AE1168 | H1993 | Interferon Î³ | | AE1169 | H596 | No treatment | | AE1170 | H596 | No treatment | | AE1171 | H596 | No treatment | | AE1172 | H596 | Crizotinib + Hepatocyte growth factor (HGF) | | AE1173 | H596 | Crizotinib +HGF | | AE1174 | H596 | Crizotinib +HGF | | AE1175 | H596 | Hepatocyte growth factor (HGF) | | AE1176 | H596 | Hepatocyte growth factor (HGF) | | AE1177 | H596 | Hepatocyte growth factor (HGF) | | AE1178 | H596 | Interferon Î³ | | AE1179 | H596 | Interferon Î³ | | AE1180 | H596 | Interferon Î³ | |  |  |

Part e

Cell types: (4 cell types)

1. EBC1 – 9 samples
2. H1573 – 6 samples
3. H1993 – 6 samples
4. H596 – 12 samples

Treatments: (6 types of treatments)

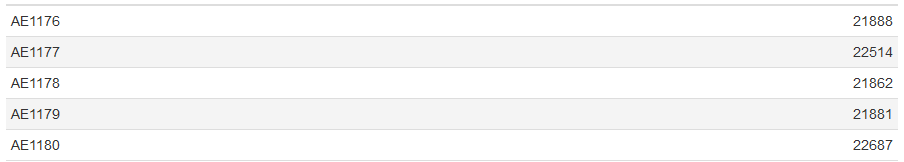
1. No treatment – 12 samples
2. Crizotinib – 3 samples
3. Interferon Î³ - 12 samples
4. Crizotinib + Hepatocyte growth factor (HGF) – 1 sample
5. Crizotinib +HGF – 2 samples
6. Hepatocyte growth factor (HGF) – 3 samples

Expressed Genes:









Highly expressed Genes:

I used excel command in counts file for each row: COUNTIF and got the following result

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| |  |  | | --- | --- | | AE1148 | 6601 | | AE1149 | 7346 | | AE1150 | 6082 | | AE1151 | 6955 | | AE1152 | 6935 | | AE1153 | 7270 | | AE1154 | 5759 | | AE1155 | 6826 | | AE1156 | 6407 | | AE1157 | 6938 | | AE1158 | 6109 | | AE1159 | 6675 | | AE1160 | 7066 | | AE1161 | 5855 | | AE1162 | 7193 | | AE1163 | 6717 | | AE1164 | 6092 | | AE1165 | 6595 | | AE1166 | 7059 | | AE1167 | 6227 | | AE1168 | 6981 | | AE1169 | 7173 | | AE1170 | 6082 | | AE1171 | 6627 | | AE1172 | 5986 | | AE1173 | 6769 | | AE1174 | 6523 | | AE1175 | 6643 | | AE1176 | 5917 | | AE1177 | 6441 | | AE1178 | 5553 | | AE1179 | 5823 | | AE1180 | 6678 | |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
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Filtered data.frame:

For the following 2 treatments:



I have a total of 15 samples

Genes differentially expressed with threshold < 0.05:

There are 353 genes with adjusted p-value < 0.05

Genes differentially expressed with threshold < 0.01:

There are 182 genes with adjusted p-value < 0.01

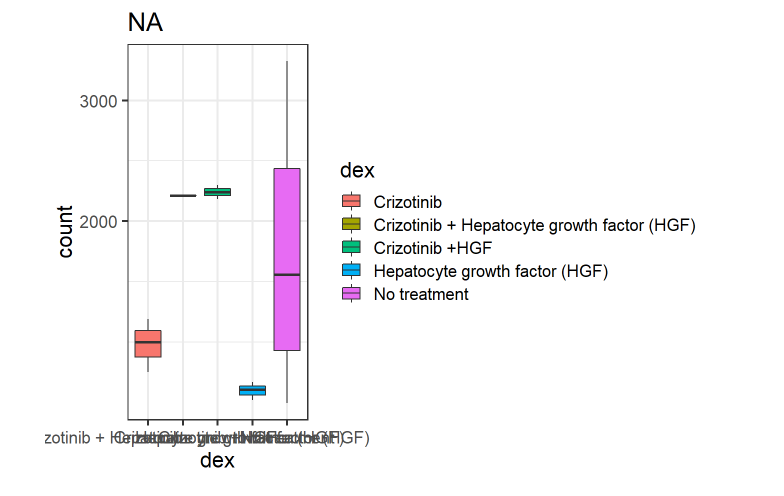
Log2fold change:

There are 3220 with log fold change above 2

There are 233 with log fold change below -2

How significant is the effect of the treatment on gene expression levels?

As we can see in the box plot:



It seems like HGF is the only treatment which is significant on the gene expression.