



**COLLEGE OF MEDICINE  
AND LIFE SCIENCES**

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**THE UNIVERSITY OF TOLEDO**

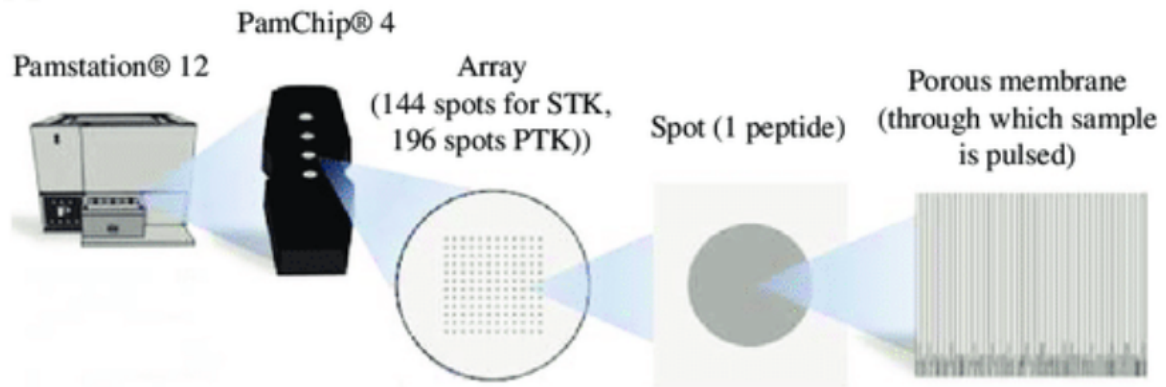
# Kinase Array Report (STK)

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{The Department of Neurosciences at the University of Toledo Medical Center}

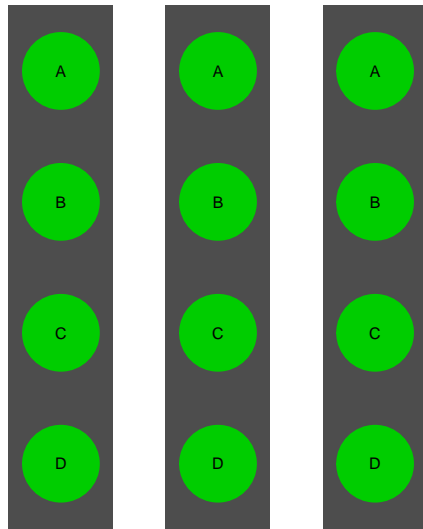
## Introduction

**Background** The Pamstation12 instrument provides a profiling of kinase activity of cell or tissue samples. The device is loaded with either serine/threonine or tyrosine microarray chips. Each chip has 4 wells so four samples can be loaded on a single chip, and the Pamstation12 can accommodate 3 chips per run. The microarray represents 144 (STK chip) or 196 (PTK chip) reporter peptides that can be phosphorylated by serine/threonine or tyrosine kinases. The device measures the degree of the phosphorylation in real time by detecting fluorescently labeled antibodies at different exposure times. The list of peptides present in each microarray can be viewed here: [STK chip](#), [PTK chip](#)



**Samples Info** Schizophrenia vs. Control: Run 1, Pair 1, Chip 1,2, & 3

**Run Design** Designing the placement of the samples on the chips and arrays is important to consider due to the variability across different chips and batches. During the run some wells are subject to fail and their data cannot be analyzed and shown below as red.

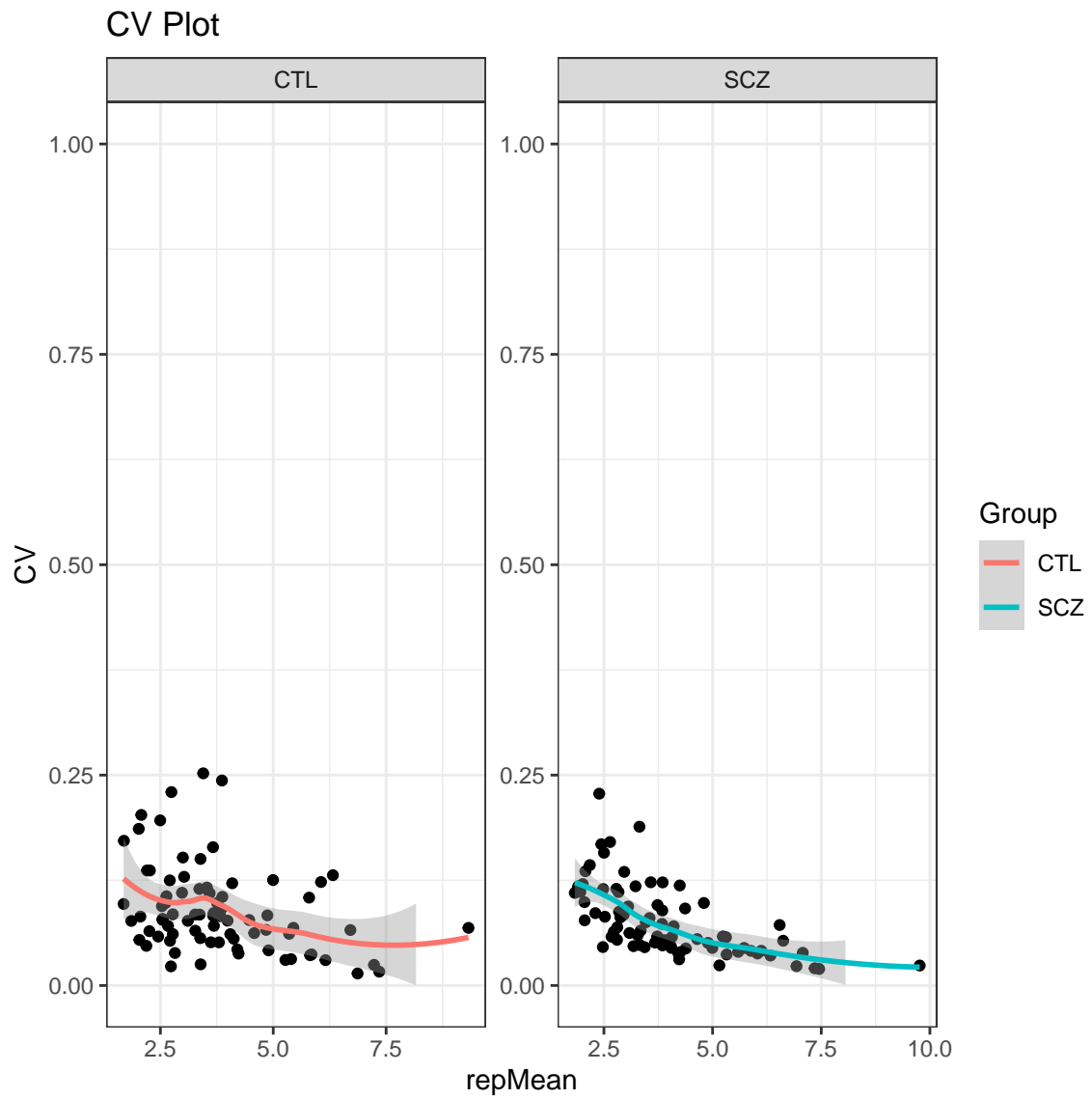


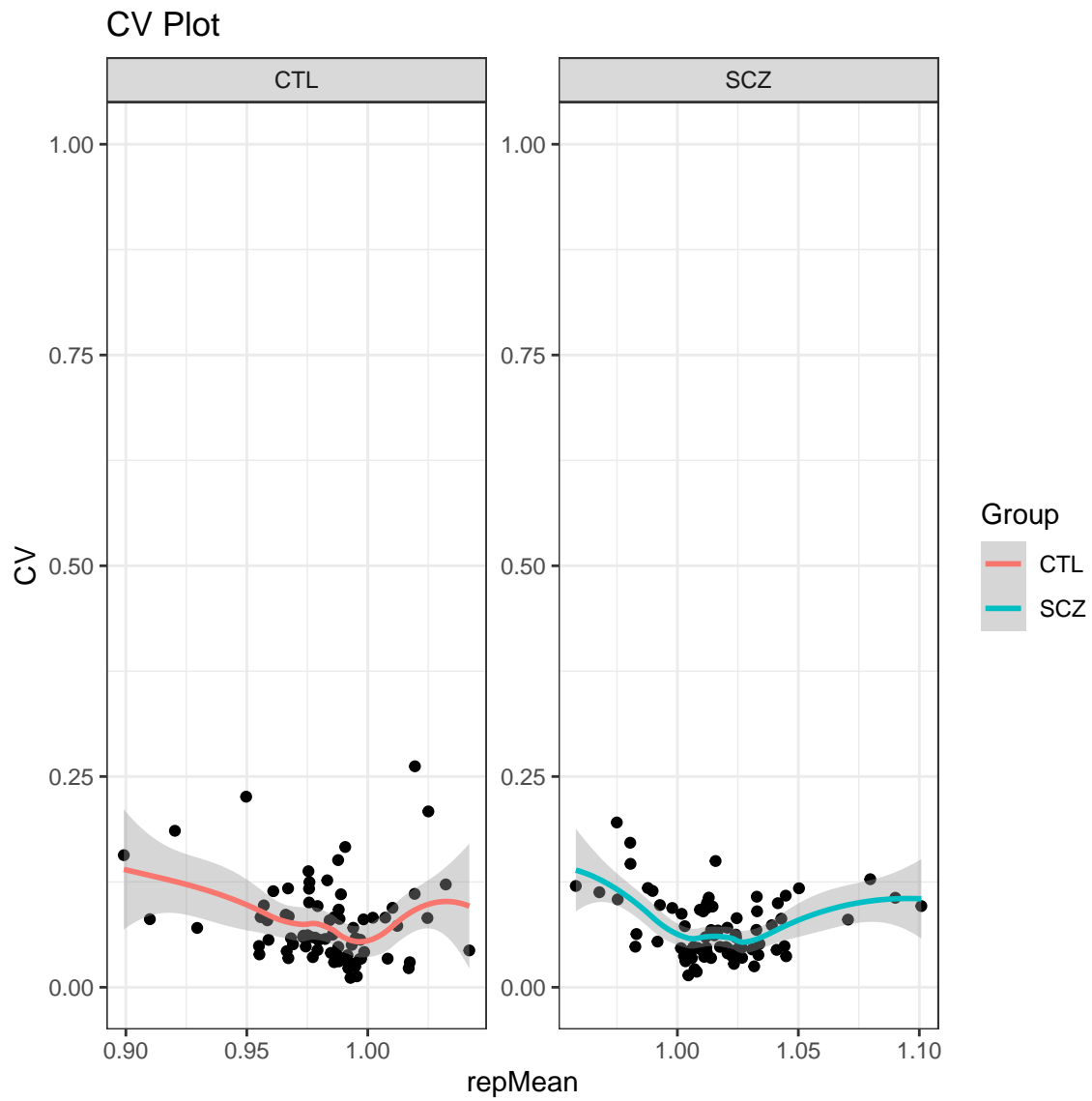
## Results

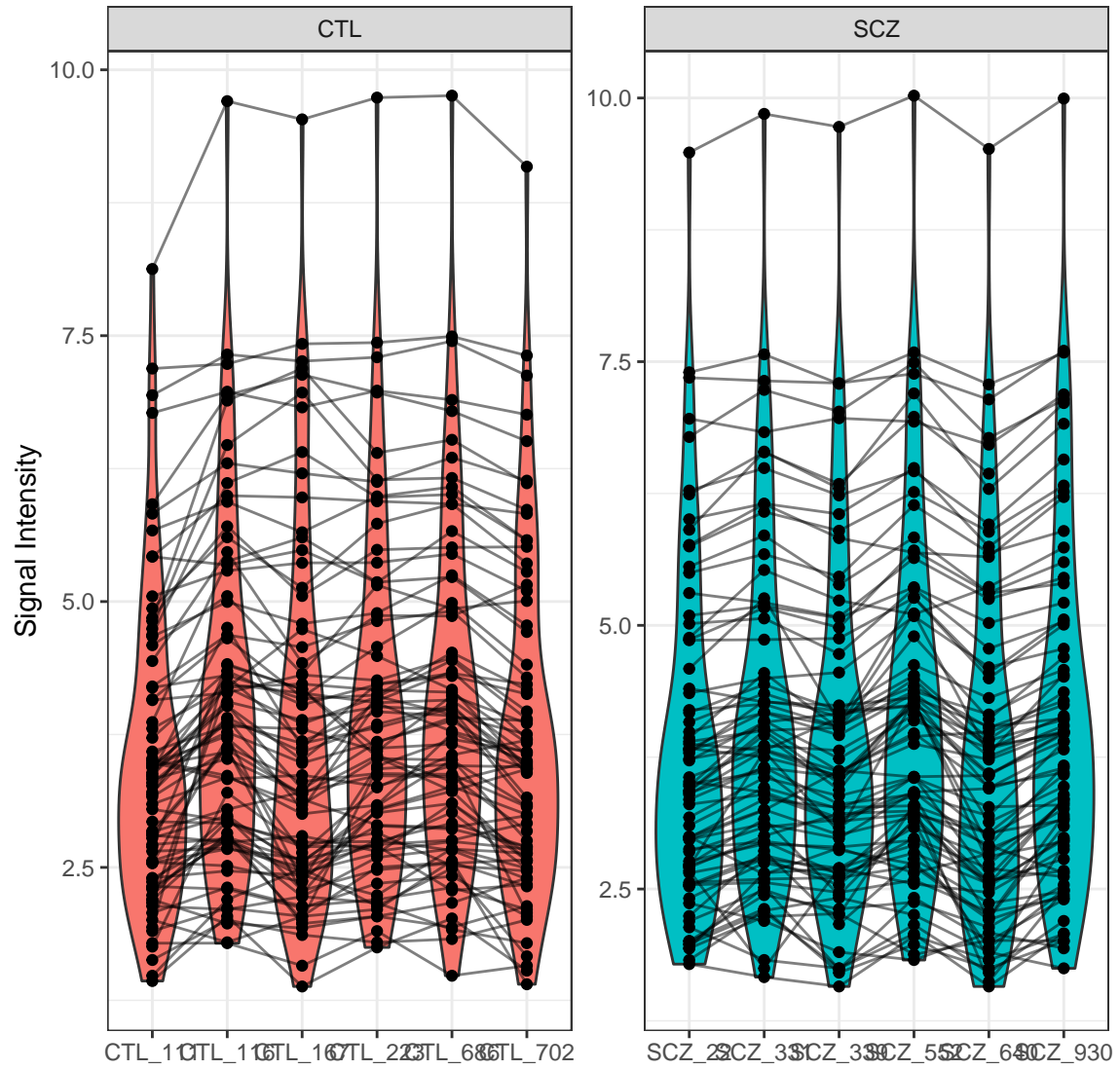
**Image Analysis** The first step of analyzing the run is to convert the images taken by the PamStation of each array at different exposure times to numerical values. This is done by the Bionavigator software developed by Pamgene. The software recognizes the grid of the array with the aid of the searching algorithm (Pamgrid) to correctly identify each spot on the array. The numbers produced by this software represent the median value of the foreground pixels minus the median value of the background pixels to produce the median signal minus background (*Median\_SigmBg*).

**Data Tidying and Modeling** The raw data is then transformed to be tidy for an easier analysis, modeling, and visualizing. In order to combine the values from different exposure times into a single value, a simple linear regression model of the *Median\_SigmBg* as a function of exposure time is fitted. The slope of the model fit and  $R^2$  are then used for quality control and samples comparison. The slope is also scaled by multiplying by 100 and log2 transformed (*Slope\_Transformed*).

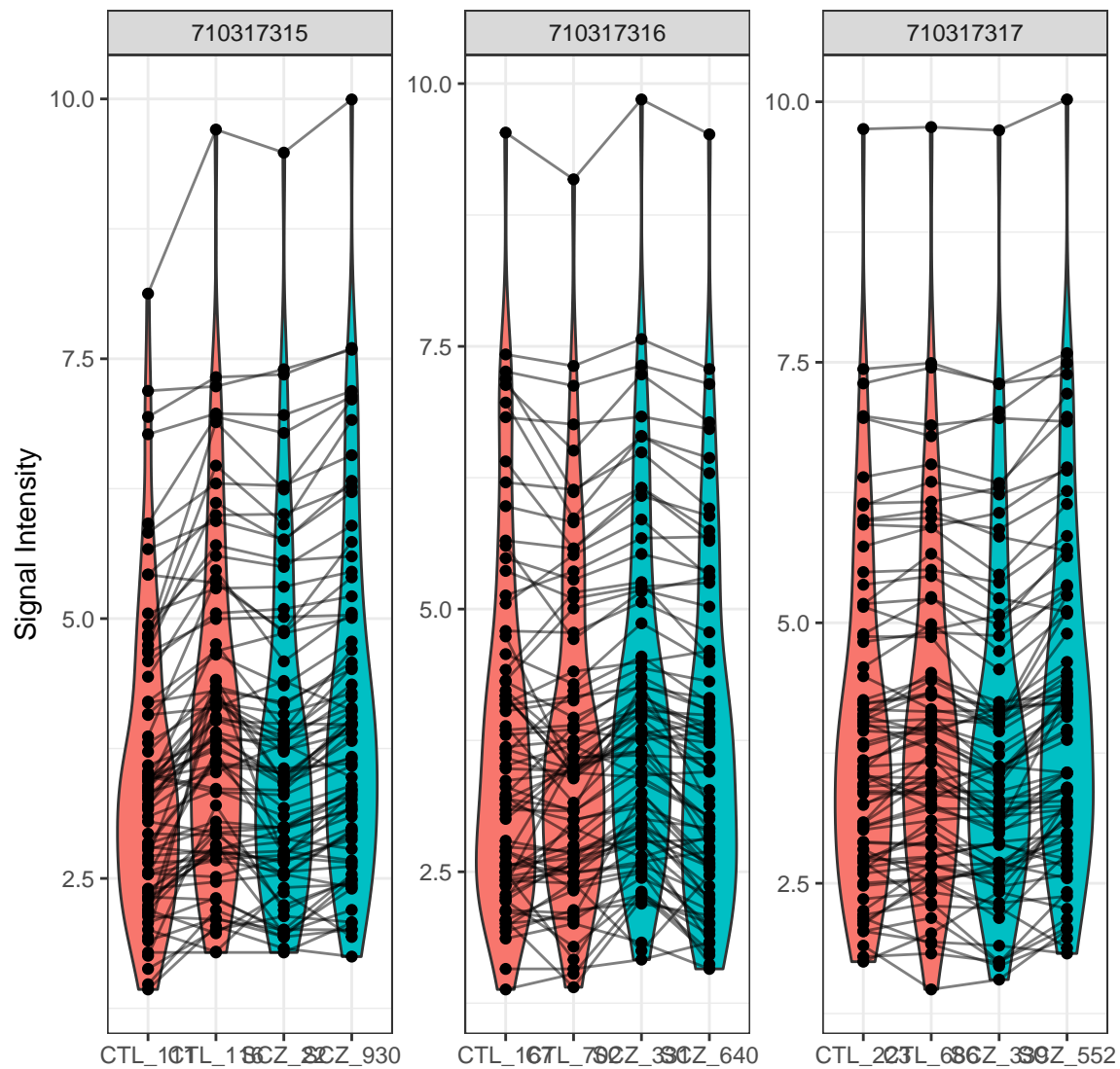
**Global Signal Intensity** For a global signal intensity across all samples/groups, a heatmap is constructed based on the *Slope\_Transformed* values. This heatmap represents all the peptides present on the chip except the positive/internal controls and peptides that failed to pass QC. The heatmap is scaled by row to highlight the peptide signal differences across the samples. A hierarchical unsupervised clustering is applied both on the peptides and the samples to potentially group similar signatures.

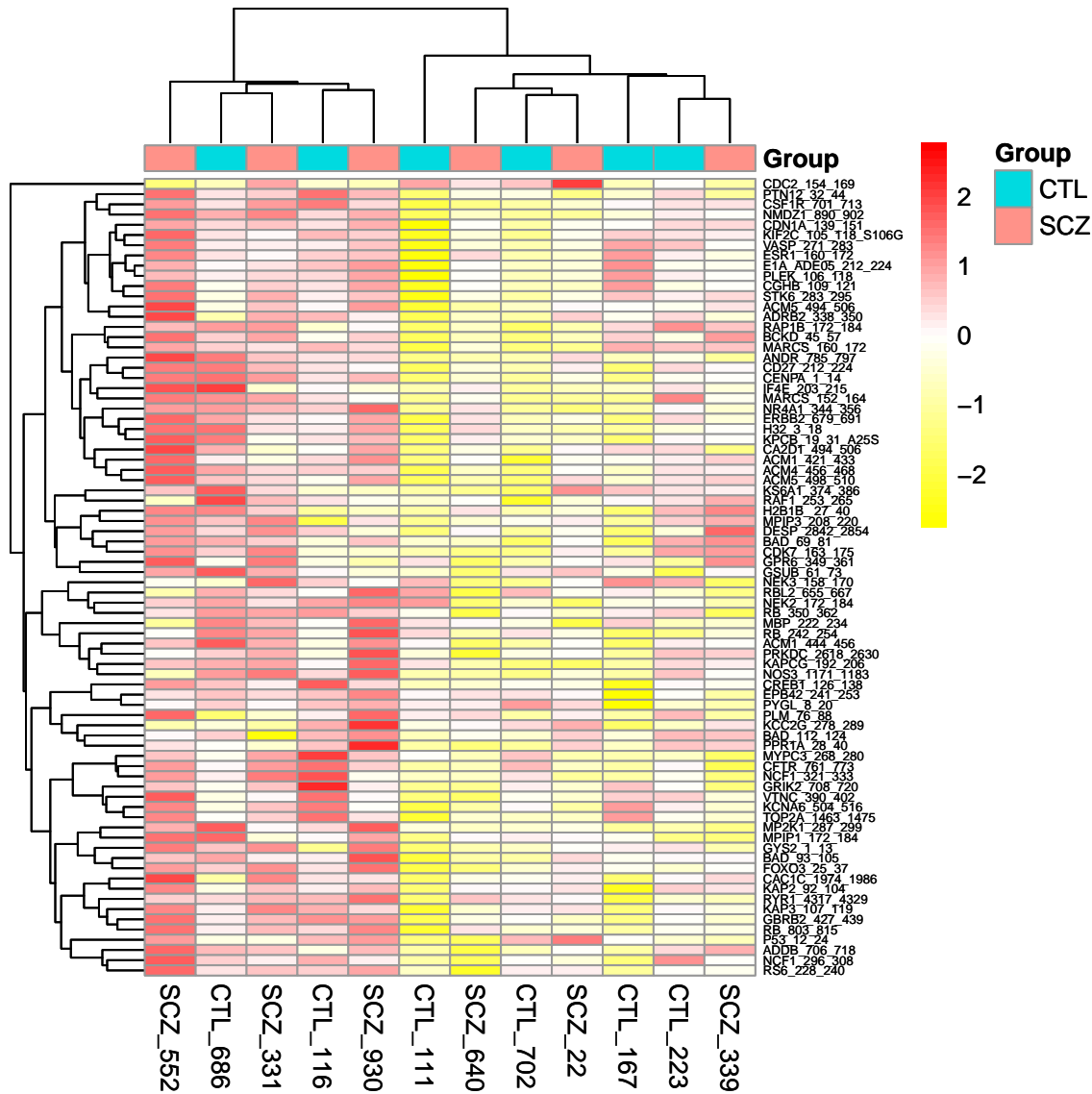


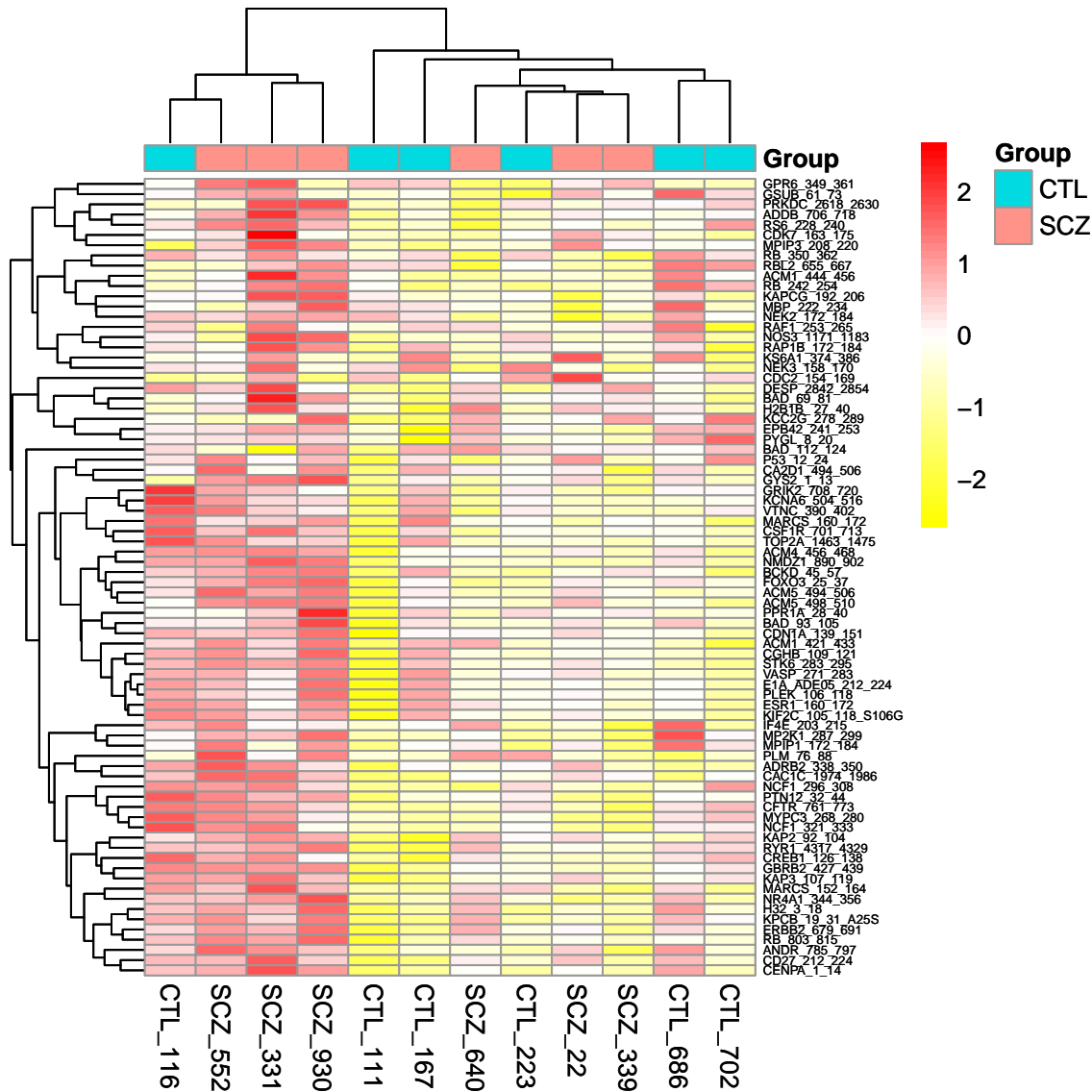


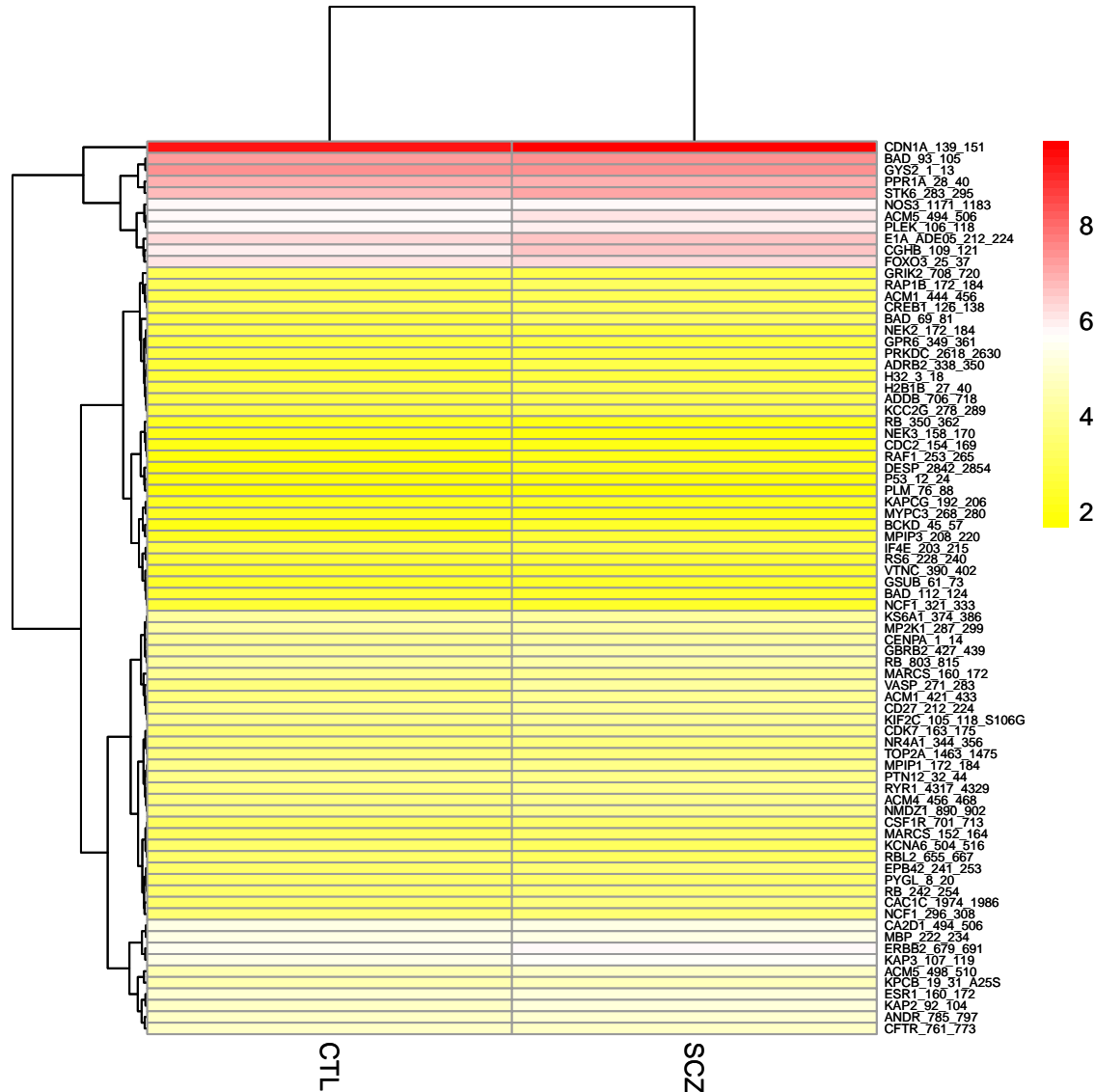












**Group Comparison** To compare between samples, a two-group comparison is performed. In this case, the two group comparisons are:

- Control vs. Schizophrenia (Pair 3.1)

The *Slope\_Transformed* ratio between each group, paired by chip, is calculated to represent the final peptide signal to be used to calculate the fold change. Based on the fold change, peptides that pass a certain fold change threshold are considered significant hits. Also, quality control steps applied in each comparison to filter out peptides that do not reach specific criteria:

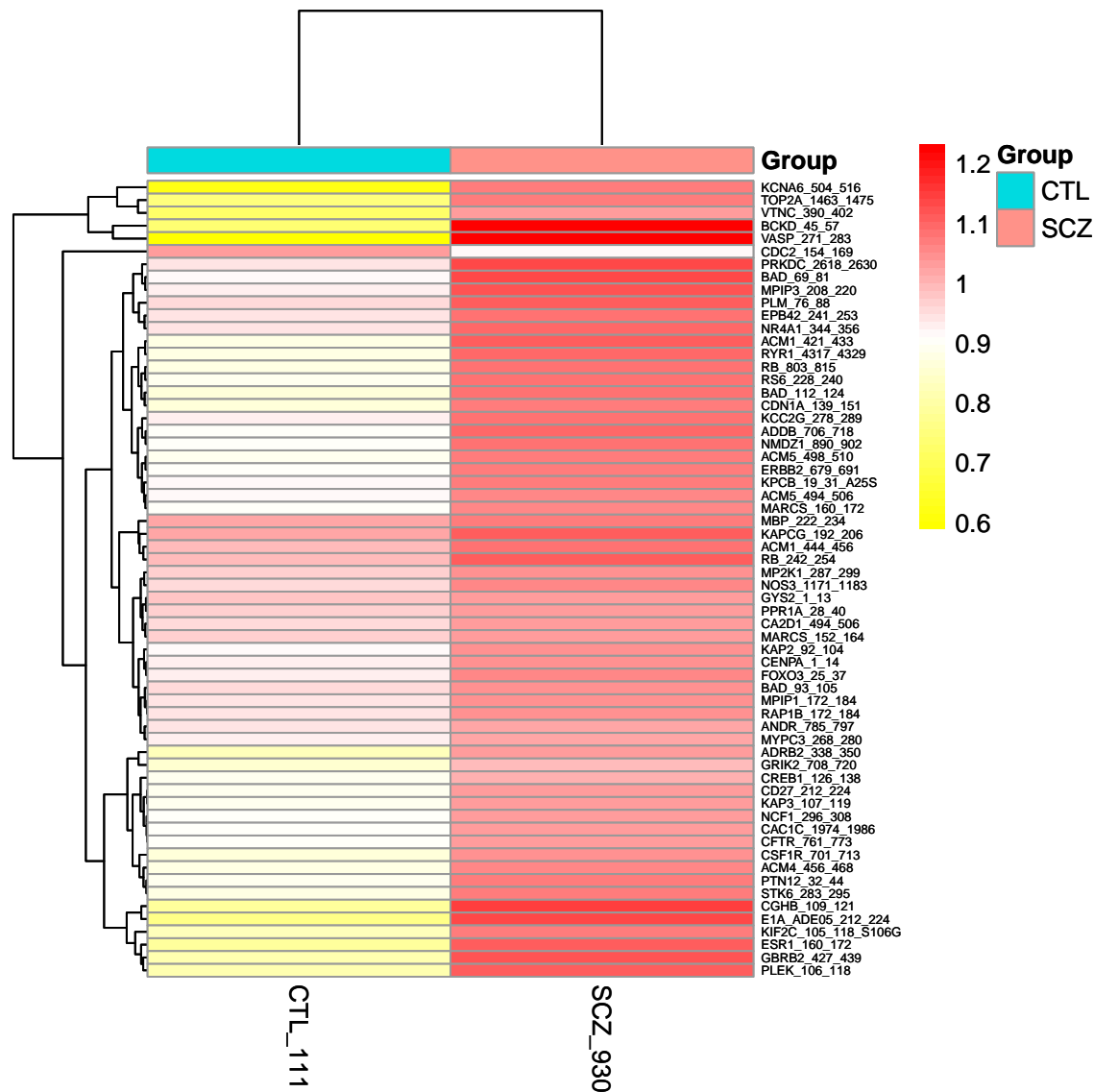
- The *Medain\_SigmBg* at max exposure 200ms must be above a certain value

- $R^2$  of the linear model fit must be above a threshold value

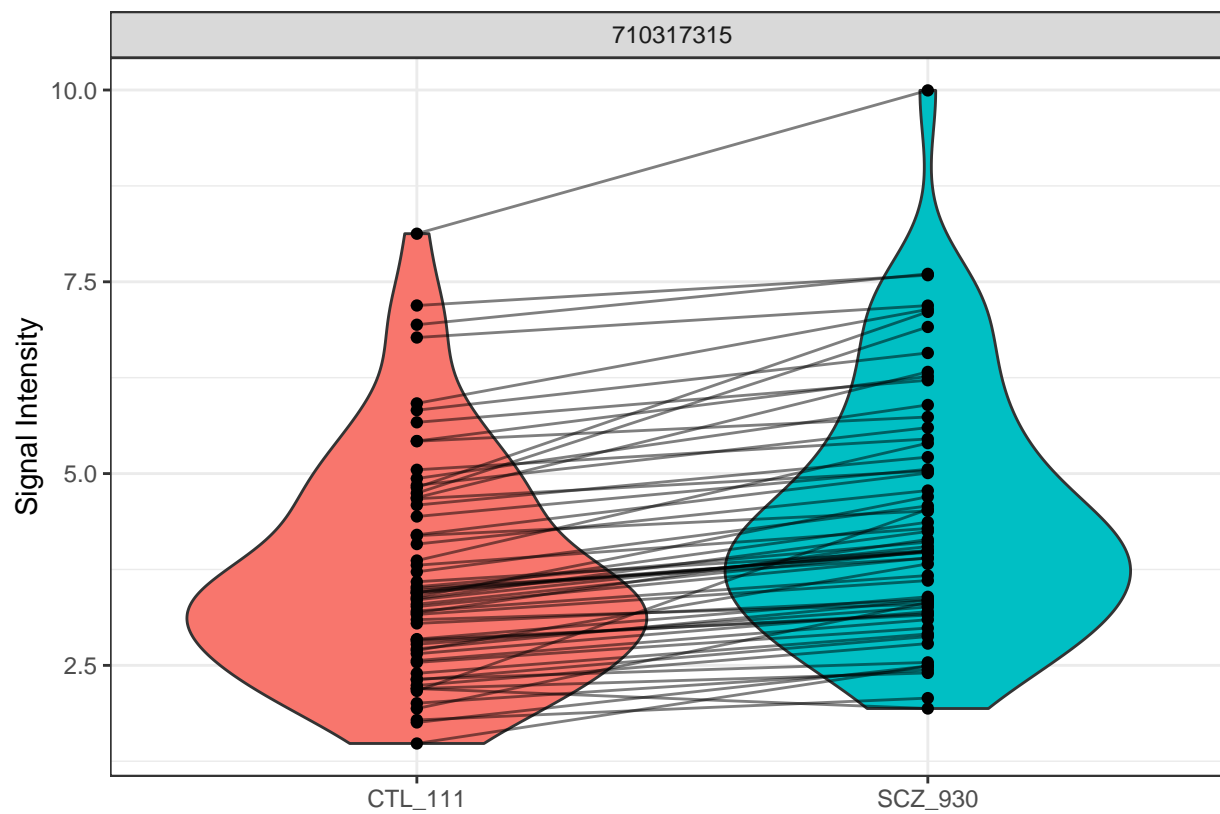
These *Filtering Parameters* (fold change threshold, QC criteria) can be modified to adjust the stringency of the analysis. The *Filtering Parameters* that are used for this analysis:

- The *Medain\_SigmBg* at max exposure *200ms* must be equal or above 5
- $R^2$  of the linear model fit must be above or equal 0.9
- Log fold change (LFC) cutoffs at (0.2,0.3)

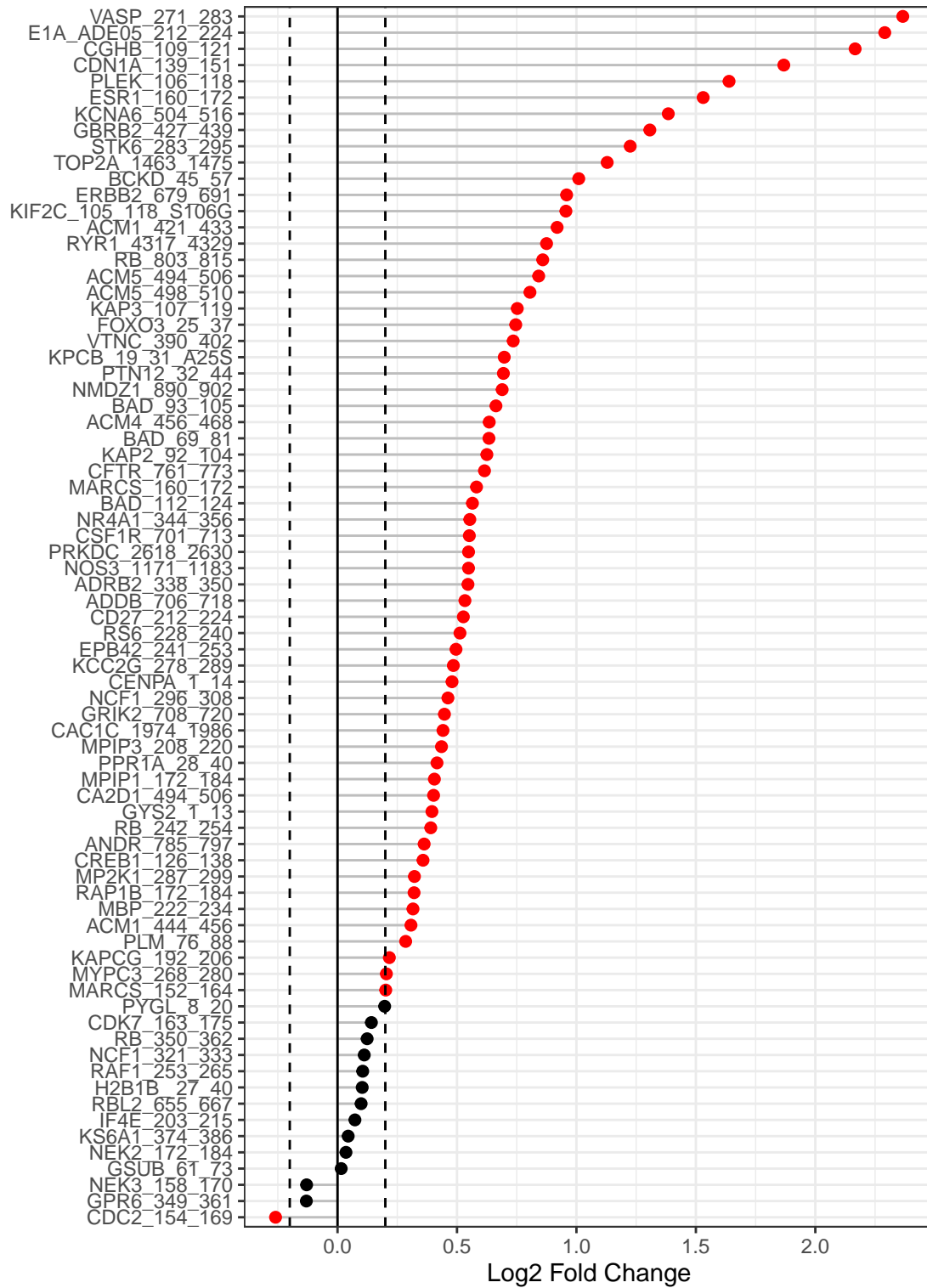
**Schizophrenia vs. Control (Pair 3.1)** After applying the *Filtering Parameters* for this group comparison, only 62/141 peptides carried forward in the analysis (i.e. 62 hits). Below are some figures to visualize the differences between these samples for considering these hits.



## Run3 Comp1

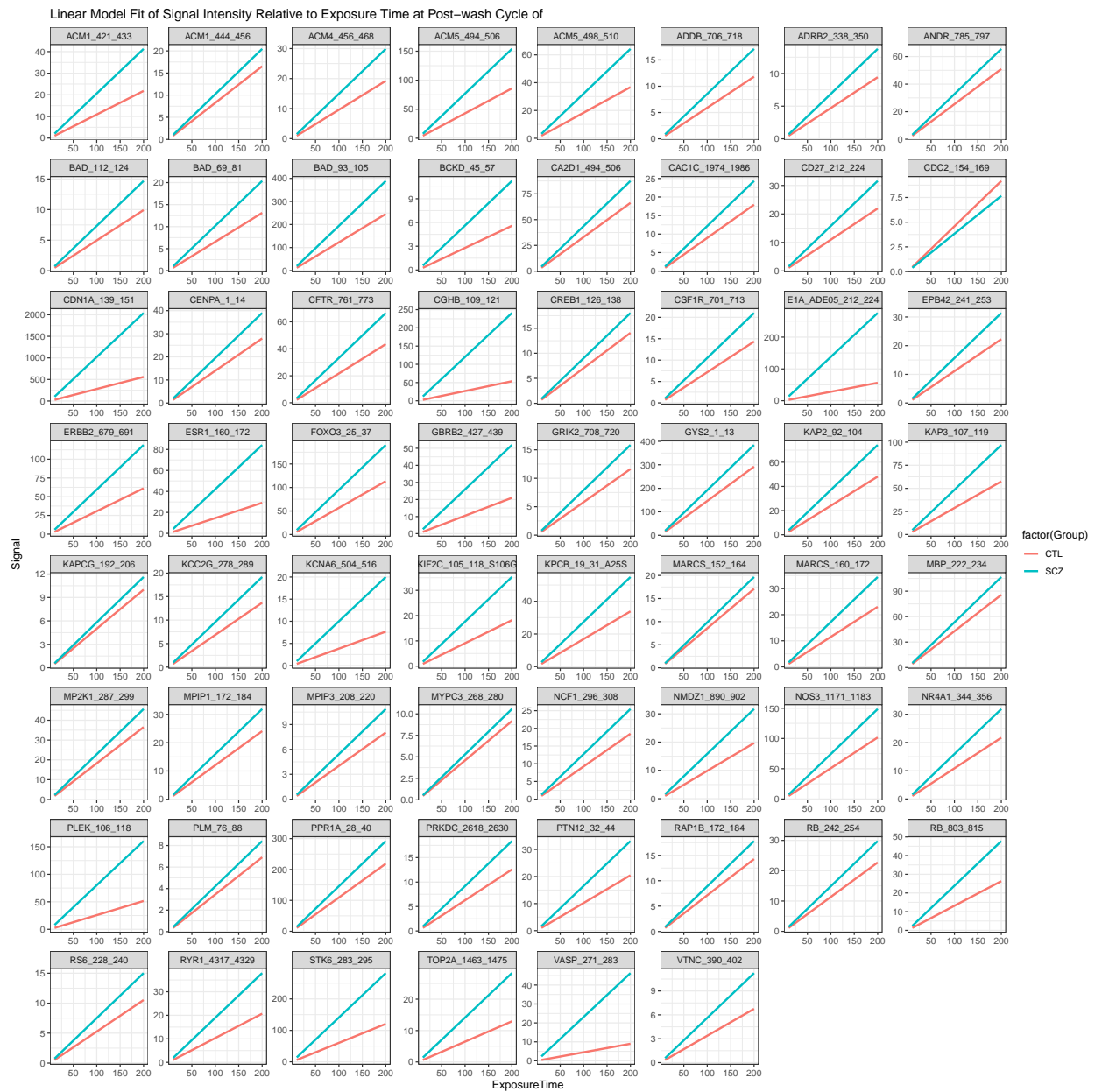


## Run3 Comp1





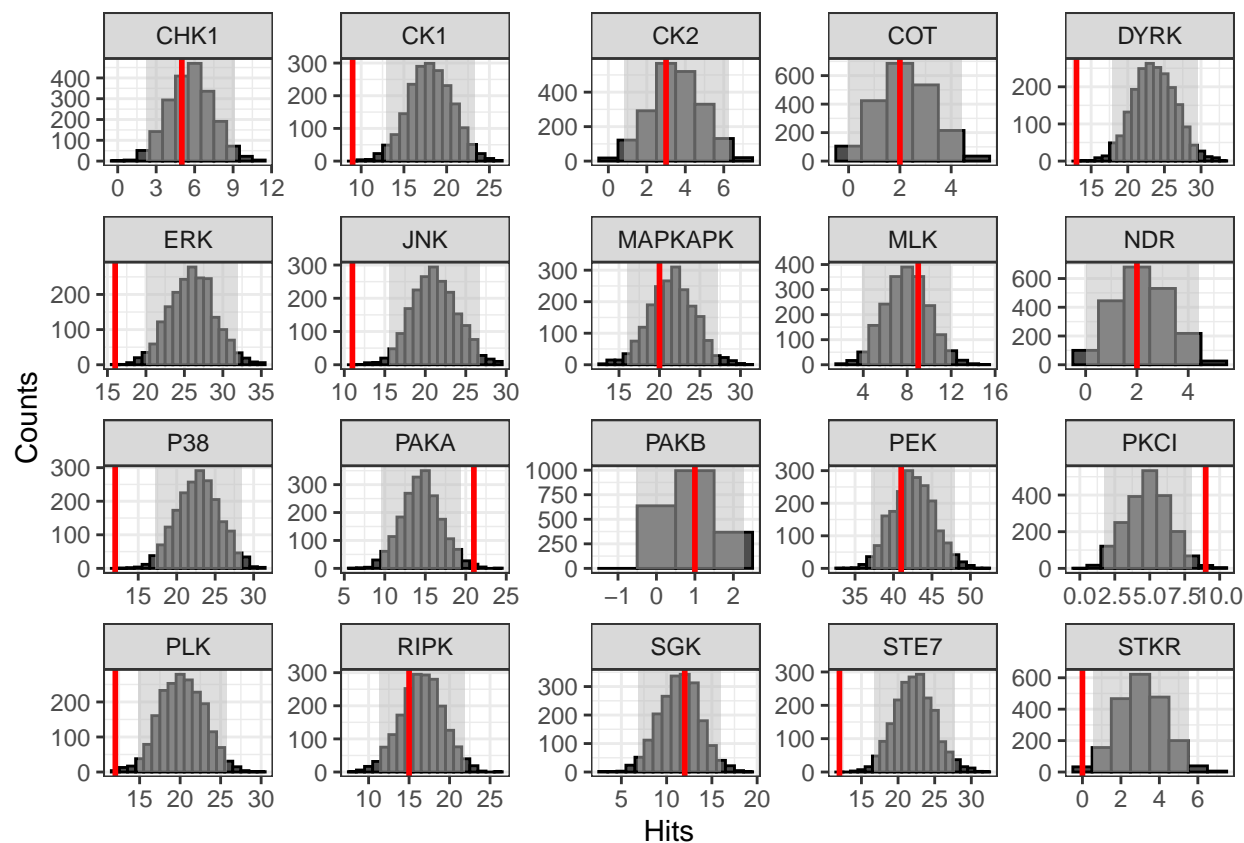
## Run3 Comp1



**Run3 Comp1**

**Upstream Kinase Analysis** The lab carefully curated and mapped the kinases that can act and phosphorylate each peptide present on the chip. This was achieved by using multiple sources including GPS 3.0, Kinexus Phosphonet, PhosphoELM and PhosphoSite Plus. Based on that association between peptides and kinases, a random sampling analysis is performed for these hits. This is done by using Kinome Random Sampling Analyzer (*KRSA*). *KRSA* is a software tool developed by the lab to perform the random sampling analysis. The basic idea of *KRSA* is: For each iteration (2000 iterations performed in this analysis), the same number of hits are randomly selected from the total 141/or 193 peptides present on the chip. Predicted kinases are then mapped to this sample list of peptides and number of kinases are determined. The kinase count from the actual hits and random sampling is then compared to determine the significance.

Kinase	Observed	SamplingAvg	SD	Z
P38	12	22.792	2.806	-3.846
STE7	12	22.250	2.743	-3.737
DYRK	13	23.653	2.910	-3.660
JNK	11	21.151	2.797	-3.629
CK1	9	18.084	2.589	-3.508
ERK	16	25.998	2.978	-3.357
PLK	12	20.262	2.742	-3.013
PAKA	21	14.530	2.450	2.641
PKCI	9	4.880	1.569	2.627
STKR	0	3.070	1.246	-2.464
NMO	1	4.846	1.619	-2.376
PKA	33	26.462	2.880	2.270
STE11	1	4.366	1.483	-2.270
CDK	38	43.989	2.730	-2.194
MST	6	10.999	2.300	-2.174
DMPK	51	45.301	2.677	2.129
PKG	27	21.087	2.803	2.109
AUR	8	4.844	1.568	2.013
VRK1	0	2.185	1.088	-2.009
PIM	37	31.241	2.968	1.941
PDK1	22	27.728	3.019	-1.897
LKB	2	4.860	1.565	-1.828
RAD53	19	14.498	2.515	1.790
AKT	22	17.619	2.655	1.650
PKN	2	0.892	0.697	1.590



Kinase	meanLFC		
	0.2	0.25	0.3
P38	-3.85	-3.75	-3.52
STE7	-3.74	-3.26	-3.60
DYRK	-3.66	-3.68	-3.50
JNK	-3.63	-3.55	-3.49
CK1	-3.51	-3.07	-2.91
ERK	-3.36	-3.77	-3.38
PLK	-3.01	-2.57	-2.85
PAKA	2.64	2.53	2.27
PKCI	2.63	2.20	2.28
STKR	-2.46	-2.23	-2.22
NMO	-2.38	-2.31	-2.13
PKA	2.27	1.99	1.97
STE11	-2.27	-2.12	-2.02
CDK	-2.19	-2.20	-2.46
MST	-2.17	-2.39	-2.24
DMPK	2.13	1.90	2.04
PKG	2.11	1.82	1.29
AUR	2.01	1.48	1.66

VRK1	-2.01	-1.93	-1.87
PIM	1.94	2.11	2.09
PDK1	-1.90	-2.11	-2.27
LKB	-1.83	-2.29	-2.19
RAD53	1.79	1.66	1.52
AKT	1.65	2.04	2.21
PKN	1.59	0.25	0.27
RSK	1.55	1.80	1.51
PKCH	1.54	0.69	0.78
PKD	1.49	1.47	1.32
GRK	-1.39	-1.18	-1.13
MARK	-1.38	-1.26	-1.19
PKCD	1.34	1.52	1.70
PRKDC	-1.29	-1.25	-1.11
NAK	-1.28	-1.20	-1.17
TTK	-1.27	-1.20	-1.15
NUAK	-1.26	-1.19	-1.17
HAL	-1.24	-1.20	-1.19
TLK	-1.24	-1.17	-1.17
IKK	-1.20	-1.51	-1.56
PASK	1.19	1.15	1.21
BRSK	1.18	1.19	1.21
WNK	1.16	1.15	1.20
FRAY	1.12	1.23	1.44
GSK	-1.06	-1.34	-1.21
NEK	-1.04	-0.84	-0.71
CAMK1	-1.04	-0.85	-0.76
ATR	-1.02	-0.87	-0.76
TAO	-0.93	-0.87	-0.82
SLK	-0.92	-0.87	-0.86
KHS	-0.91	-0.83	-0.83
ULK	-0.90	-0.86	-0.80
CLK	-0.89	-0.84	-0.81
MOS	-0.89	-0.84	-0.82
NIK	-0.88	-0.85	-0.83
CAMKK	-0.88	-0.82	-0.84
MTOR	-0.87	-1.59	-1.39
PKCA	0.86	1.10	1.55
BUD32	-0.86	-0.85	-0.80
PDHK	0.85	0.70	0.71
PHK	0.85	0.51	1.01
BARK2	0.81	0.85	0.93
CAMK2	-0.79	-1.06	-1.01
ATM	-0.77	-0.68	-0.62
MSN	-0.72	-0.69	-0.68

QIK	-0.72	-0.57	-0.27
MELK	0.71	0.56	0.76
DAPK	-0.70	-0.94	-0.78
RAF	-0.70	-0.45	-0.34
MLCK	0.70	0.86	0.96
IRAK	-0.67	-1.04	-0.95
AMPK	-0.67	-0.48	-0.30
RIPK	-0.60	-0.69	-0.92
PEK	-0.57	-0.57	-0.82
MAPKAPK	-0.56	-0.18	0.04
MLK	0.52	0.20	0.39
CHK1	-0.40	-0.27	-0.19
CK2	-0.39	-0.22	-0.18
SGK	0.25	0.50	0.68
COT	-0.20	-0.09	-0.92
PAKB	0.19	0.22	0.28
NDR	-0.18	-0.09	0.03

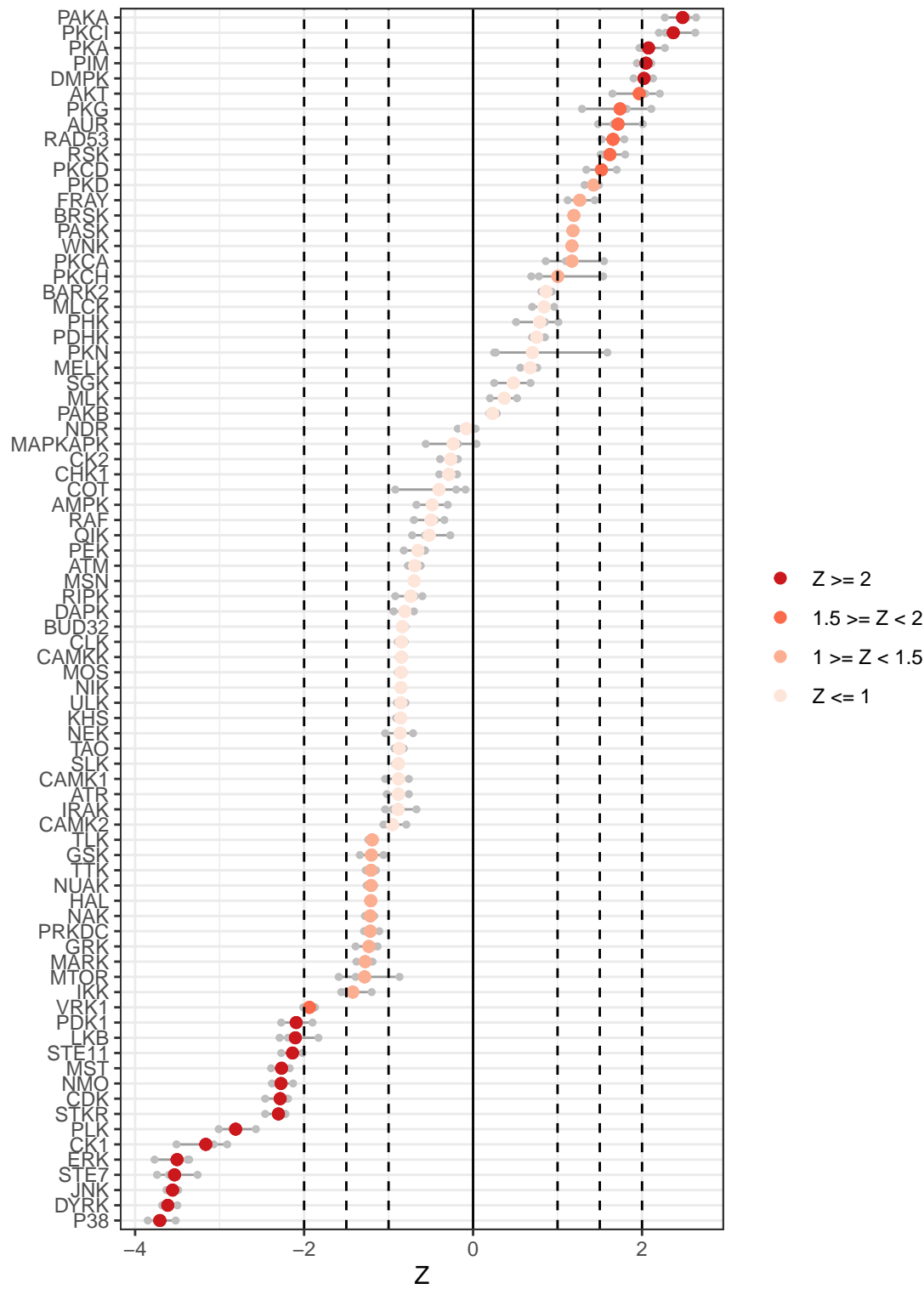
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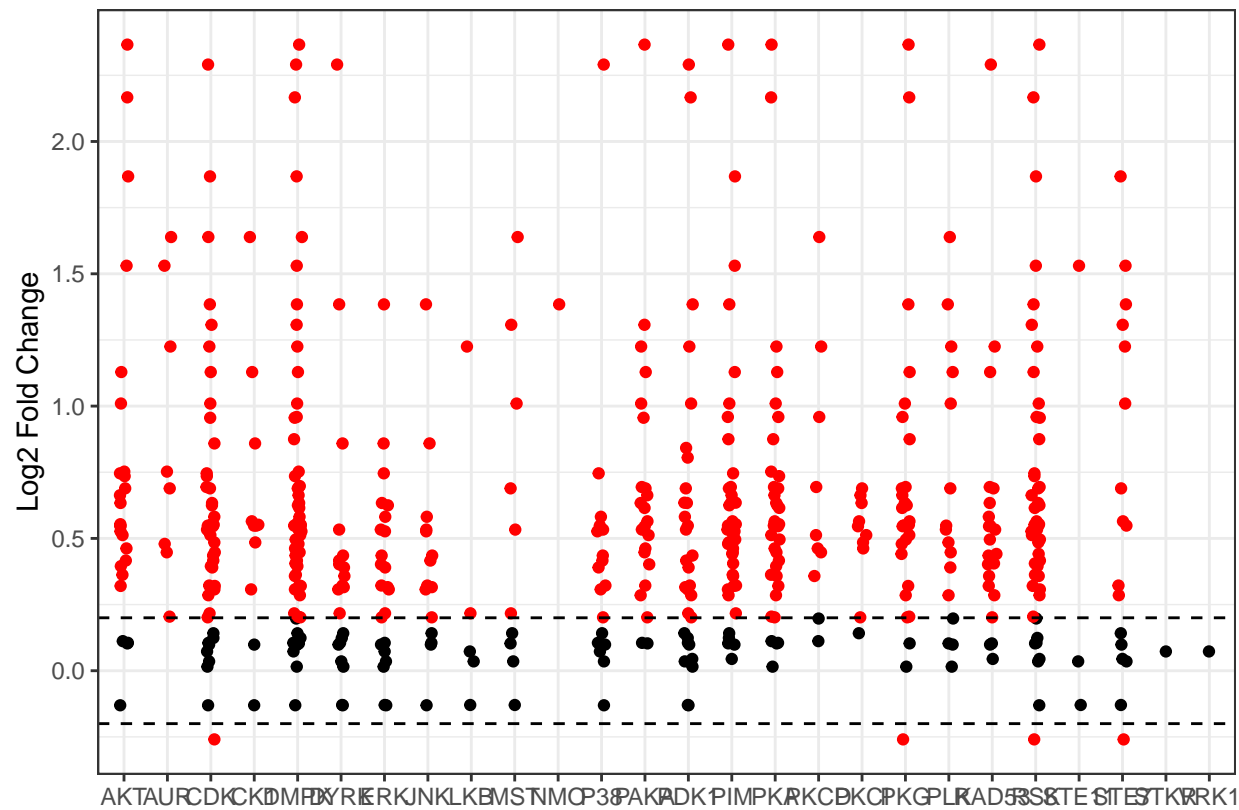
Method	NumberOfPeptides
meanLFC.0.2	62
meanLFC.0.25	59
meanLFC.0.3	57

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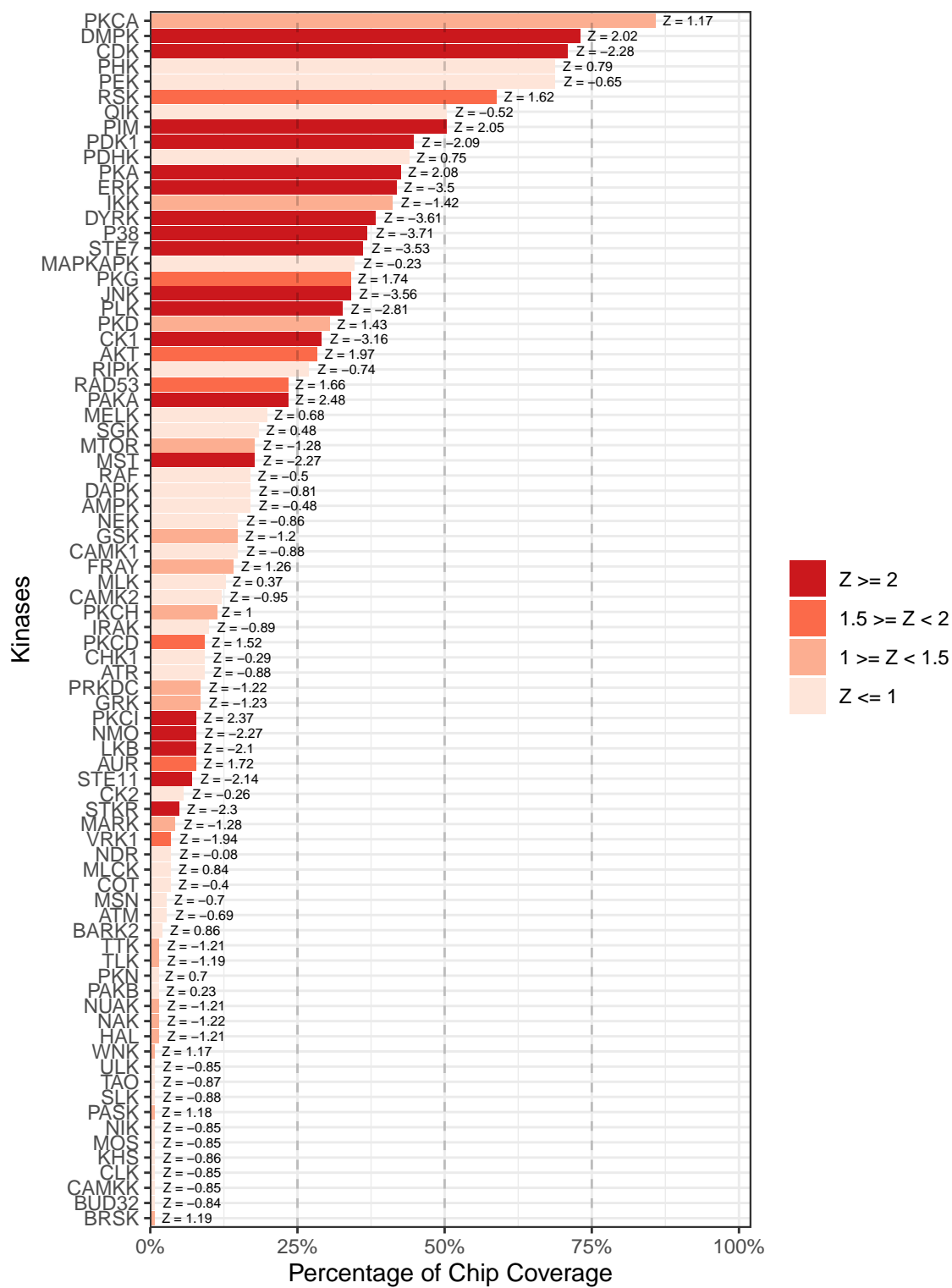
Run3 Comp1



Run3 Comp1

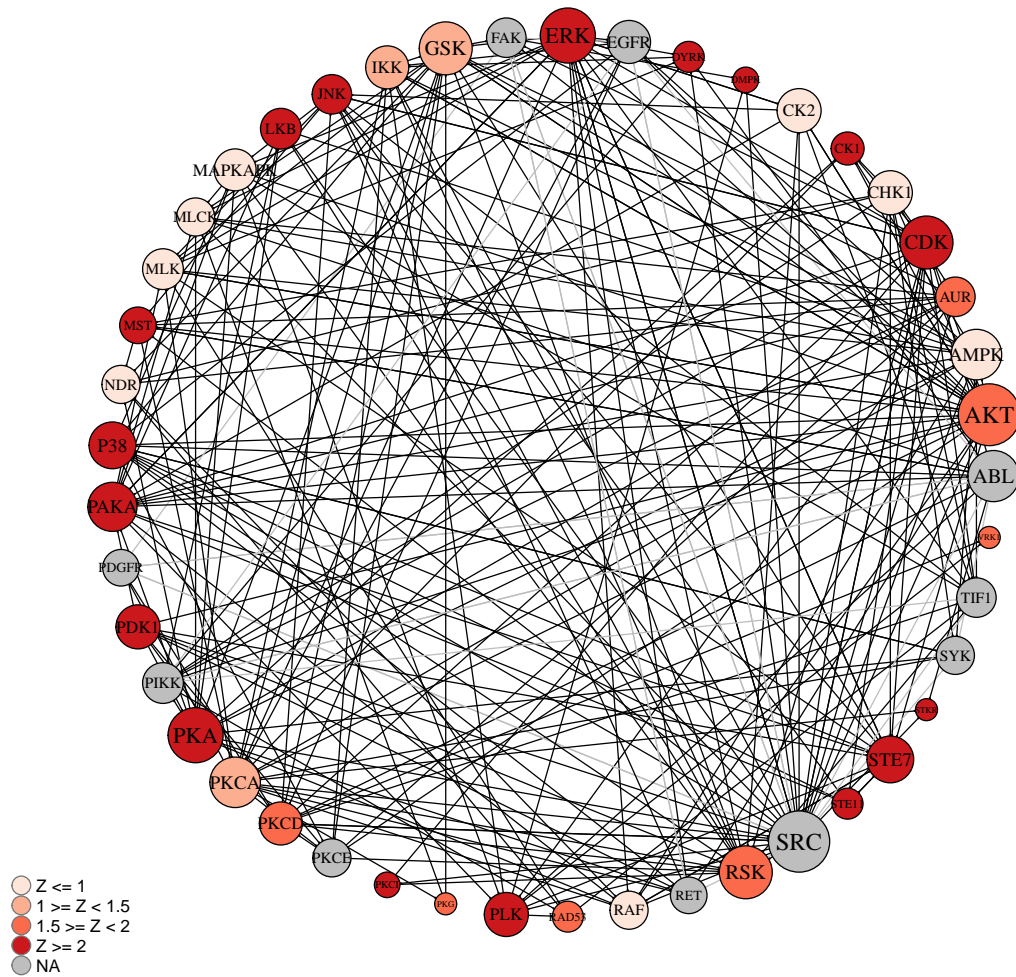


## Run3 Comp1





## Run3 Comp1



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##      purrr    readr      tidyr      tibble  ggplot2  tidyverse
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```