# Nanostring Analysis for Dataset X

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# **Guiding Questions**

Which immune cell type (and other) to compare with what we learned from flow cytometry? Did PD1 elicit any changes in expression profile compared with IgG?

What can we learn about IFNg treatment.immune cells activated?

## What are the characteristics of the samples?

#### Basic Setup

##		${\tt Sample.Name}$	${\tt RNA.Solution}$	${\tt Tumor}$	Fraction	${\tt Treatment}$
##	1	P0003.S1	RNA Later	P0003	large fragments	None
##	2	P0003.S3	RNA Later	P0003	single cell flow	None
##	3	P0004.S1	RNA Later	P0004	large fragments	None
##	4	P0004.S2	RNA Later	P0004	None	None
##	5	P0004.S3	RNA Later	P0004	single cell flow	None
##	6	P0010.IFNy	RNA Later	P0010	None	IFNy
##	7	P0010.IgG	RNA Later	P0010	None	IgG
##	8	P0010.S1	RNA Later	P0010	large fragments	None
##	9	P0010.S2	RNAdvance	P0010	None	None
##	10	P0010aPD1	RNAdvance	P0010	None	aPD1
##	11	P0011.S1	RNAdvance	P0011	large fragments	None
##	12	P0011.S2	RNAdvance	P0011	None	None

## What is being quantified?

Number of Nanostring Controls

What Gene functions are being quantified?

Gene
Cell.Type
Adaptive.Immunity
Apoptosis
Cell.Cycle

 $\mathbf{X}$ 

Cellular.Stress

Complement.System

Death.Receptor.Signaling

Extracellular.matrix.organization

Fc.Receptor.Signaling

Innate.Immunity

Interferon.Signaling

Interleukin.Signaling

NF.kB

MAPK.Signaling

Metabolism

TLR.Signaling

VEGF.Signaling

Wnt.Signaling

#### How many genes represent each function type Information?

Cell.Type	n
	712
B-cells	4
CD45	1
CD8 T cells	2
Cytotoxic cells	8
DC	4
Exhausted CD8	4
Macrophages	2
Mast cells	2
Neutrophils	3
NK CD56dim cells	3
NK cells	2
T-cells	5
Th1 cells	1
Treg	1

Cellular.Stress	n
-	723
+	31

Complement.System	n
-	720
+	34

Death.Receptor.Signaling	n
-	736
+	18

Extracellular.matrix.organization	n
-	714
+	40

Fc.Receptor.Signaling	n
-	681
+	73

n
733 21

Interferon.Signaling	n
-	664
+	90

$$\begin{array}{c|c} \underline{\text{Interleukin.Signaling}} & \underline{n} \\ - & 631 \\ + & 123 \end{array}$$

MAPK.Signaling	n
_	689
+	65

Metabolism	n
-	712
+	42

VEGF. Signaling	n
-	698
+	56

Wnt.Signaling	n
-	734
+	20

#### What comparisons can be made?

Fraction	n
large fragments	4
None	6
single cell flow	2

RNA.Solution	n
RNA Later	8
RNAdvance	4

Tumor	n
P0003	2
P0004	3
P0010	5
P0011	2

Treatment	n
aPD1	1
IFNy	1
IgG	1
None	9

## Can we group the samples?

PCA plots give an idea what similarties are to be expected from the samples that are in it.

 $\operatorname{PCA}$  - Calculates variability across entire dataset for each gene - Groups components - Using these components it allows to check for bias and grouping within samples

```
## Importance of components:

## PC1 PC2 PC3 PC4 PC5 PC6 PC7

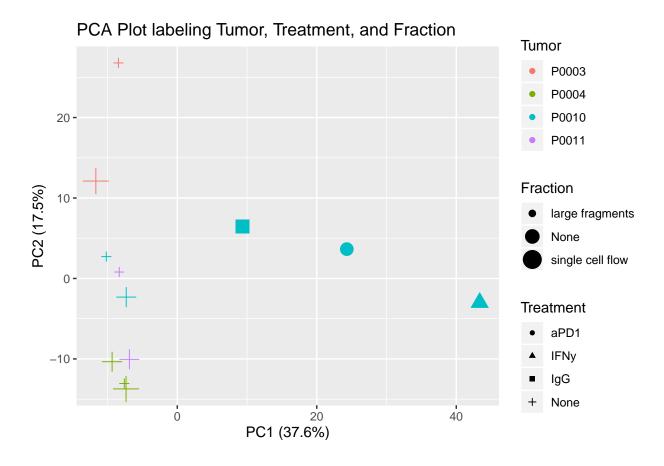
## Standard deviation 17.1568 11.7095 11.0791 8.76368 7.71650 5.47066 4.79097

## Proportion of Variance 0.3755 0.1749 0.1566 0.09796 0.07595 0.03817 0.02928
```

```
## Cumulative Proportion 0.3755 0.5503 0.7069 0.80487 0.88082 0.91899 0.94827 ## PC8 PC9 PC10 PC11 PC12 PC12 Proportion of Variance 0.02065 0.01555 0.01186 0.00367 0.000e+00 Cumulative Proportion 0.96892 0.98447 0.99633 1.00000 1.000e+00 ## Joining, by = "Sample.Name"
```

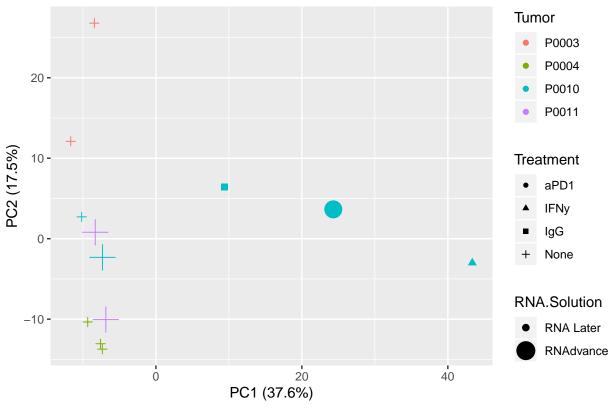
#### Samples Separate by treatment

## Warning: Using size for a discrete variable is not advised.



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## Immune Cell Type Composition?

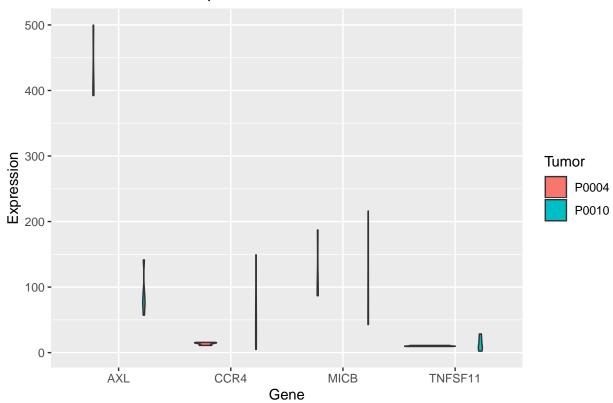
What can we learn about IFNg treatment.immune cells activated? Which immune cell type (and other) to compare with what we learned from flow cytometry? PD1 elicit response?

```
## Joining, by = "Sample.Name"
```

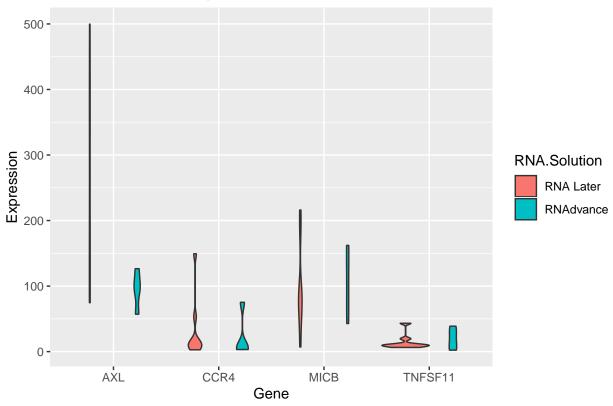
## Warning: Column `Sample.Name` joining character vector and factor, coercing into
## character vector

<sup>\*</sup>Missing Flow Cytometry data

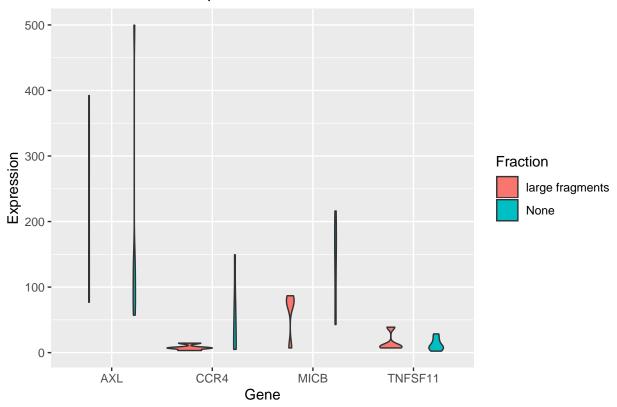




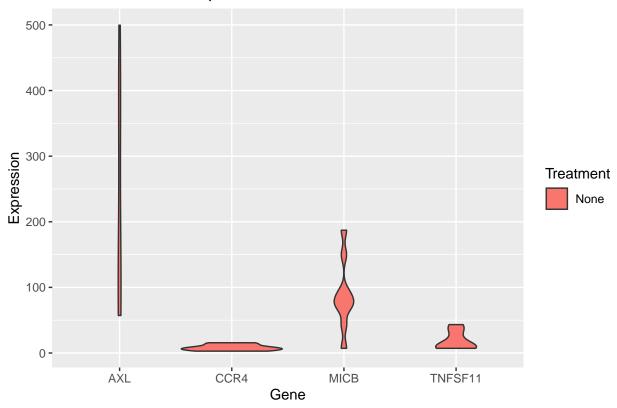








# Is there a relationship for RNA Solution?



### Heatmaps of Each Immune Cell Type

## Joining, by = "Sample.Name"

