# Data

Non-Small Cell Lung Cancer

Squamous Cell Lung Cancer
Adenocarcinoma

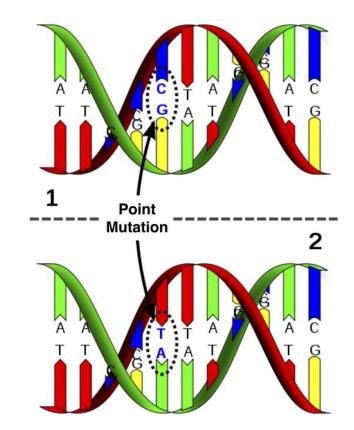
### Mutation

Mutation

389296 obs. of 9 variables

- Mutation data has:
  - SampleID
  - Chromosomal Location
    - Chr
    - Start, Stop
  - Base pair change
    - Ref: Reference
    - Alt: Alternative
  - Gene

	sample_ID	Gene Chr	Start	Stop	Ref	Alt	Amino_Acid_Change	Effect
•	Effect TCGA-49-4490-01	UBR4 chr1	19155452	19155452	C	Т	p.E2097K	missense_variant
	TCGA-49-4490-01	PLA2G2D chr1	20115562	20115562	G	Α	p. c79c	synonymous_variant
	TCGA-49-4490-01	MTF1 chr1	37822366	37822366	Α	G	p. S508P	missense_variant
	TCGA-49-4490-01	CLCA2 chr1	86443922	86443922	G	Α	p. D542N	missense_variant
	TCGA-49-4490-01	WNT2B chr1	112525957	112525957	G	C		downstream_gene_variant
	TCGA-49-4490-01	LTNGO4 chr1	151801168	151801168	C	т	p. D513N	missense variant

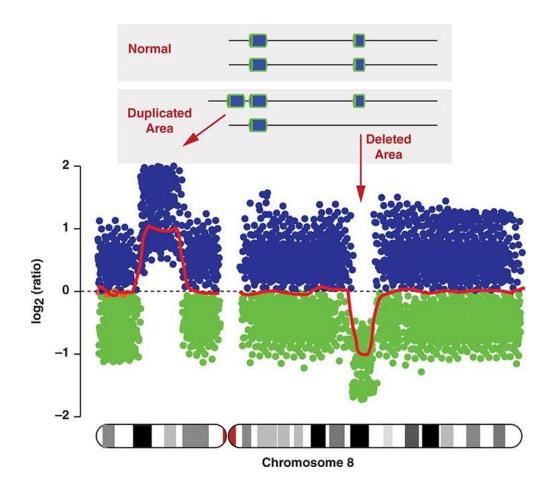


### **CNV**

CNV

24791 obs. of 1022 variables

- CNV data has:
  - Gene
  - Chromosomal location of the gene
  - Amount of DNA for a gene per sample
    - -2: 0 copies of the gene (double deletion)
    - -1: 1 copy of the gene (deletion)
    - 0: 2 copies of the gene (normal)
    - 1: 3 copies of the gene (duplication)
    - 2: 4 copies of the gene (double duplication)



```
        Gene
        Chr
        Start
        Stop
        Strand
        TCGA-18-3406-01
        TCGA-18-3407-01
        TCGA-18-3408-01
        TCGA-18-3409-01
        TCGA-18-3410-01

        A1BG
        chr19
        58345178
        58353499
        -1
        2
        1
        0
        -1
        1
        1

        A1CF
        chr10
        50799409
        50885675
        -1
        -1
        1
        0
        0
        0
        0
        0

        A2M
        chr12
        9067664
        9116229
        -1
        0
        -1
        0
        0
        1

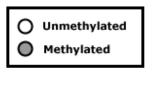
        A2ML1
        chr12
        8822472
        8887001
        1
        0
        -1
        0
        0
        1

        A3GALT2
        chr1
        33306766
        33321098
        -1
        -1
        0
        -1
        0
        0
        0
```

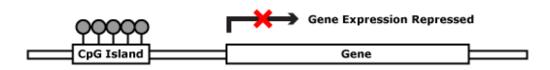
## Methylation

Methylation 485577 obs. of 914 variables

- Methylation data has:
  - probeID
  - Chromosomal location of the probe
  - Gene
  - β-value for a probe per sample
    - Ranges from 0 to 1
      - Roughly speaking 0: Unmethylated --> 1: Methylated









- Methylation studies use M-values for statistical validity
  - $M_i = \log_2(\frac{\beta_i}{1-\beta_i})$

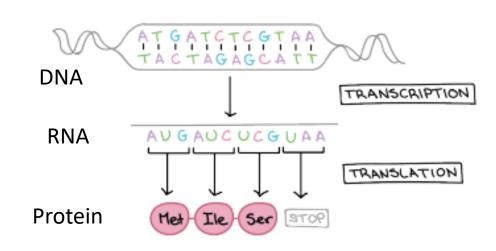
probeID	Chr	Start	Stop	Strand	Gene	Relation_CpG_Island	TCGA-44-4112-01	TCGA-NJ-A4YP-01	TCGA-22-4613-01
cg00000029	chr16	53434199	53434201	-	RBL2	N_Shore	0.34335	0.3992	0.3073
cg00000108					C3orf35		NA	NA	NA
cg00000109	chr3	172198246	172198248	-	FNDC3B		NA	NA	NA
cg00000165	chr1	90729116	90729118	+	BARHL2	s_shore	0.48315	0.5491	0.6697
cg00000236	chr8	42405775	42405777	+	VDAC3		0.85435	0.7632	0.9144
cg00000289	chr14	68874421	68874423	-	ACTN1		0.66545	0.5226	0.7565

#### THE CENTRAL DOGMA

## Gene Expression

OgeneExpression 60483 obs. of 1140 variables

- Gene Expression data has:
  - Gene
  - Chromosomal location of the gene
  - Gene Expression value for a gene per sample
    - log<sub>2</sub> transformed



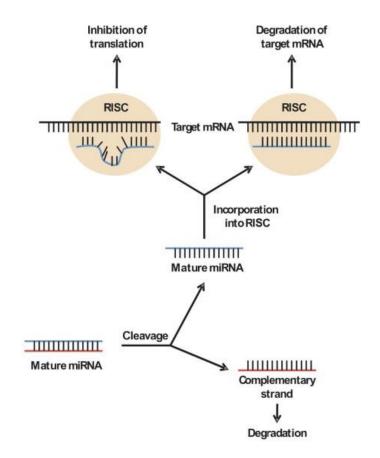
Gene	Chr	Start	Stop	Strand	TCGA-05-4244-01	TCGA-05-4249-01	TCGA-05-4250-01	TCGA-05-4382-01	TCGA-05-4384-01
TSPAN6	chrx	100627109	100639991	_	4.159317	3.985334	4.24140648	3.384259	3.276697
TNMD	chrx	100584802	100599885	+	0.000000	0.000000	0.06642033	0.000000	0.000000
DPM1	chr20	50934867	50958555	_	4.278499	4.727652	5.22596122	4.742701	4.527401
SCYL3	chr1	169849631	169894267	_	2.109782	2.375002	1.38837836	1.537189	2.376222
Clorf112	chr1	169662007	169854080	+	1.683045	1.217652	1.58297357	1.298543	1.017860
FGR	chr1	27612064	27635277	-	3.272660	2.667326	2.90317370	3.983659	3.302965

## miRNA expression

miRNA

2281 obs. of 881 variables

- miRNA expression data has:
  - MIMATID
  - Name
  - Chromosomal location of the miRNA
  - miRNA expression value for a miRNA per sample
    - log<sub>2</sub> transformed



MIMATID Name	Chr	Start	Stop	Strand	TCGA-NJ-A4YP-01	TCGA-86-8278-01	TCGA-62-A470-01	TCGA-44-6778-01
MIMAT0000062 hsa-let-7a-5p	chr11	122146568	122146589	-	14.939725	14.771870	14.332978	14.454362
MIMAT0000063 hsa-let-7b-5p	chr22	46113691	46113712	+	14.327167	14.010682	13.384376	13.834904
MIMAT0000064 hsa-let-7c-5p	chr21	16539838	16539859	+	9.595746	9.645857	9.848584	10.302141
MIMAT0000065 hsa-let-7d-5p	chr9	94178841	94178862	+	7.405218	6.728663	7.684090	7.625472
MIMAT0000066 hsa-let-7e-5	chr19	51692793	51692814	+	9.040771	9.723797	9.878375	9.523750
MIMAT0000067 hsa-let-7f-5p	chr9	94176353	94176374	+	12.597921	12.543699	12.880784	12.667485

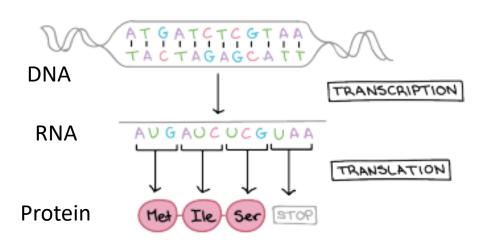
#### THE CENTRAL DOGMA

#### Proteome

Proteome

276 obs. of 694 variables

- Proteome data has:
  - ProteinID
  - Protein expression value
    - Very limited (only 355 proteins measured)



# Sample Overlap

