

PDAC gene expression analysis

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Setup

load required libraries

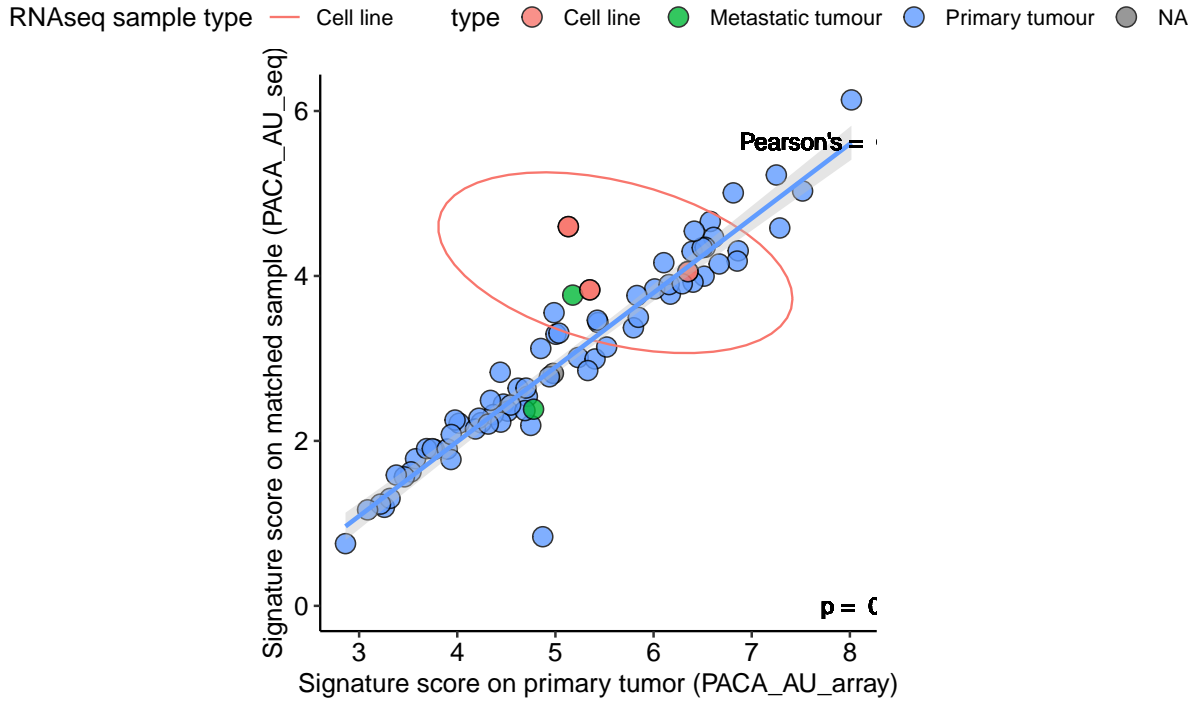
Results

Popular signatures in matched samples

```
## Registered S3 method overwritten by 'GGally':
##   method from
##   +.gg      ggplot2

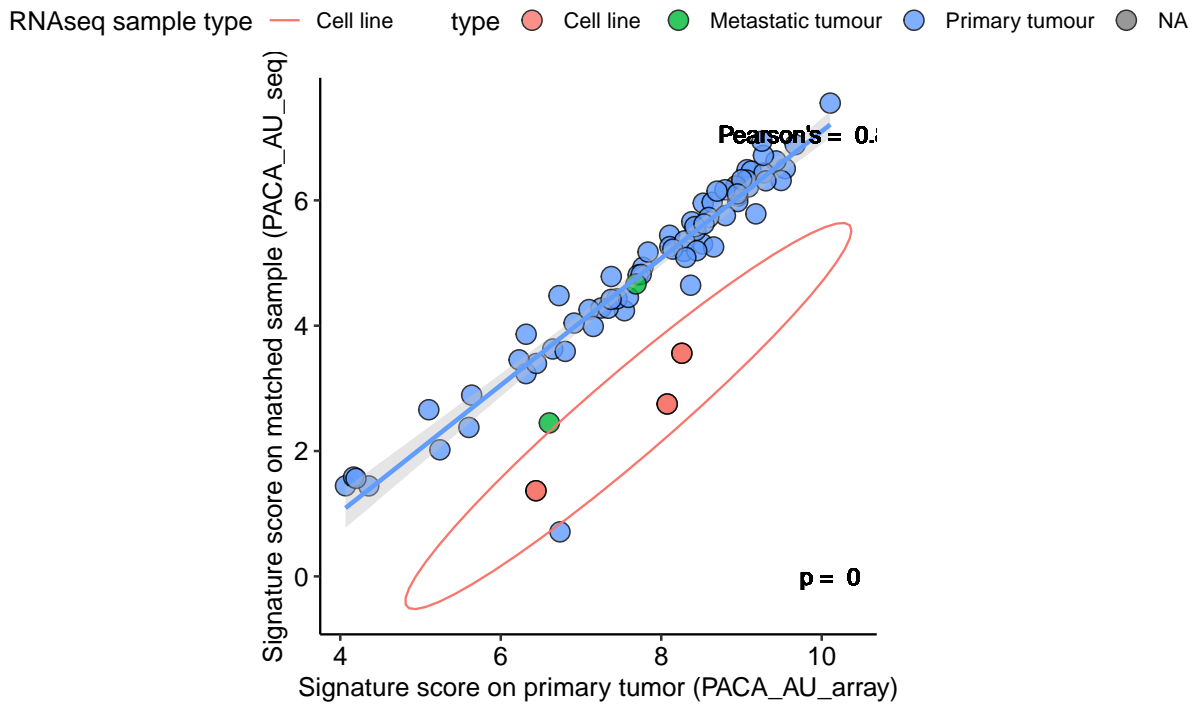
## 'geom_smooth()' using formula 'y ~ x'
```

Moffitt.Basal.25



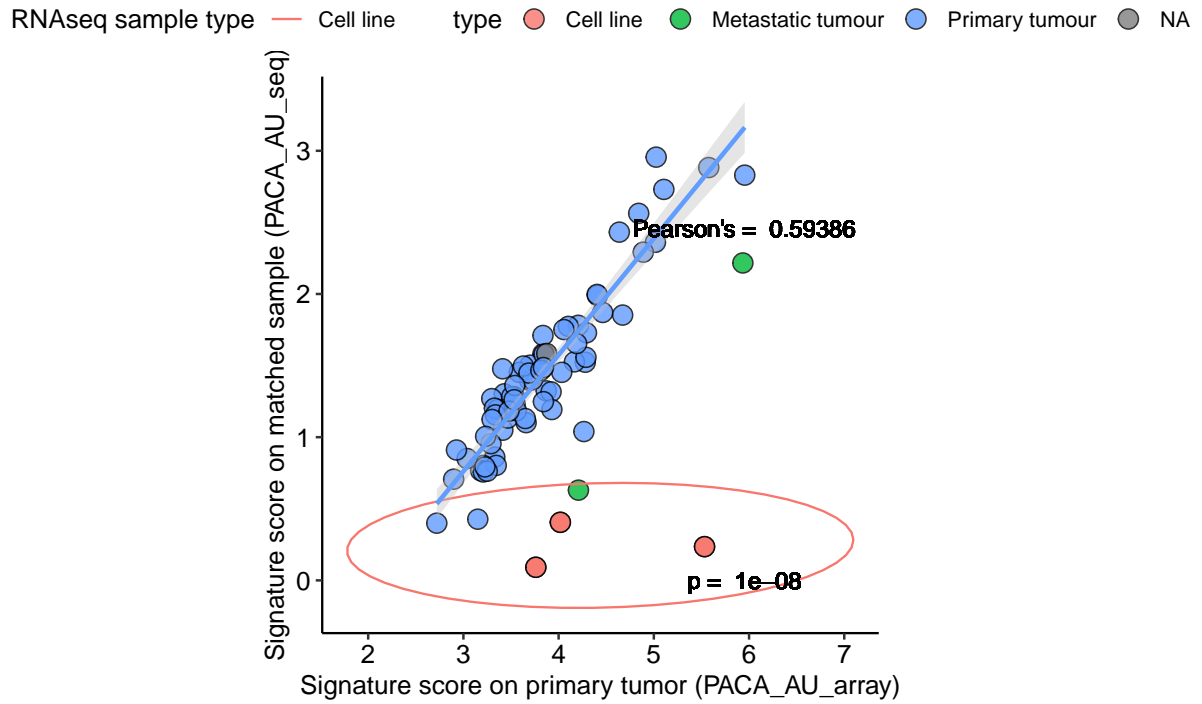
```
## 'geom_smooth()' using formula 'y ~ x'
```

Moffitt.Classical.25



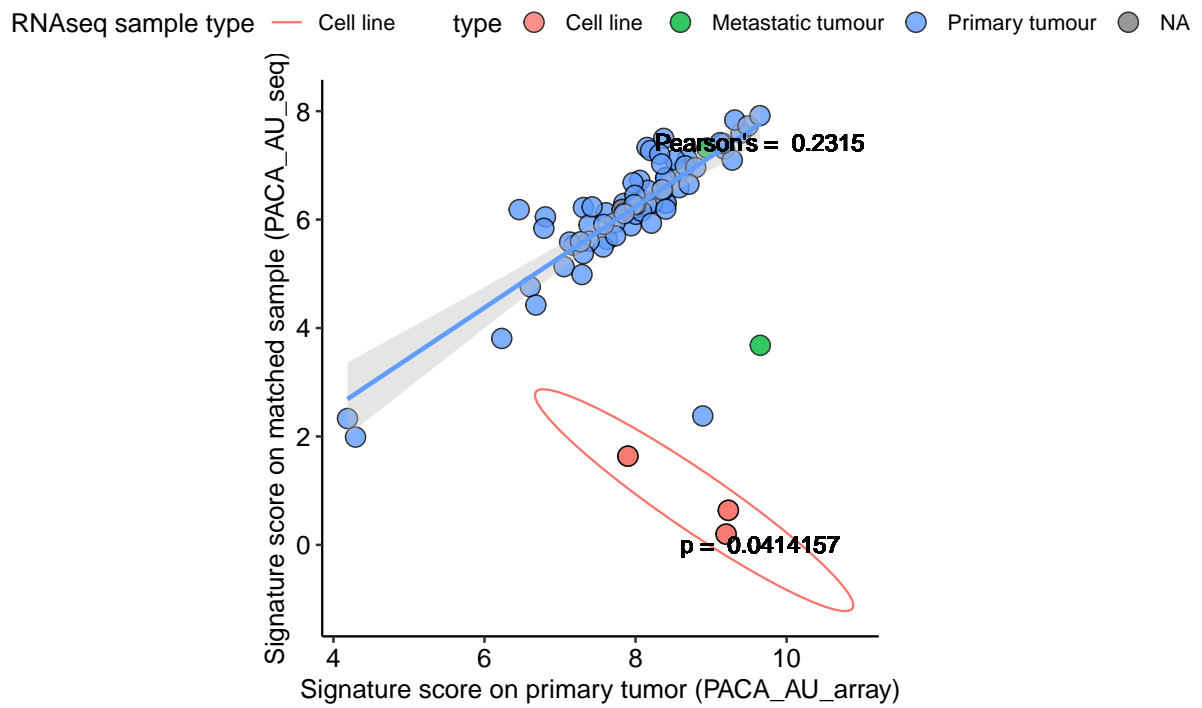
```
## 'geom_smooth()' using formula 'y ~ x'
```

Moffitt.Normal.25



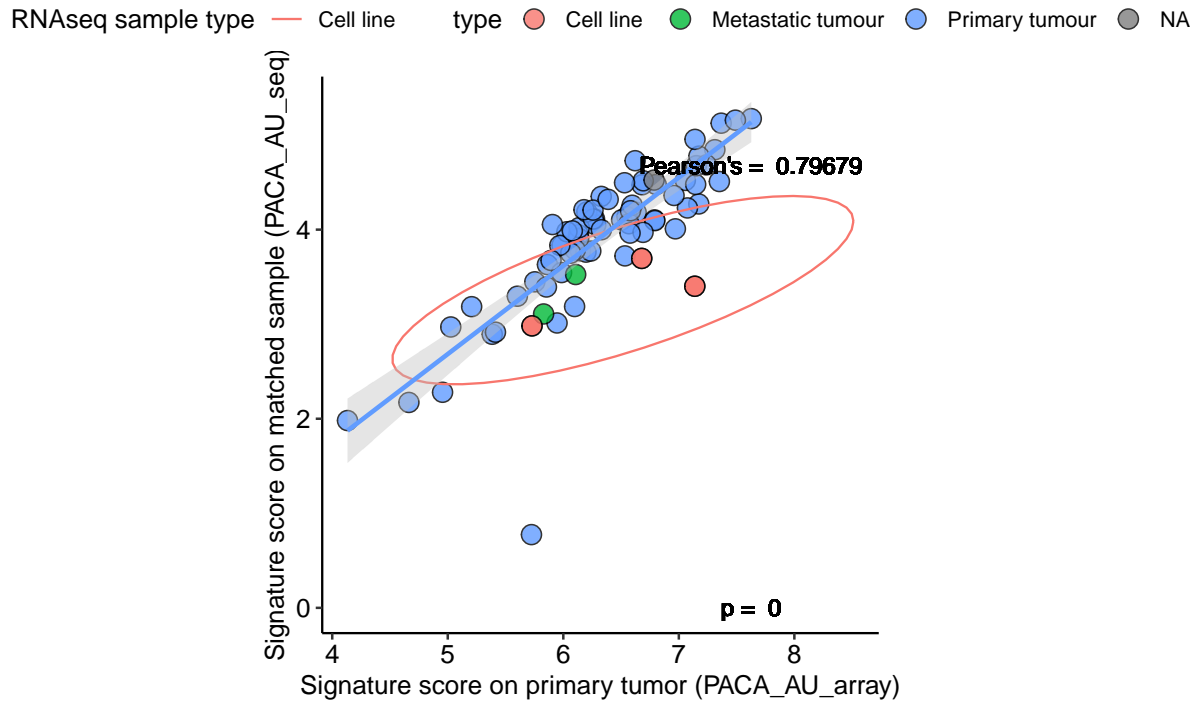
```
## 'geom_smooth()' using formula 'y ~ x'
```

Moffitt.Activated.25



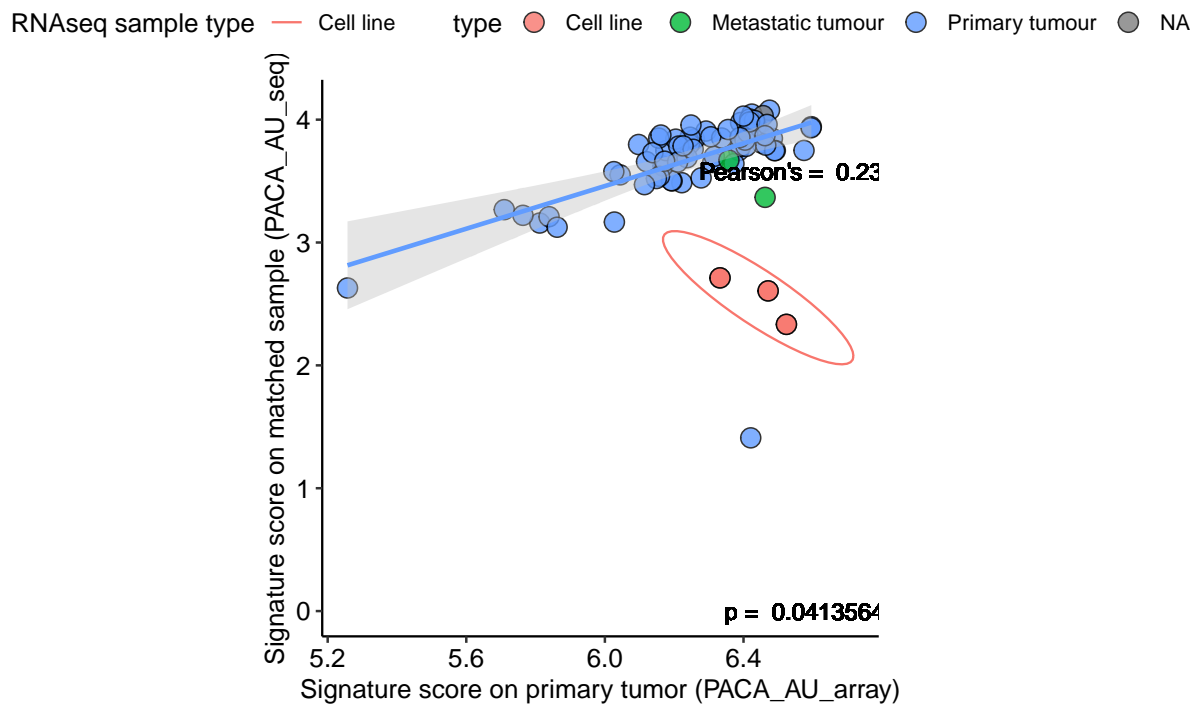
```
## 'geom_smooth()' using formula 'y ~ x'
```

Moffitt.Tumor



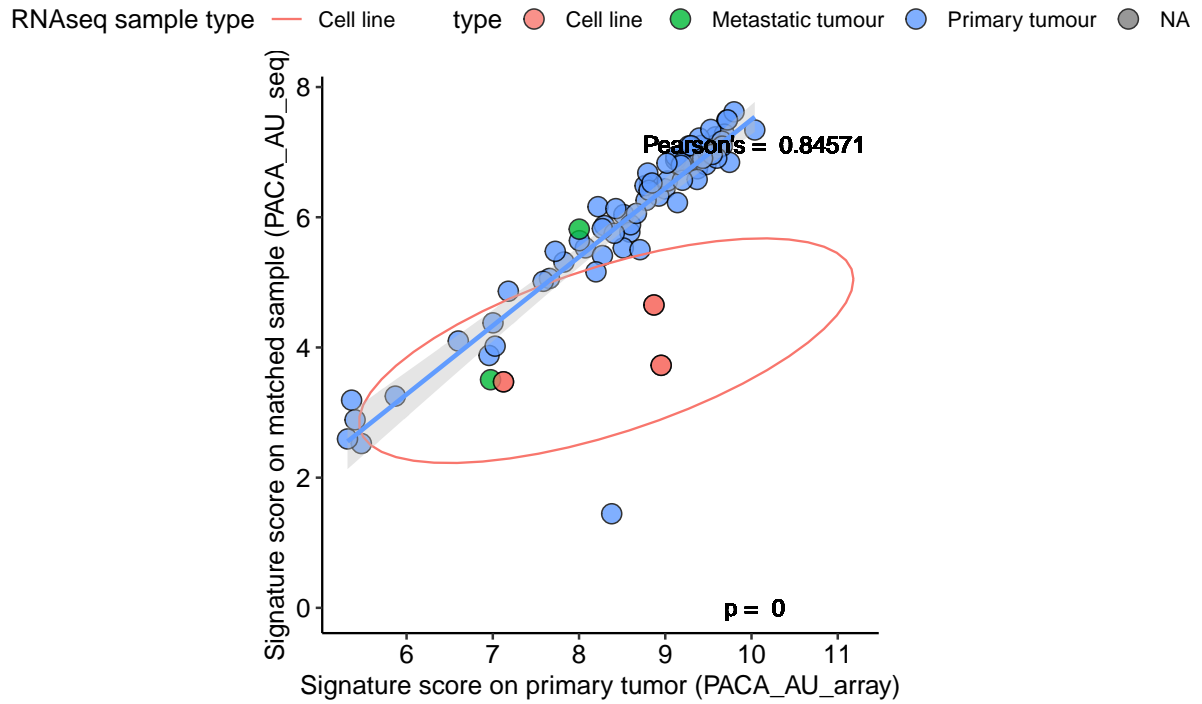
```
## 'geom_smooth()' using formula 'y ~ x'
```

Puleo.Centroids



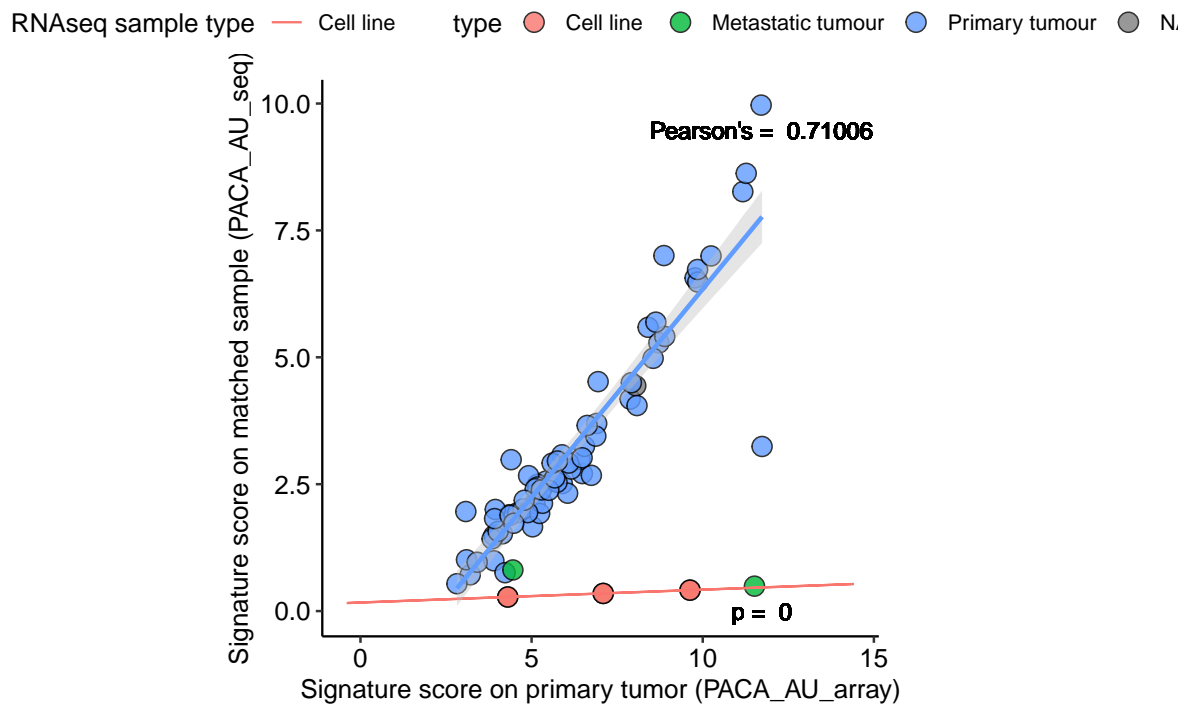
```
## 'geom_smooth()' using formula 'y ~ x'
```

Collisson.Classical



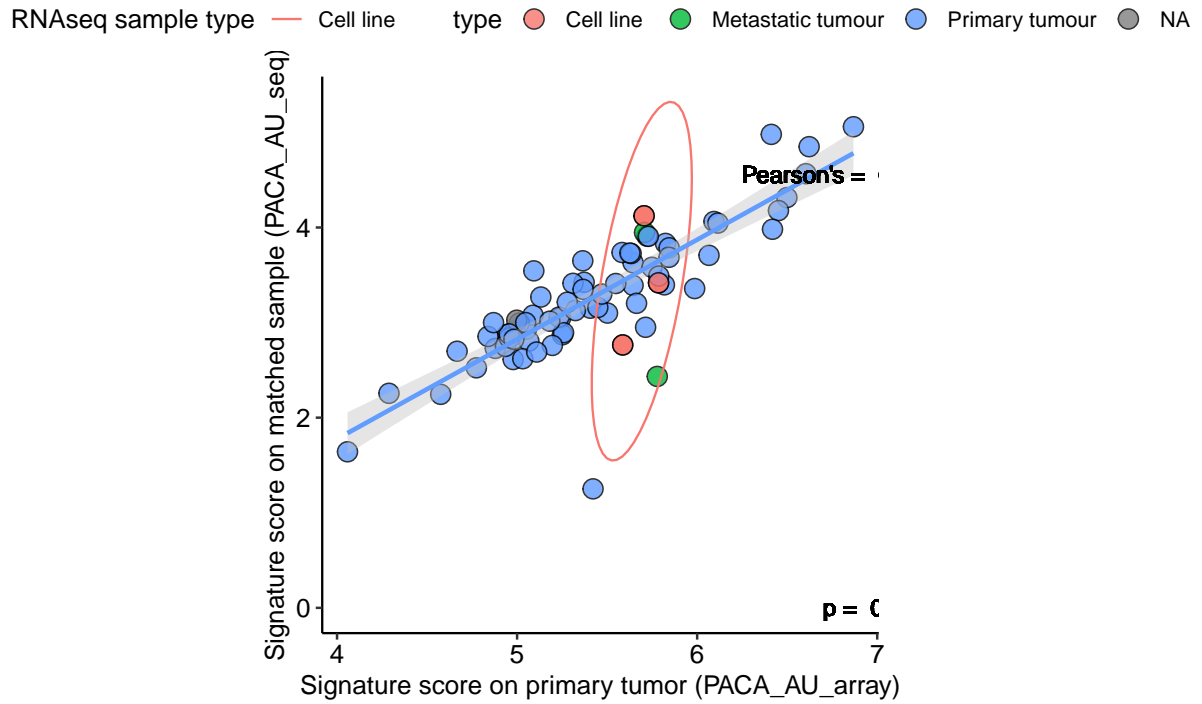
'geom_smooth()' using formula 'y ~ x'

Collisson.Exocrine



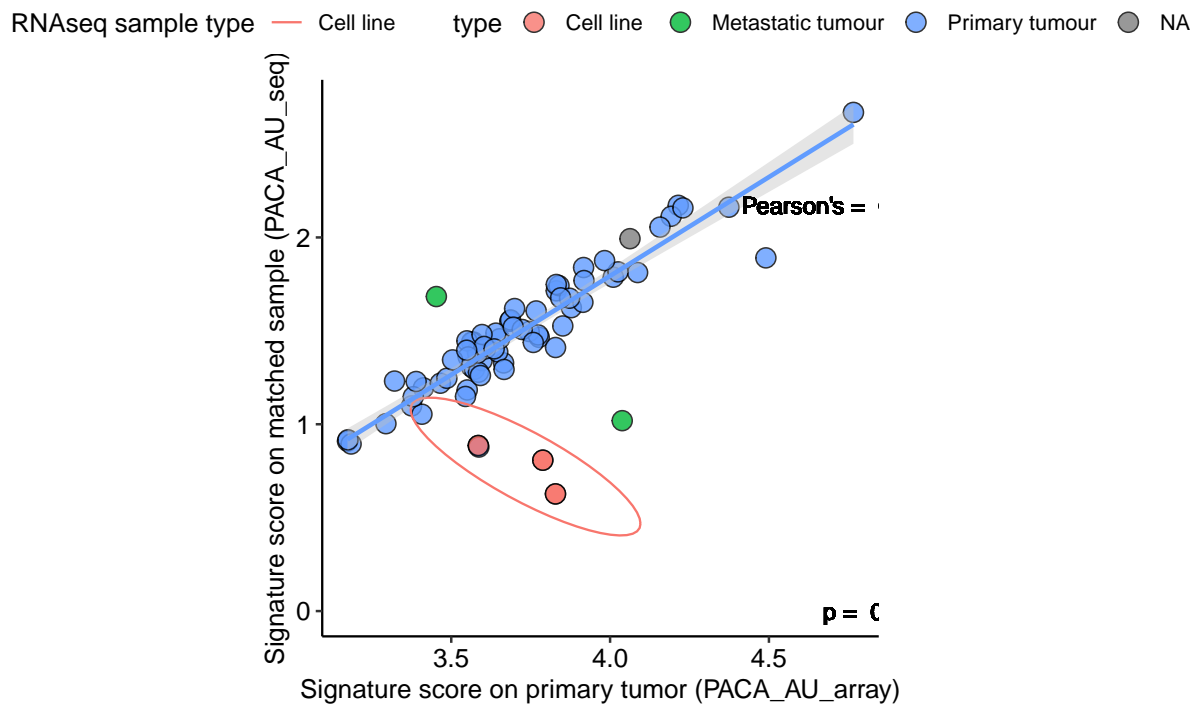
'geom_smooth()' using formula 'y ~ x'

Collisson.QM



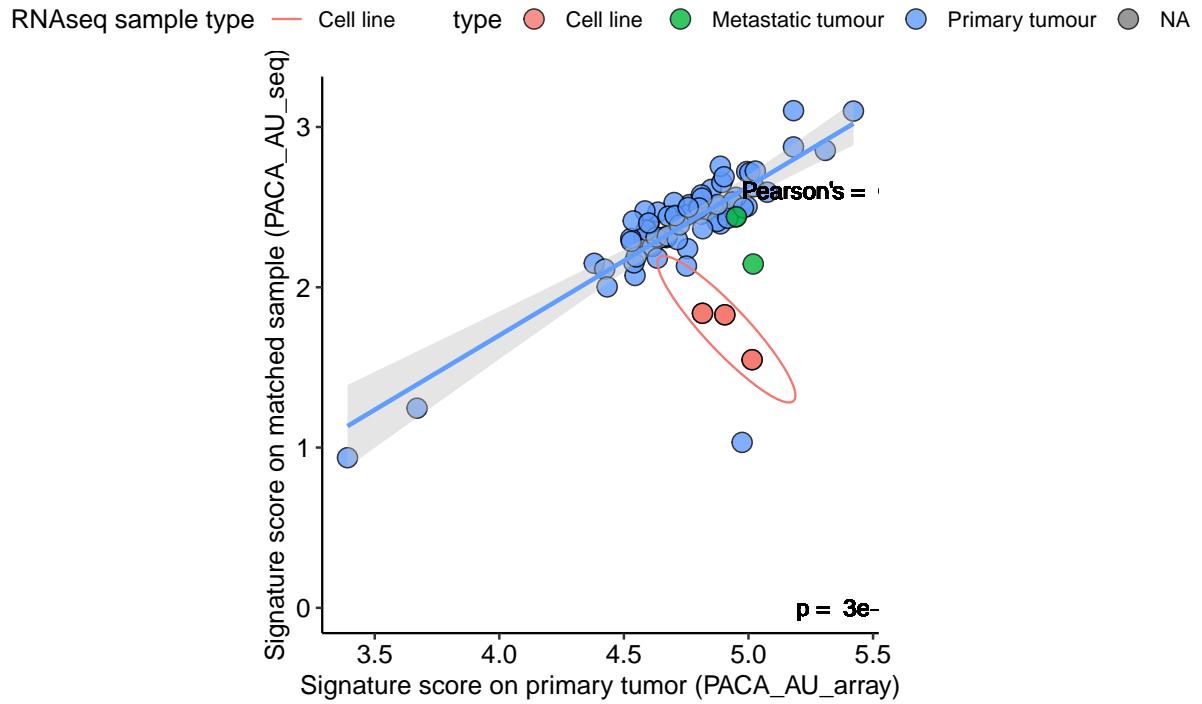
```
## 'geom_smooth()' using formula 'y ~ x'
```

ICGC.ADEX.Up



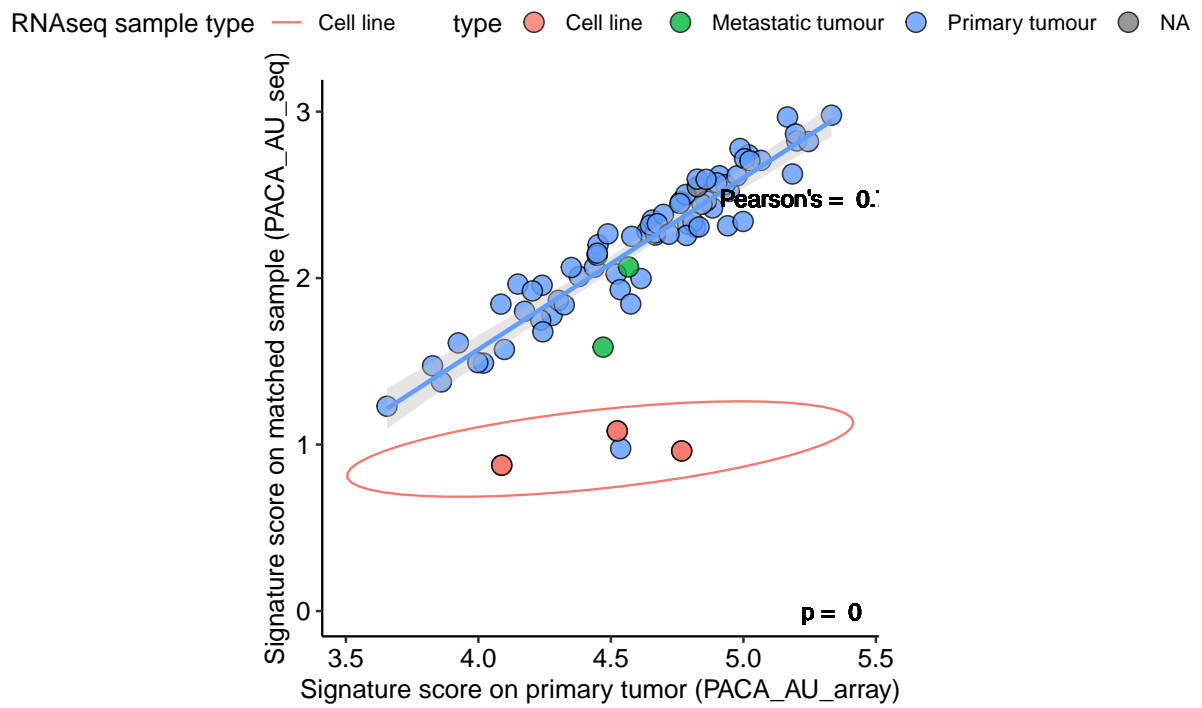
```
## 'geom_smooth()' using formula 'y ~ x'
```

ICGC.ADEX.Down



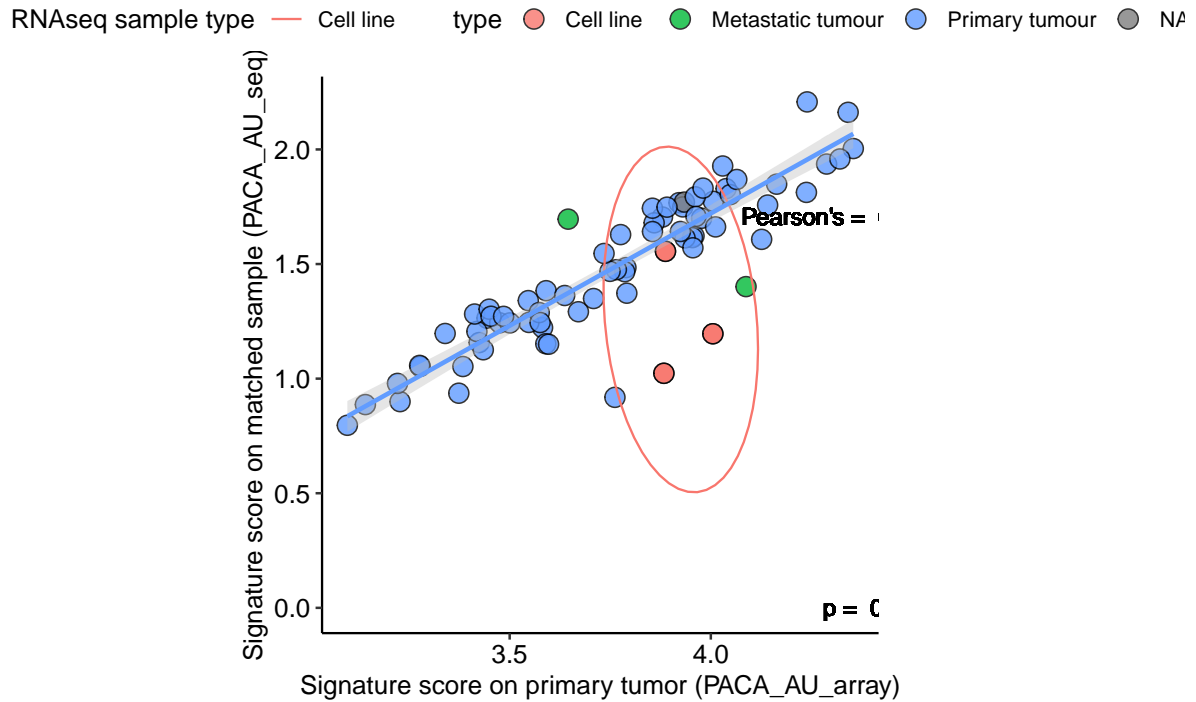
```
## 'geom_smooth()' using formula 'y ~ x'
```

ICGC.Immunogenic.Up



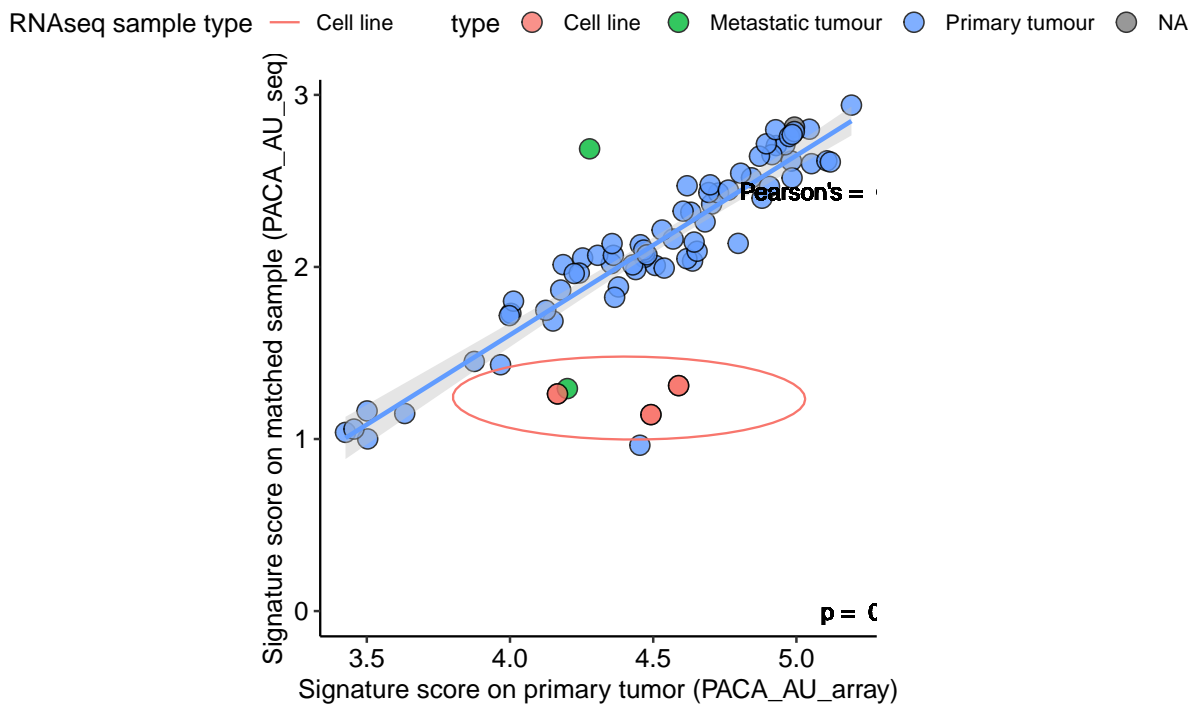
```
## 'geom_smooth()' using formula 'y ~ x'
```

ICGC.Immunogenic.Down



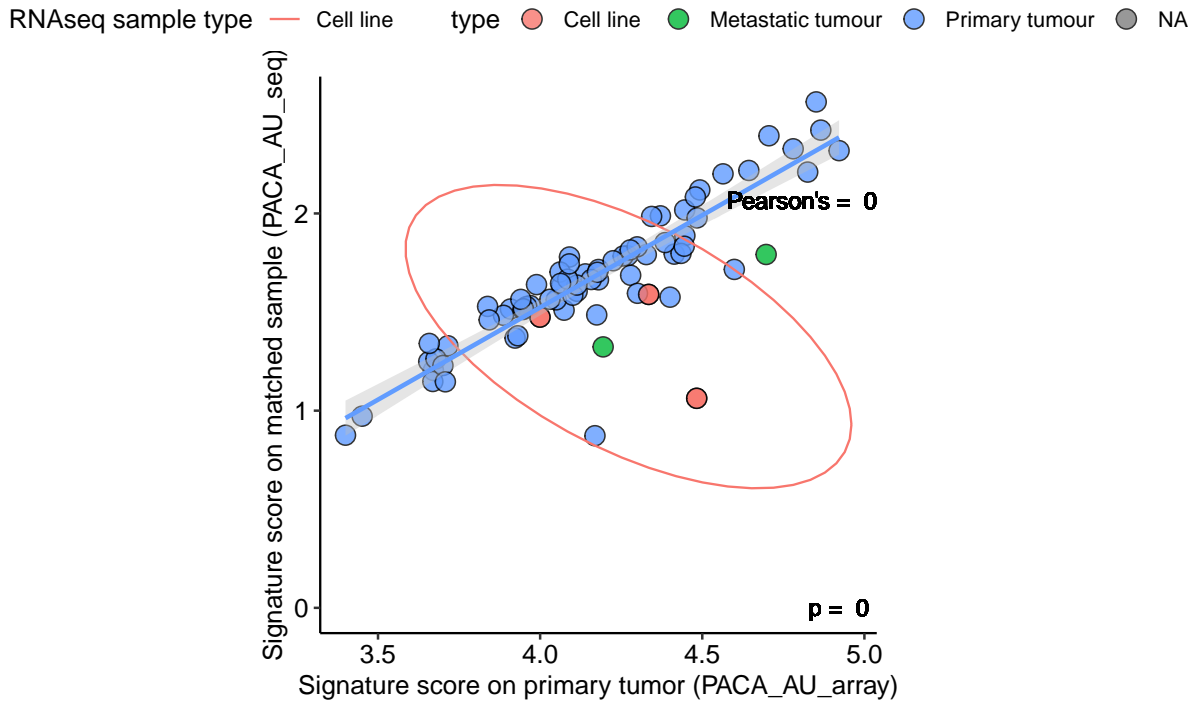
```
## 'geom_smooth()' using formula 'y ~ x'
```

ICGC.Progenitor.Up



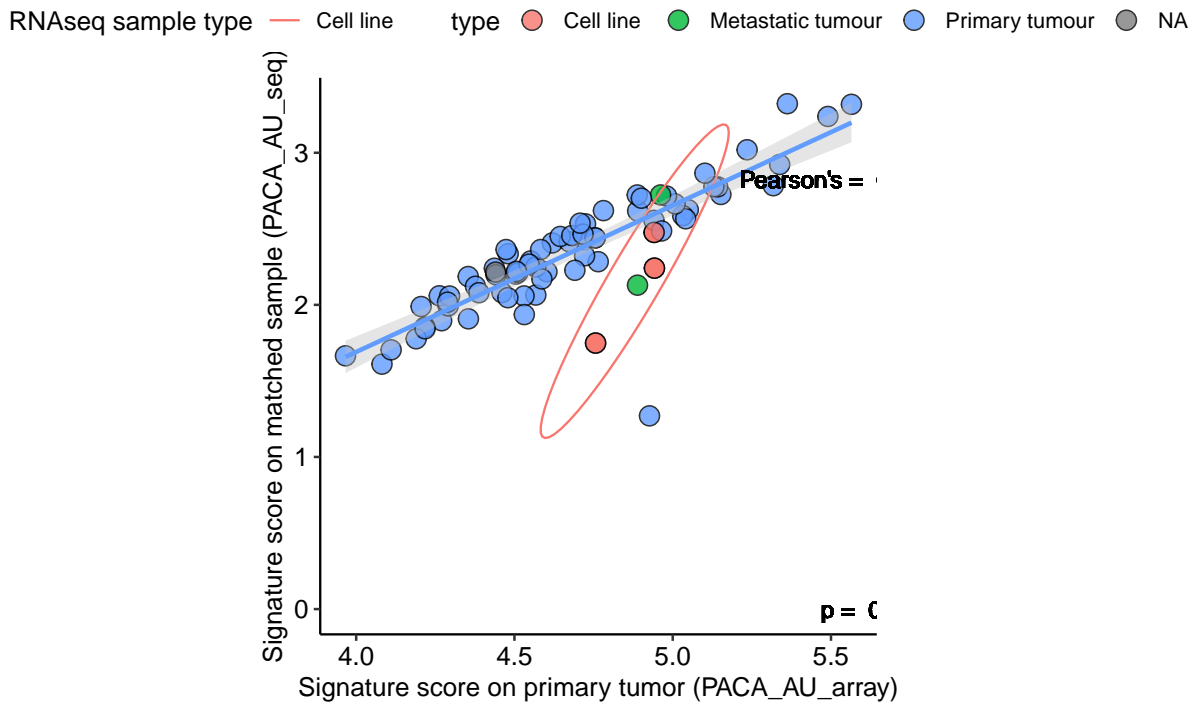
```
## 'geom_smooth()' using formula 'y ~ x'
```


ICGC.Progenitor.Down



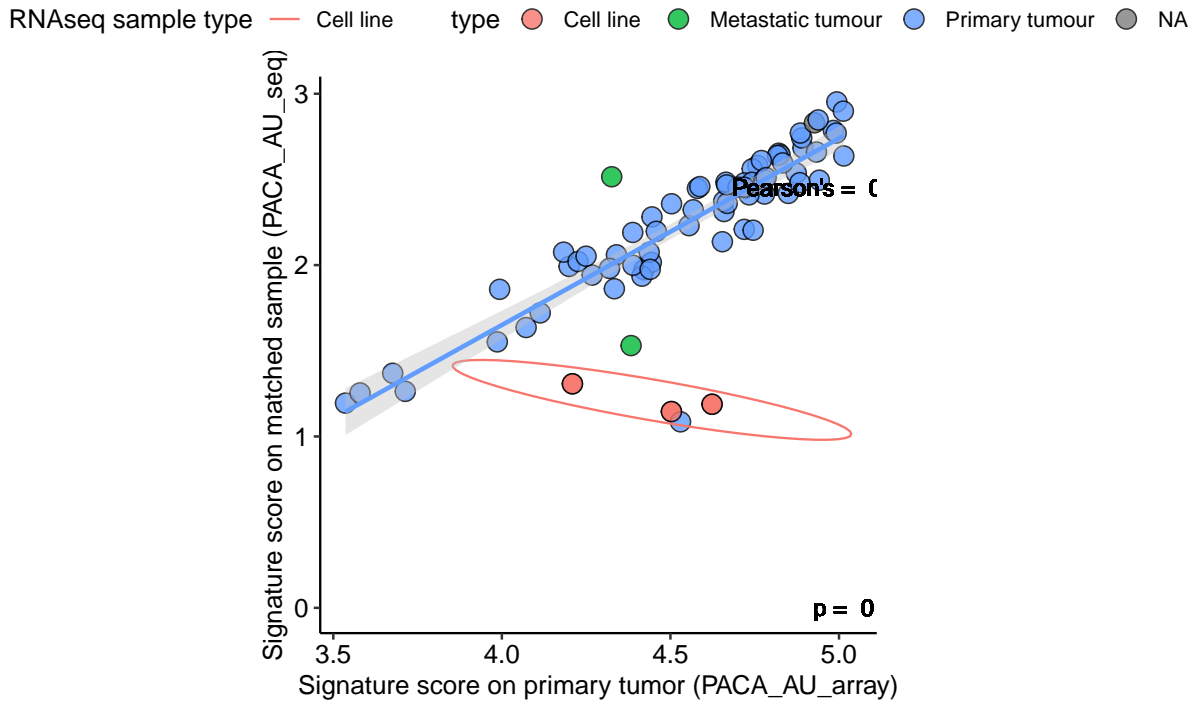
```
## 'geom_smooth()' using formula 'y ~ x'
```

ICGC.Squamous.Up



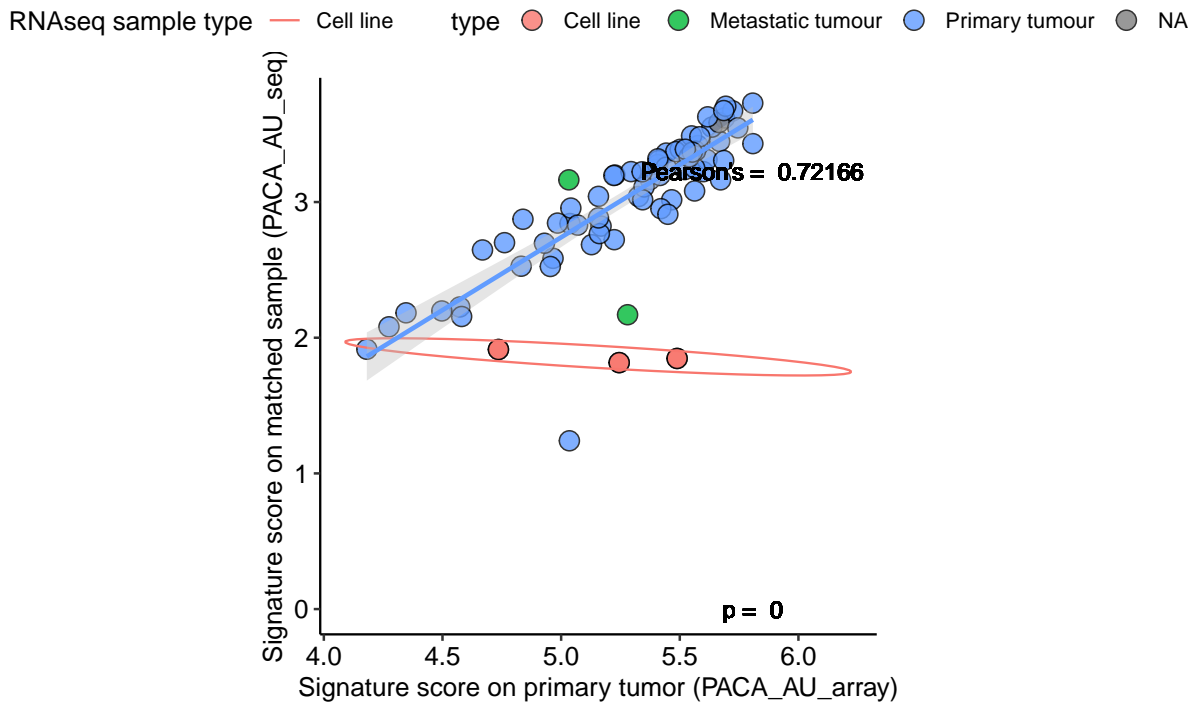
```
## 'geom_smooth()' using formula 'y ~ x'
```

ICGC.Squamous.Down



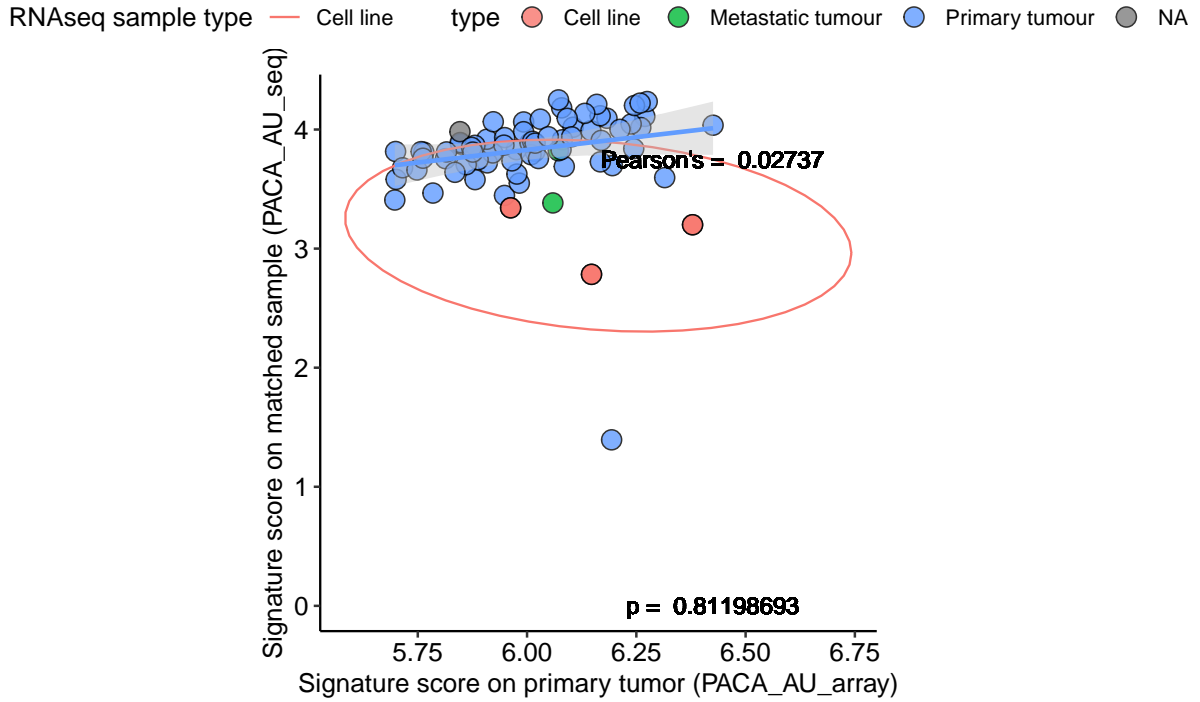
```
## 'geom_smooth()' using formula 'y ~ x'
```

ICGC.SAM



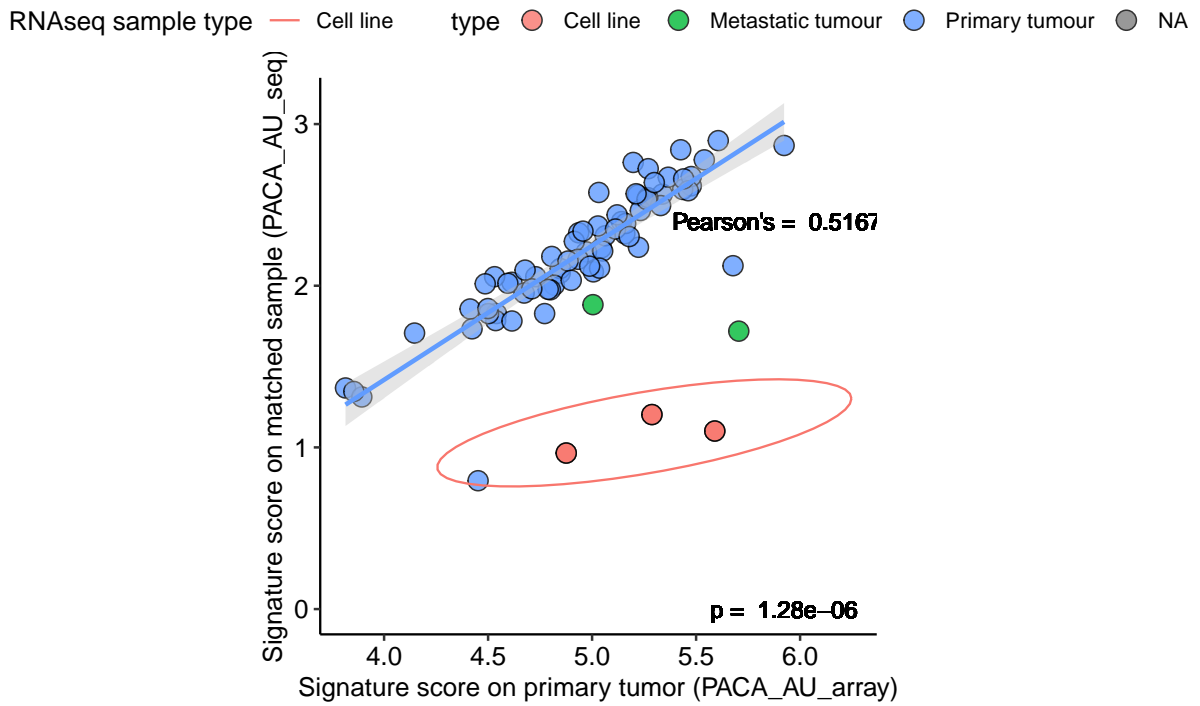
```
## 'geom_smooth()' using formula 'y ~ x'
```

Scarpa_PanNET



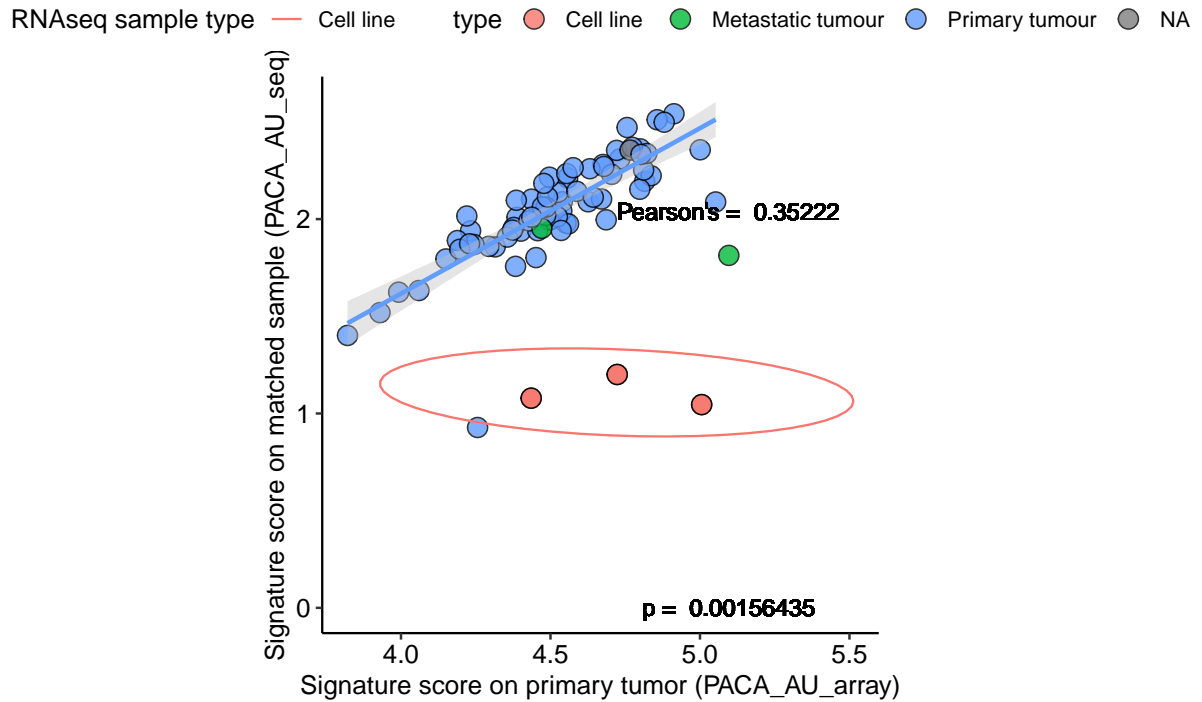
```
## 'geom_smooth()' using formula 'y ~ x'
```

Moffitt.Top5s



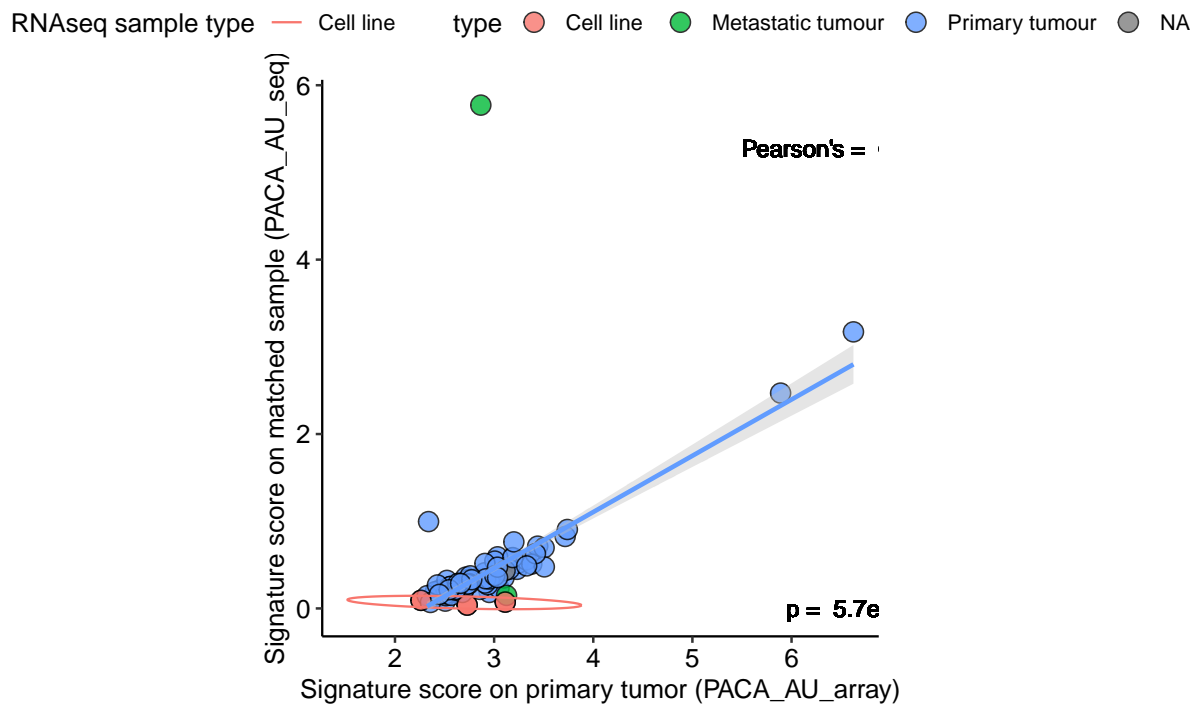
```
## 'geom_smooth()' using formula 'y ~ x'
```

Moffitt.Top25s



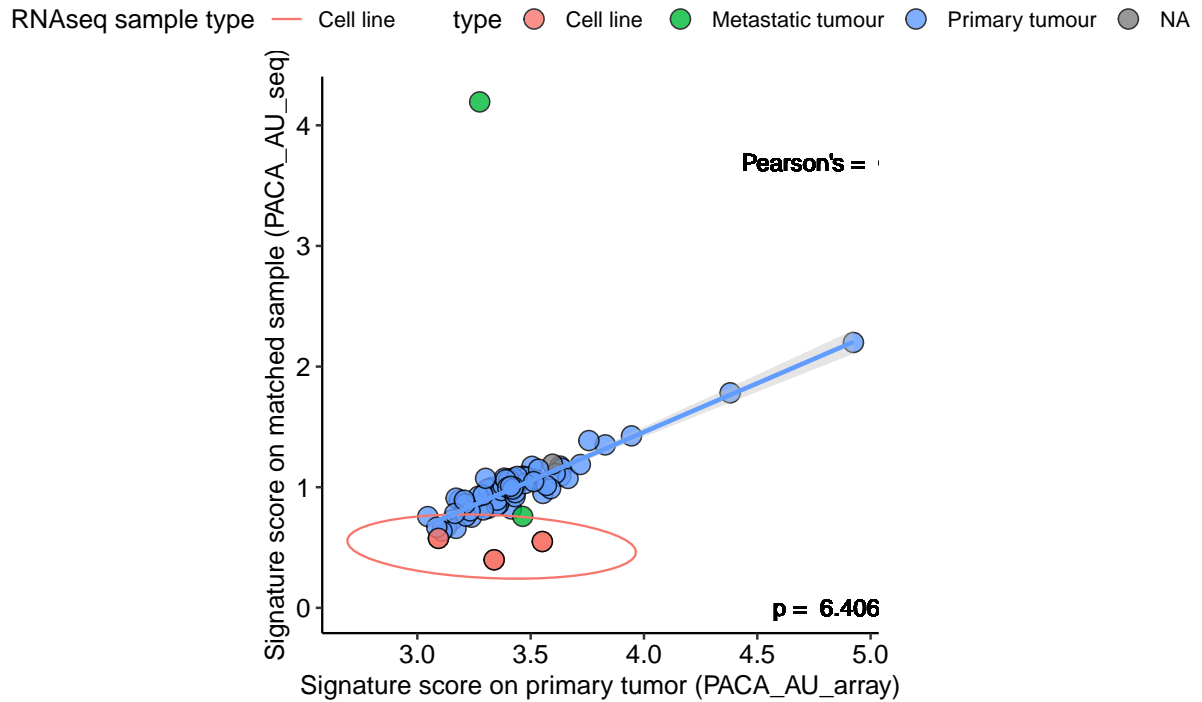
```
## 'geom_smooth()' using formula 'y ~ x'
```

Moffitt.F1_Liver.top25



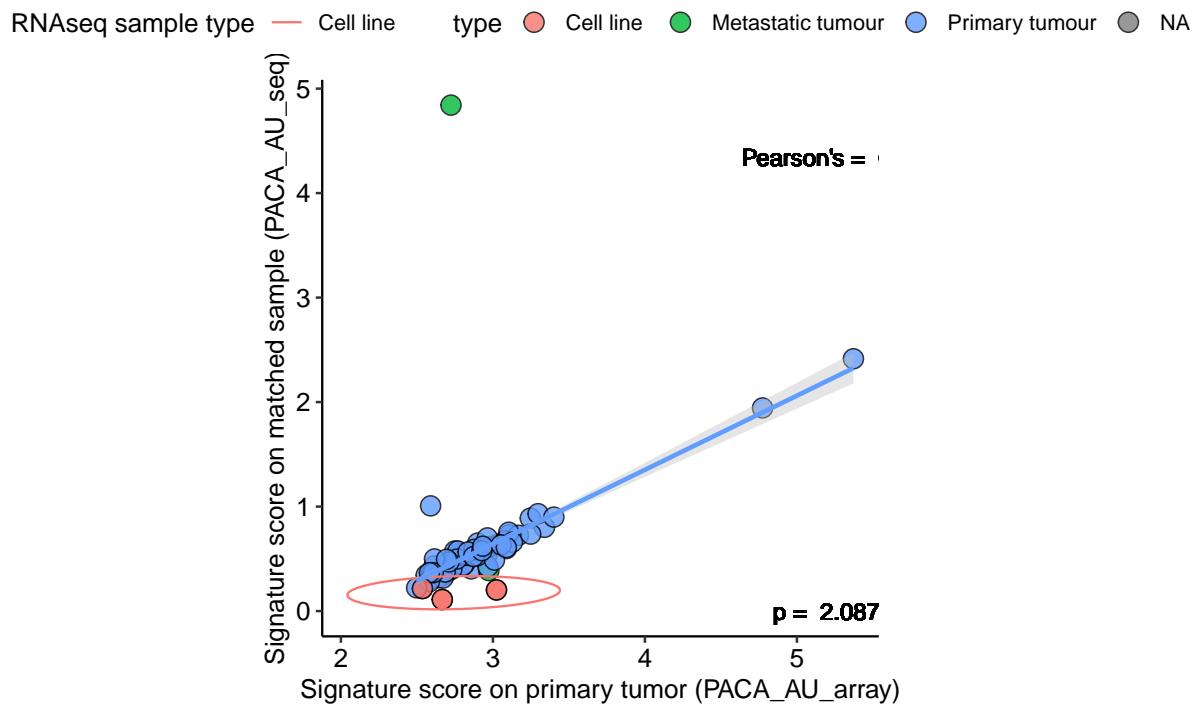
```
## 'geom_smooth()' using formula 'y ~ x'
```

Moffitt.F1_Liver.top250



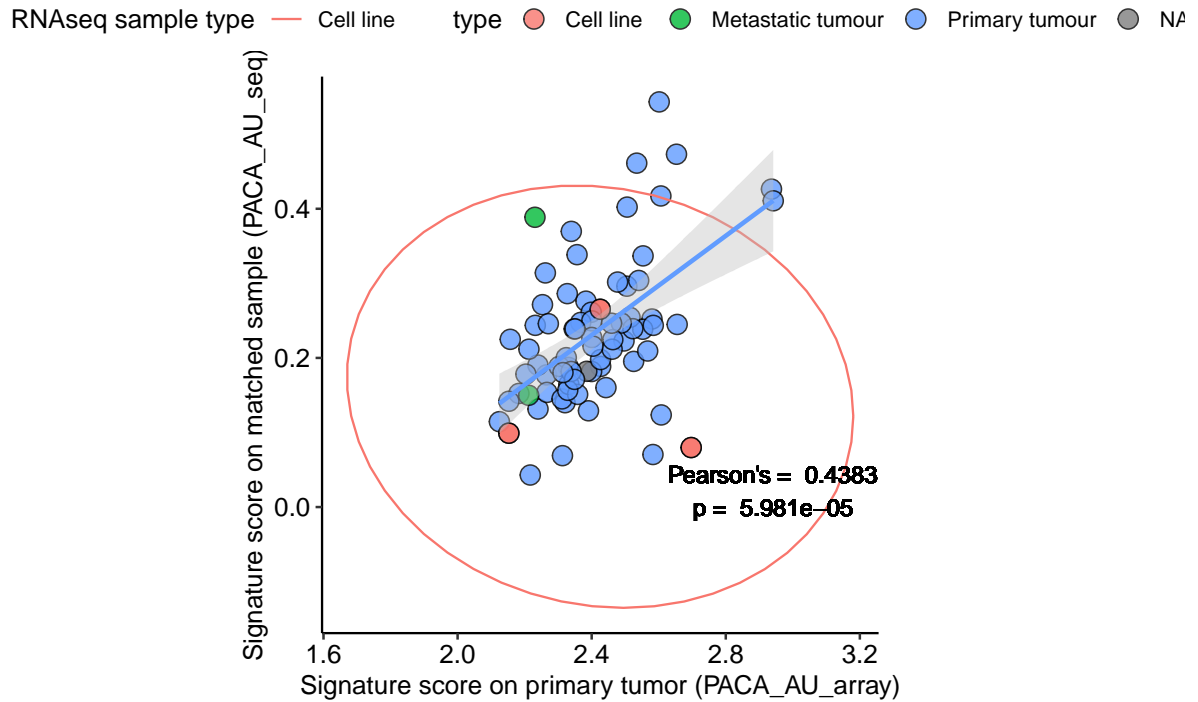
'geom_smooth()' using formula 'y ~ x'

Moffitt.F1_Liver.top100



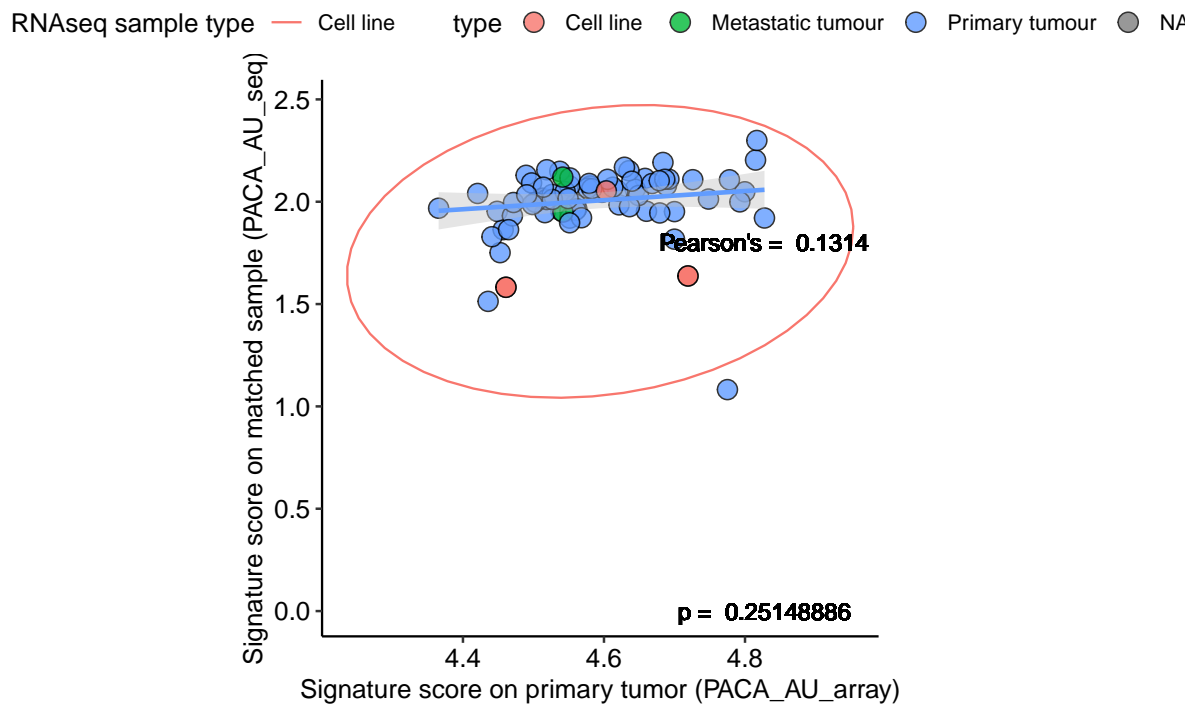
'geom_smooth()' using formula 'y ~ x'

Moffitt.F2.top25



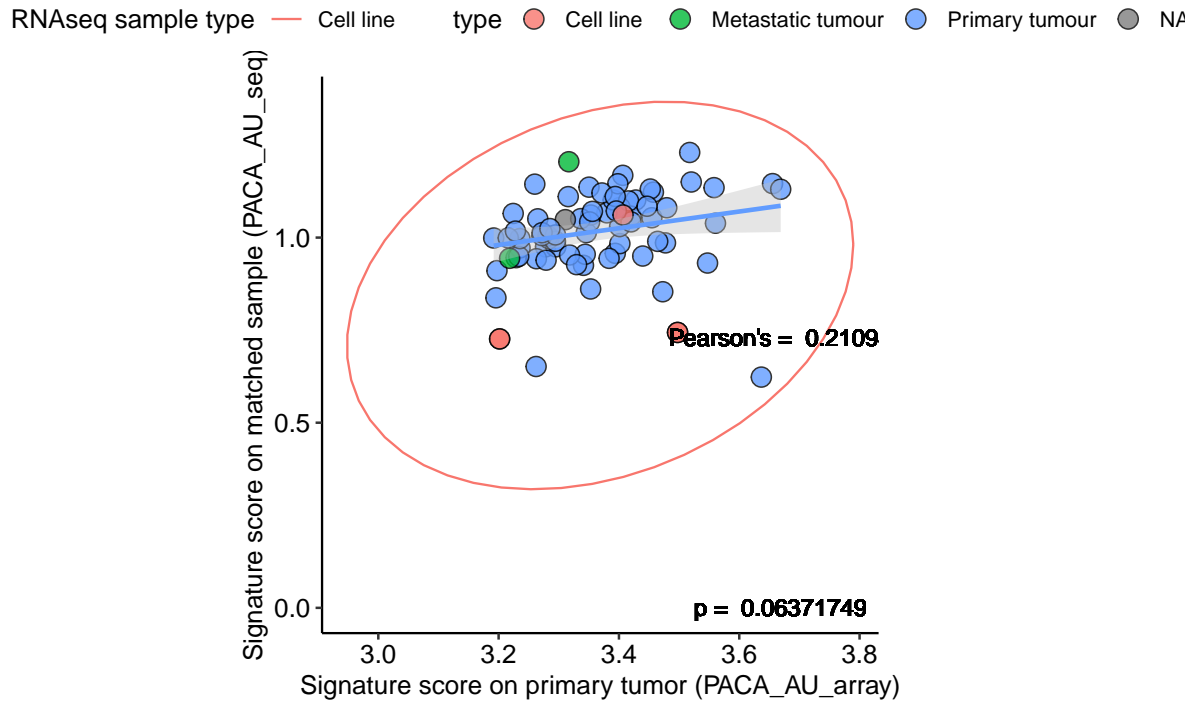
```
## 'geom_smooth()' using formula 'y ~ x'
```

Moffitt.F2.top250



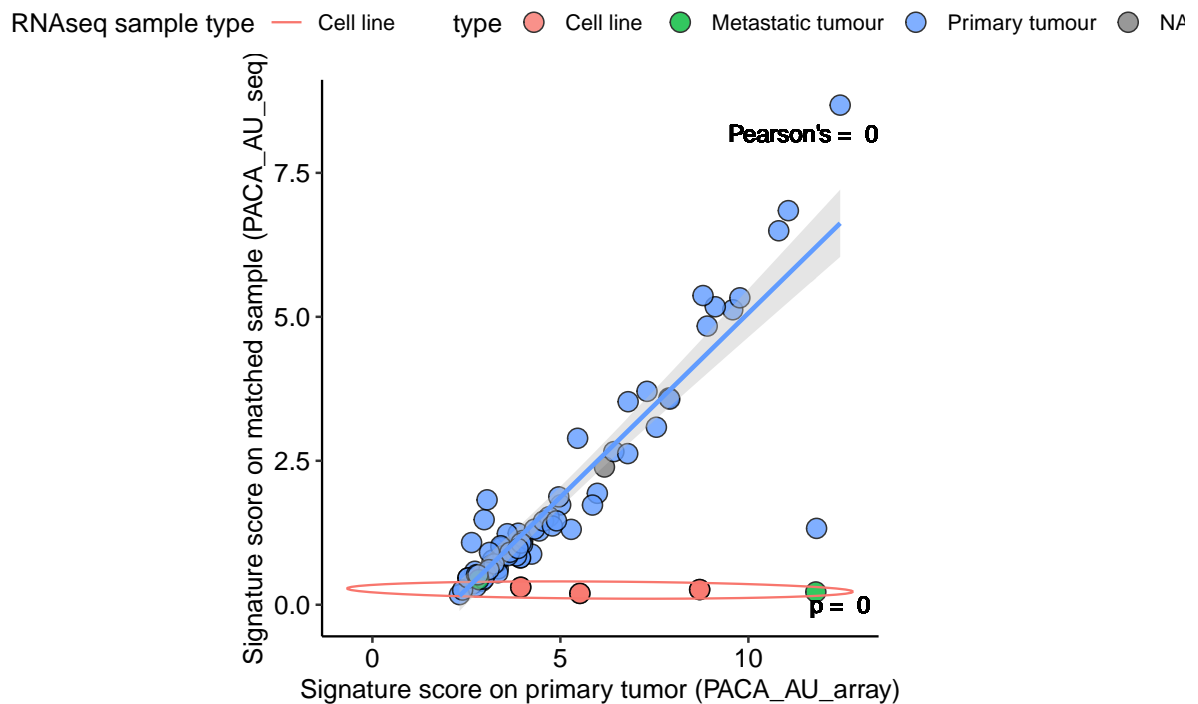
```
## 'geom_smooth()' using formula 'y ~ x'
```

Moffitt.F2.top100



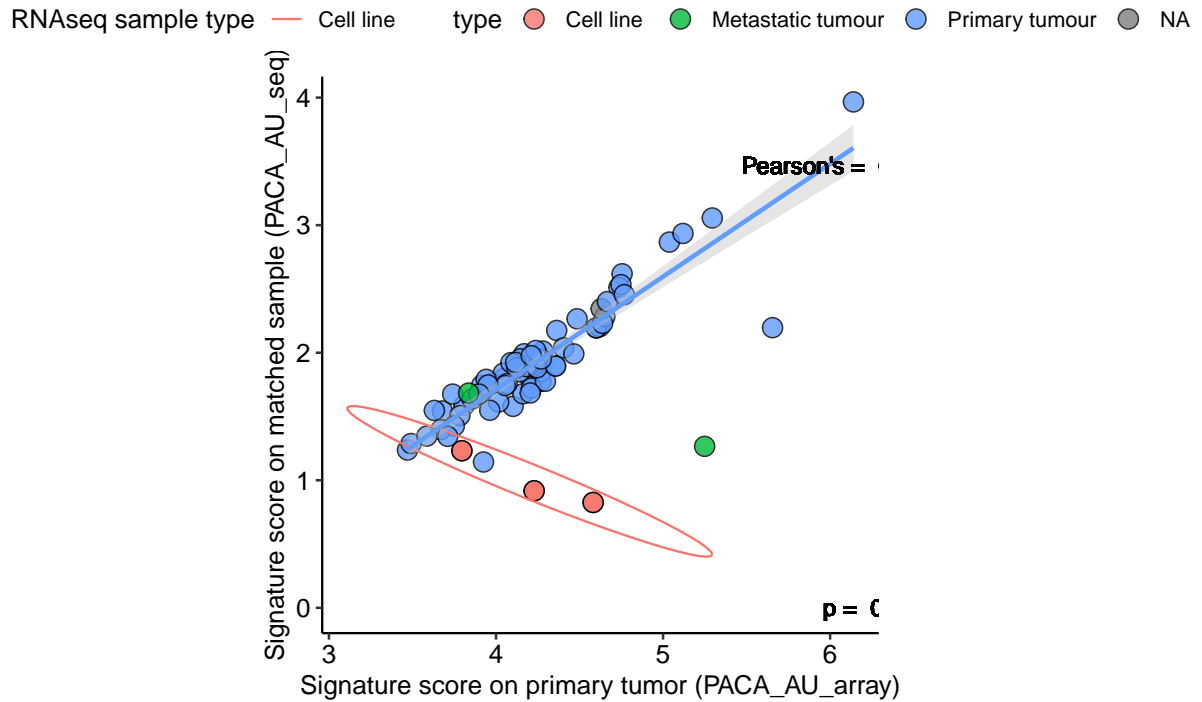
'geom_smooth()' using formula 'y ~ x'

Moffitt.F3_Exocrine.top25



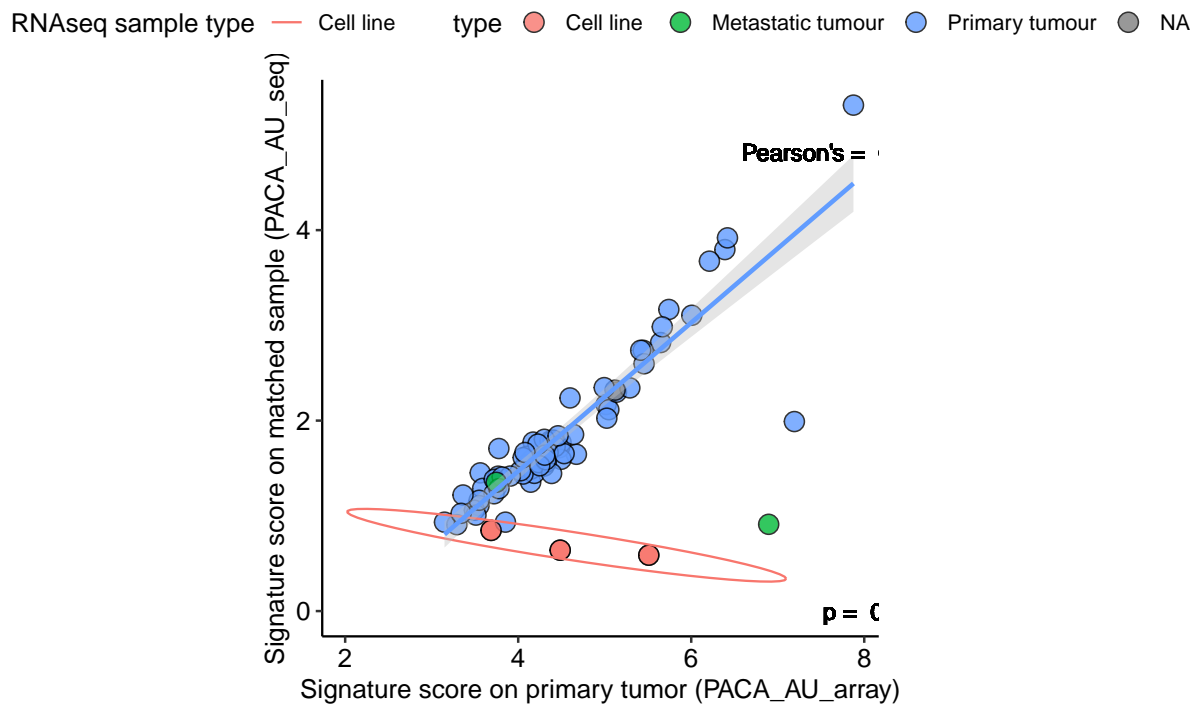
'geom_smooth()' using formula 'y ~ x'

Moffitt.F3_Exocrine.top250



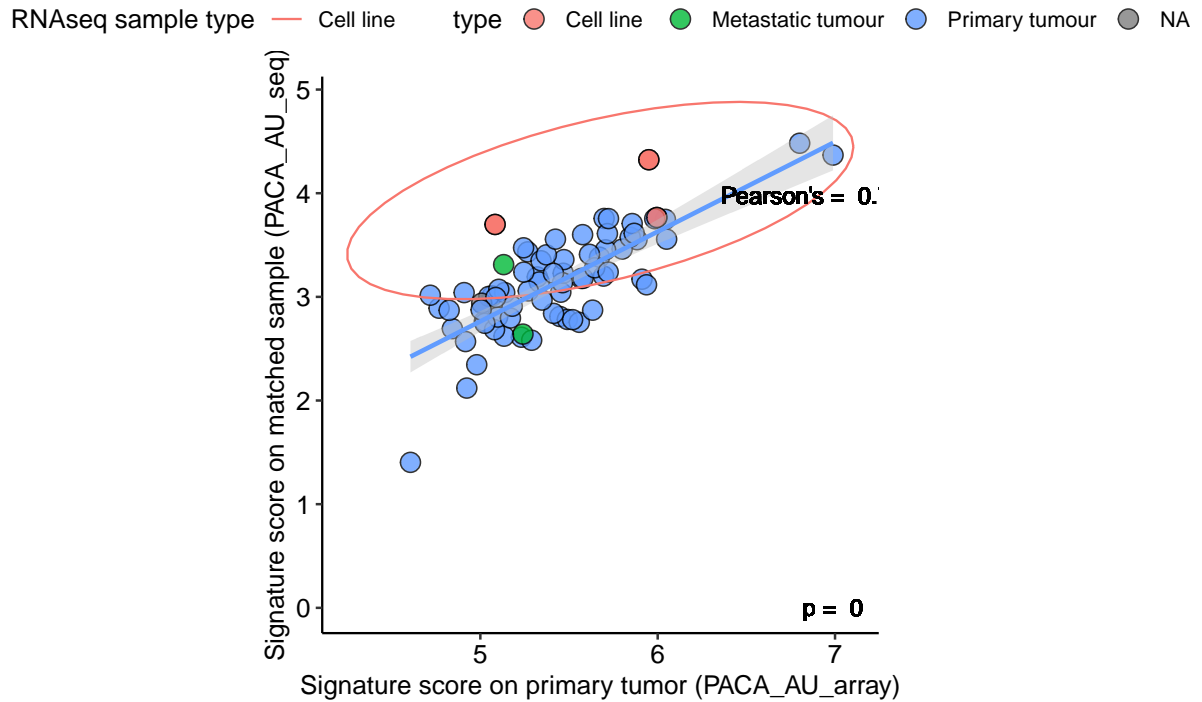
```
## 'geom_smooth()' using formula 'y ~ x'
```

Moffitt.F3_Exocrine.top100



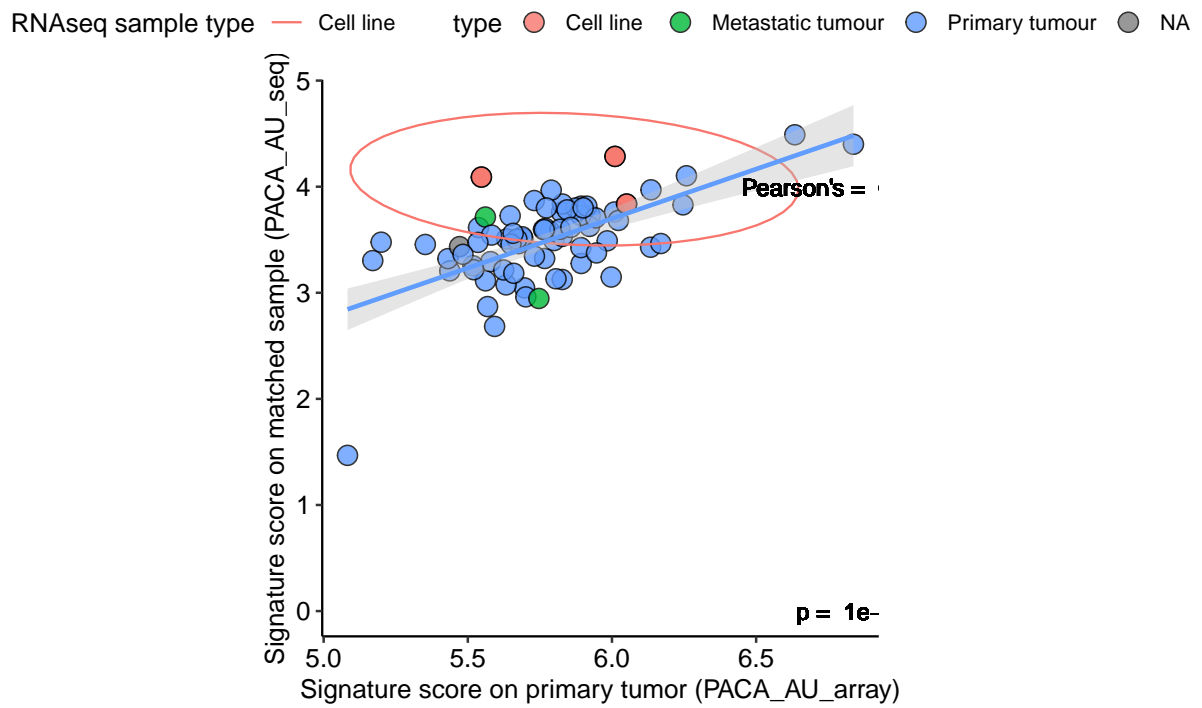
```
## 'geom_smooth()' using formula 'y ~ x'
```


Moffitt.F4_CellCycle.top25



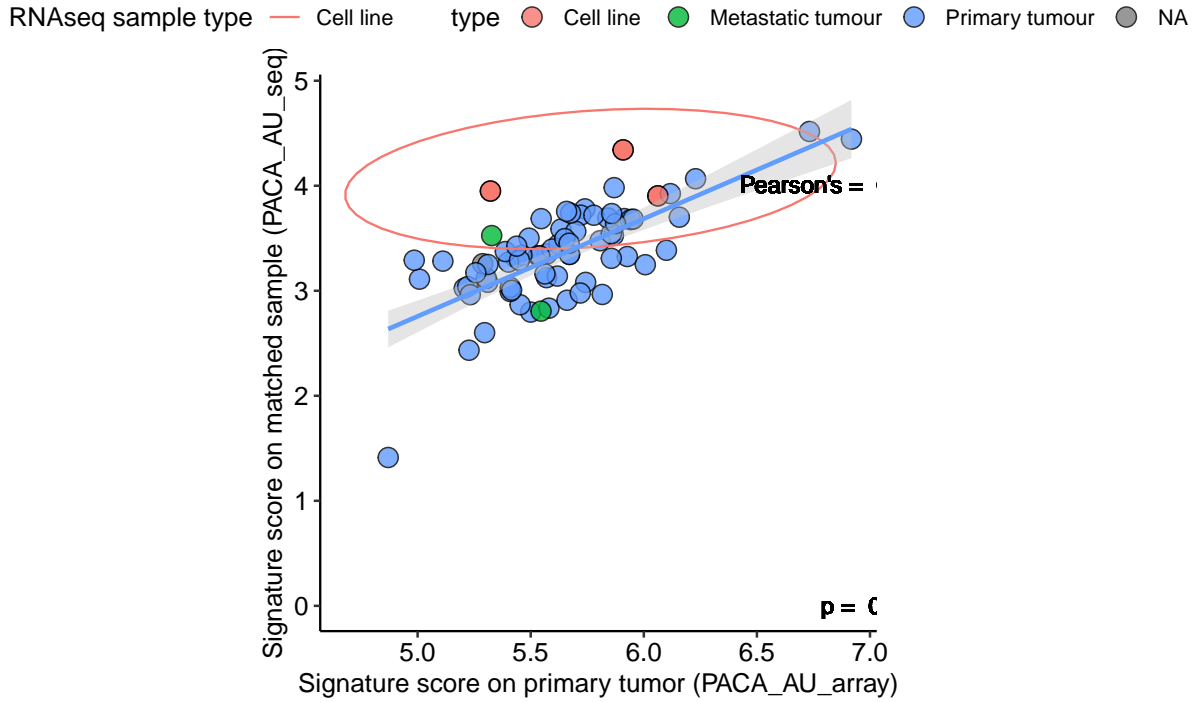
```
## 'geom_smooth()' using formula 'y ~ x'
```

Moffitt.F4_CellCycle.top250



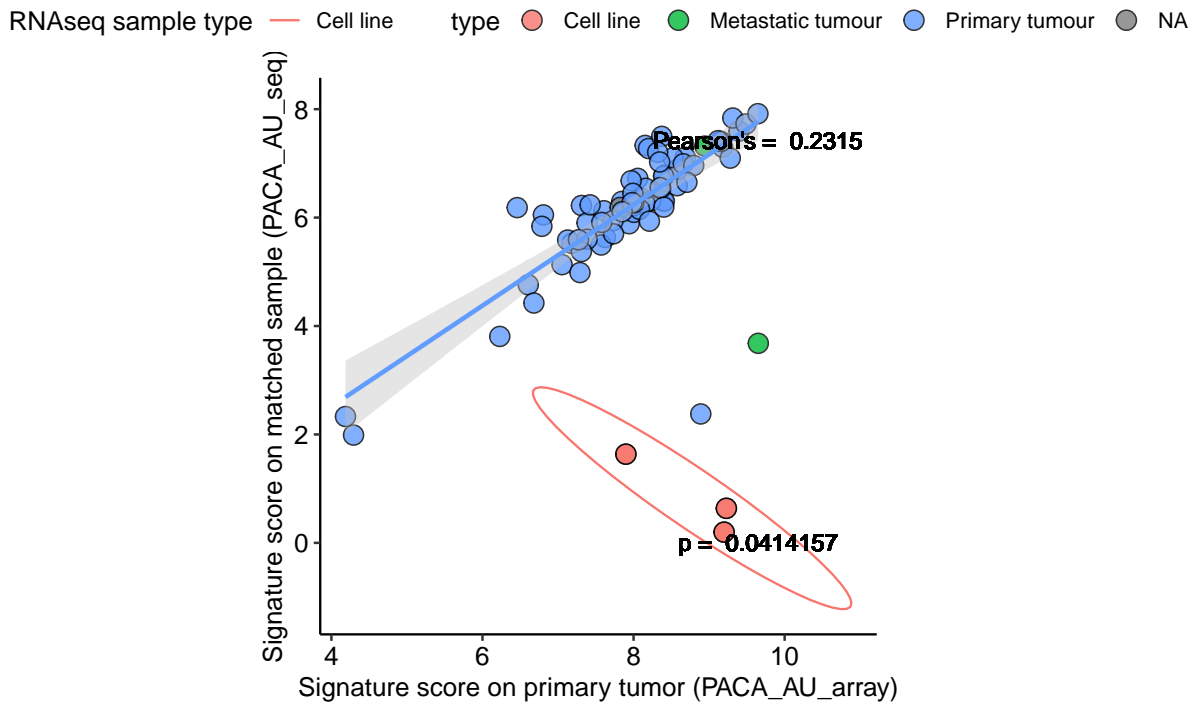
```
## 'geom_smooth()' using formula 'y ~ x'
```

Moffitt.F4_CellCycle.top100



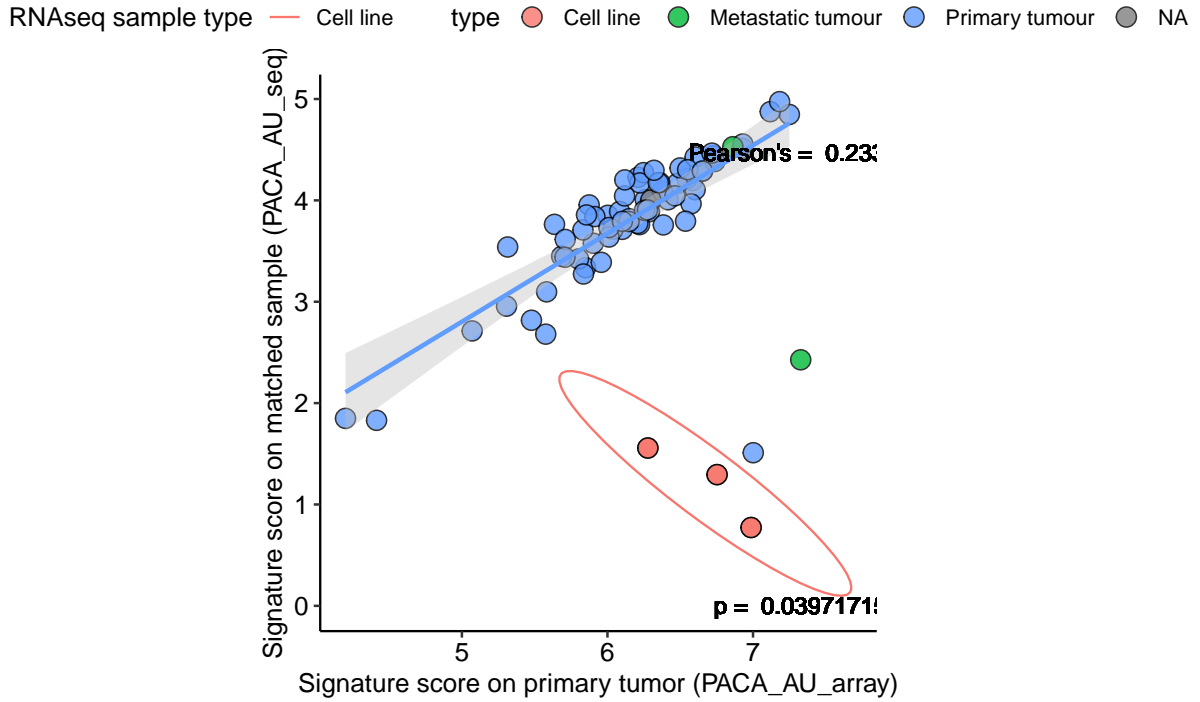
```
## 'geom_smooth()' using formula 'y ~ x'
```

Moffitt.F5_ActivatedStroma.top25



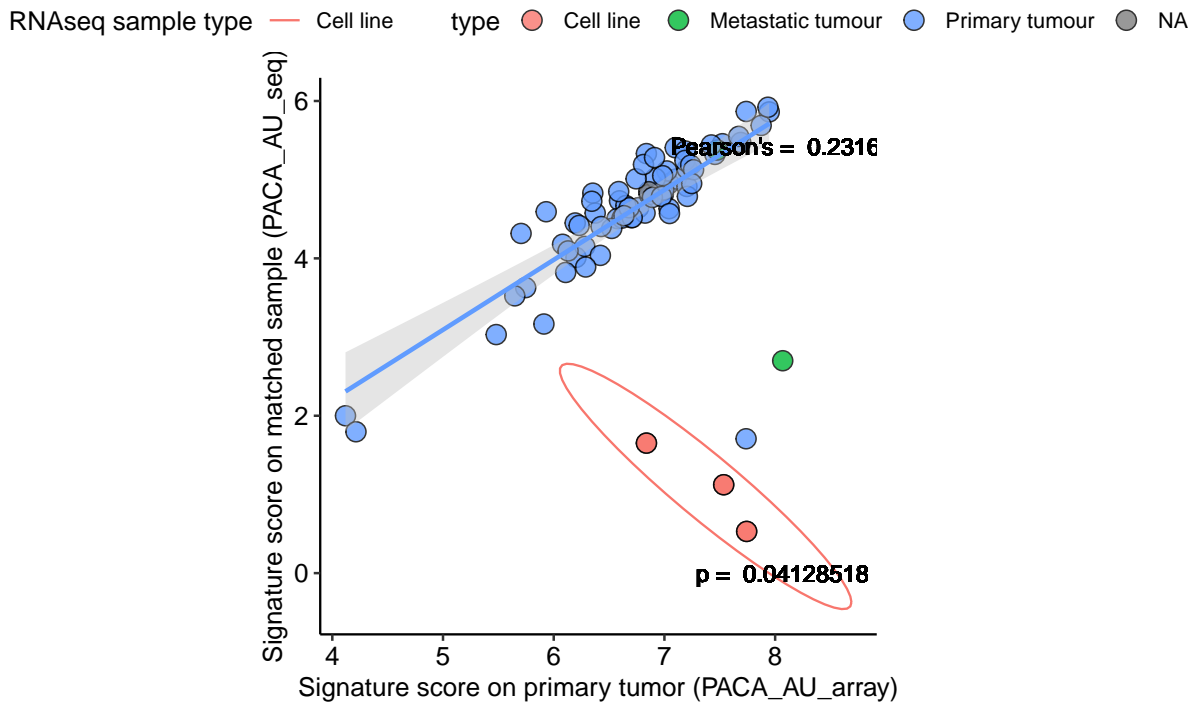
```
## 'geom_smooth()' using formula 'y ~ x'
```

Moffitt.F5_ActivatedStroma.top250



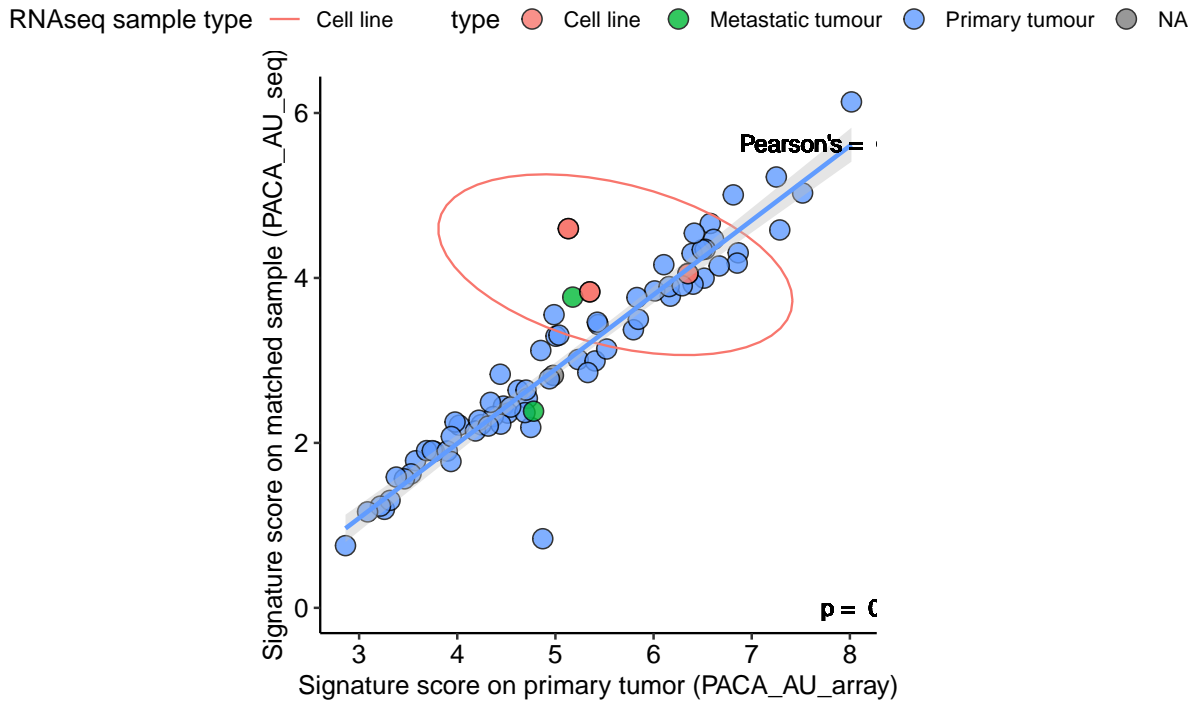
'geom_smooth()' using formula 'y ~ x'

Moffitt.F5_ActivatedStroma.top100



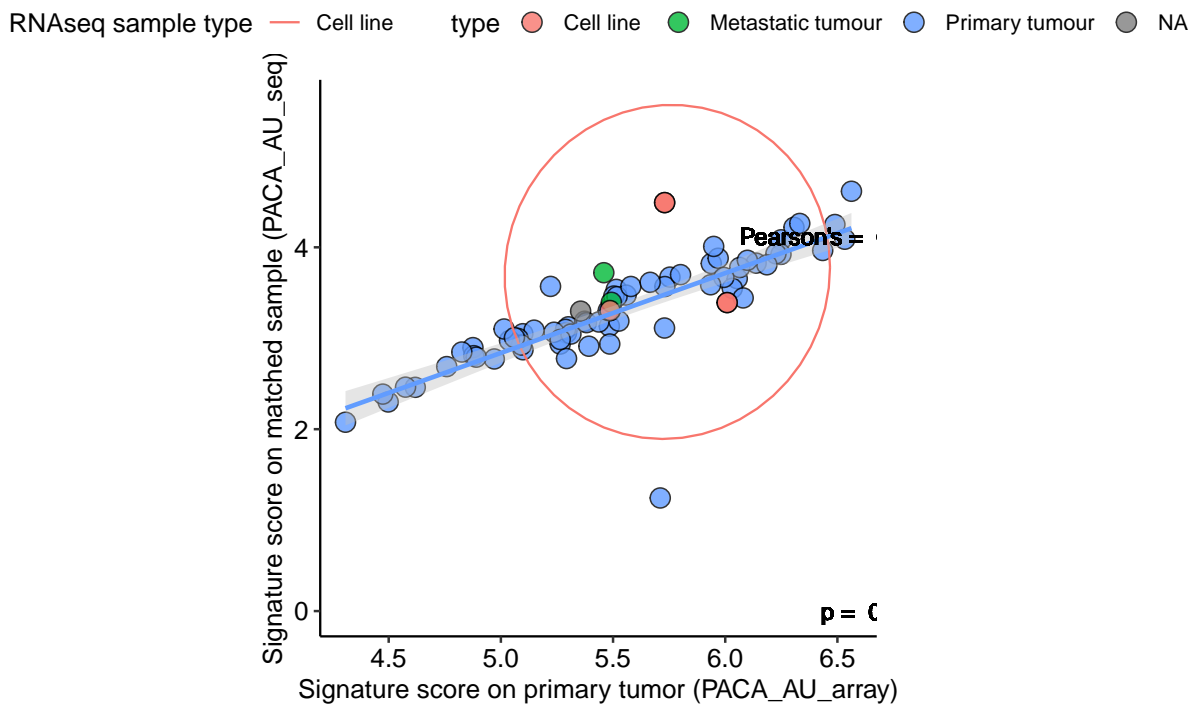
'geom_smooth()' using formula 'y ~ x'

Moffitt.F6_BasalLike.top25



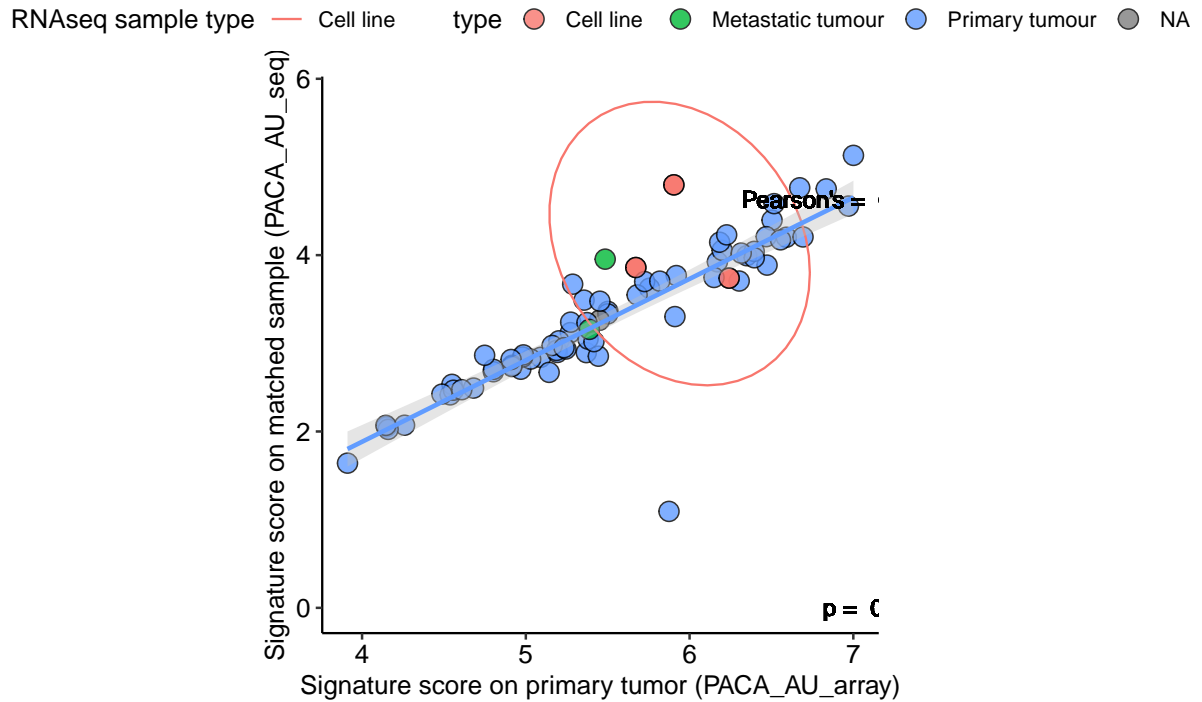
```
## 'geom_smooth()' using formula 'y ~ x'
```

Moffitt.F6_BasalLike.top250



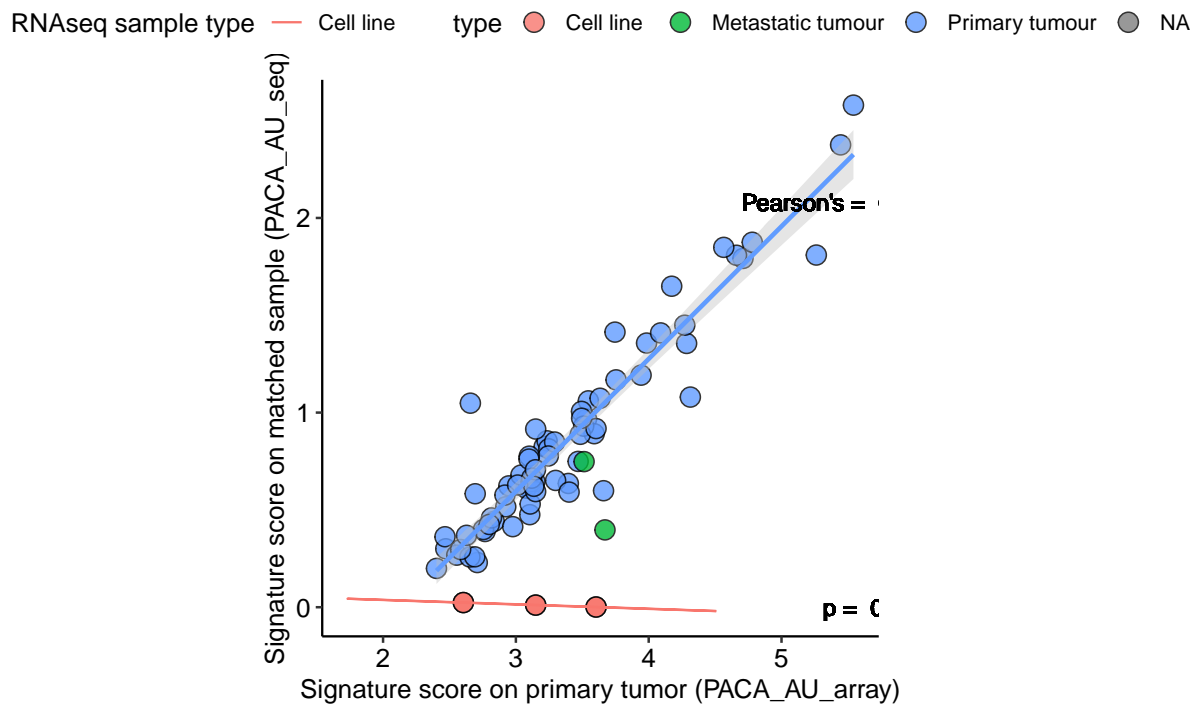
```
## 'geom_smooth()' using formula 'y ~ x'
```

Moffitt.F6_BasalLike.top100



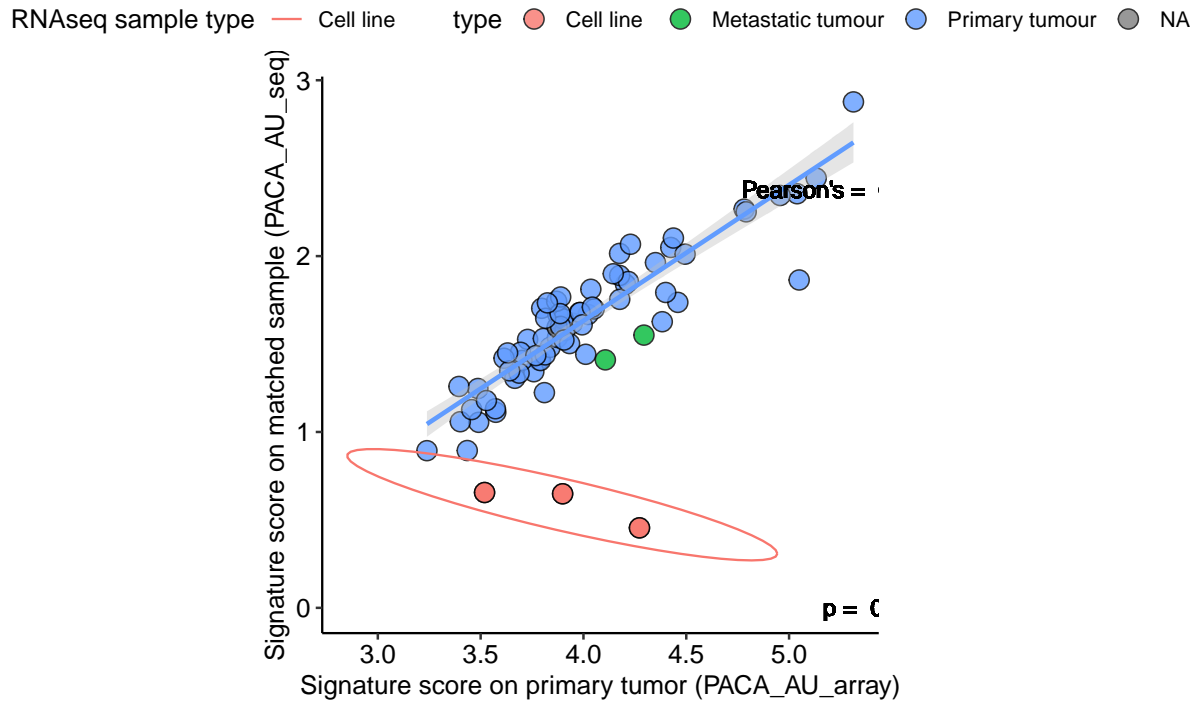
```
## 'geom_smooth()' using formula 'y ~ x'
```

Moffitt.F7_Immune.top25



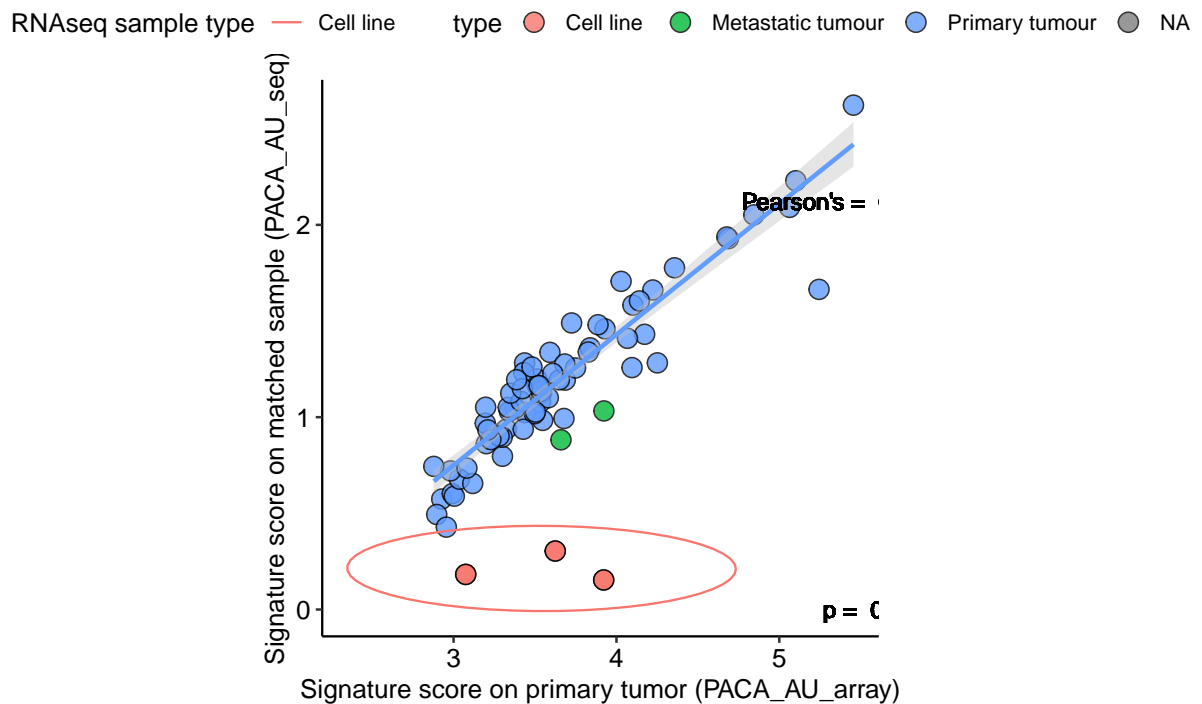
```
## 'geom_smooth()' using formula 'y ~ x'
```

Moffitt.F7_Immune.top250



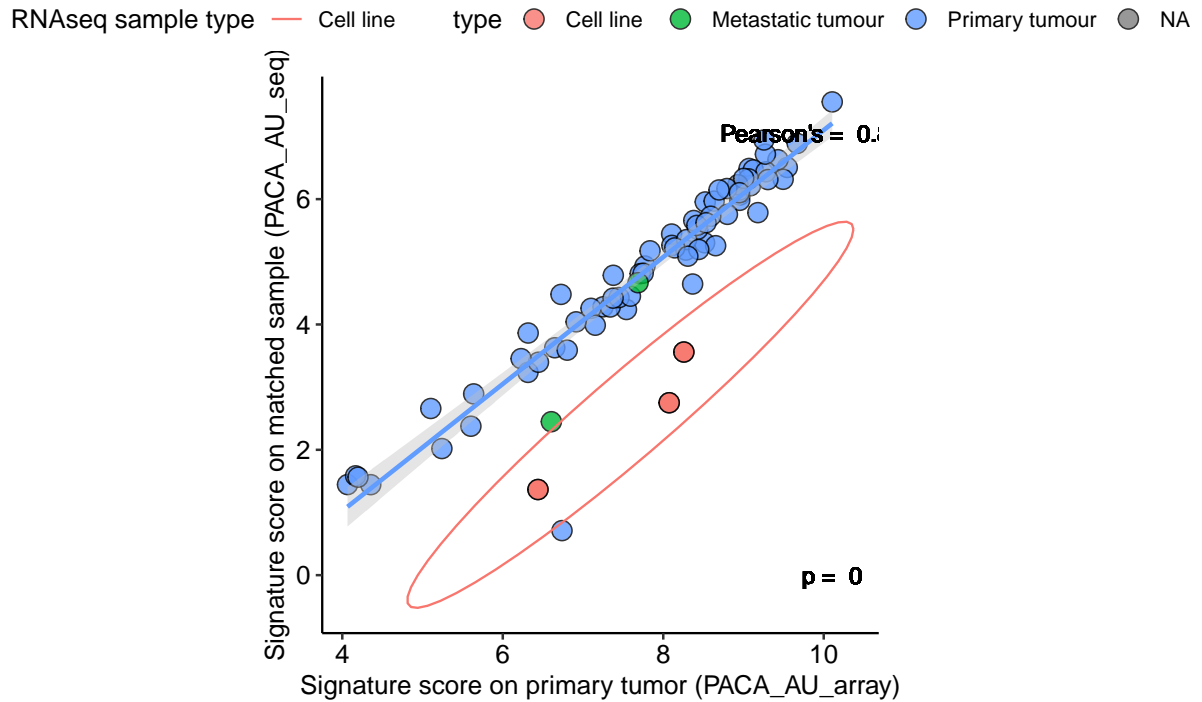
```
## 'geom_smooth()' using formula 'y ~ x'
```

Moffitt.F7_Immune.top100



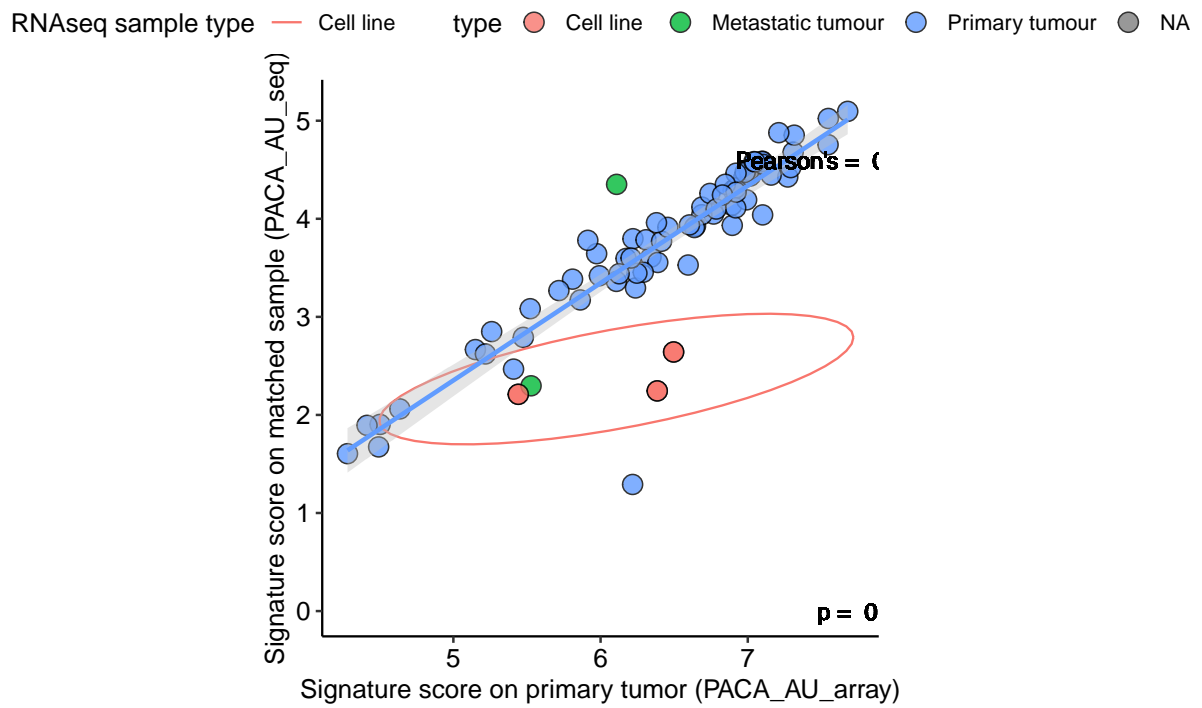
```
## 'geom_smooth()' using formula 'y ~ x'
```

Moffitt.F8_Classical.top25



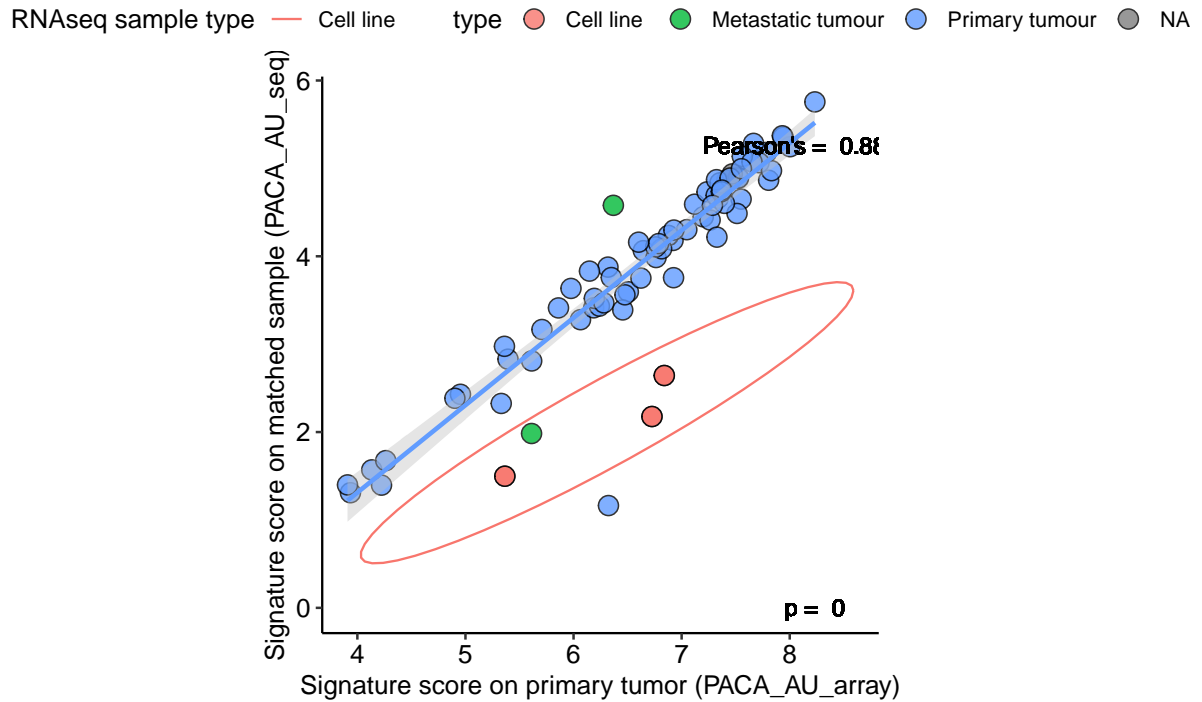
```
## 'geom_smooth()' using formula 'y ~ x'
```

Moffitt.F8_Classical.top250



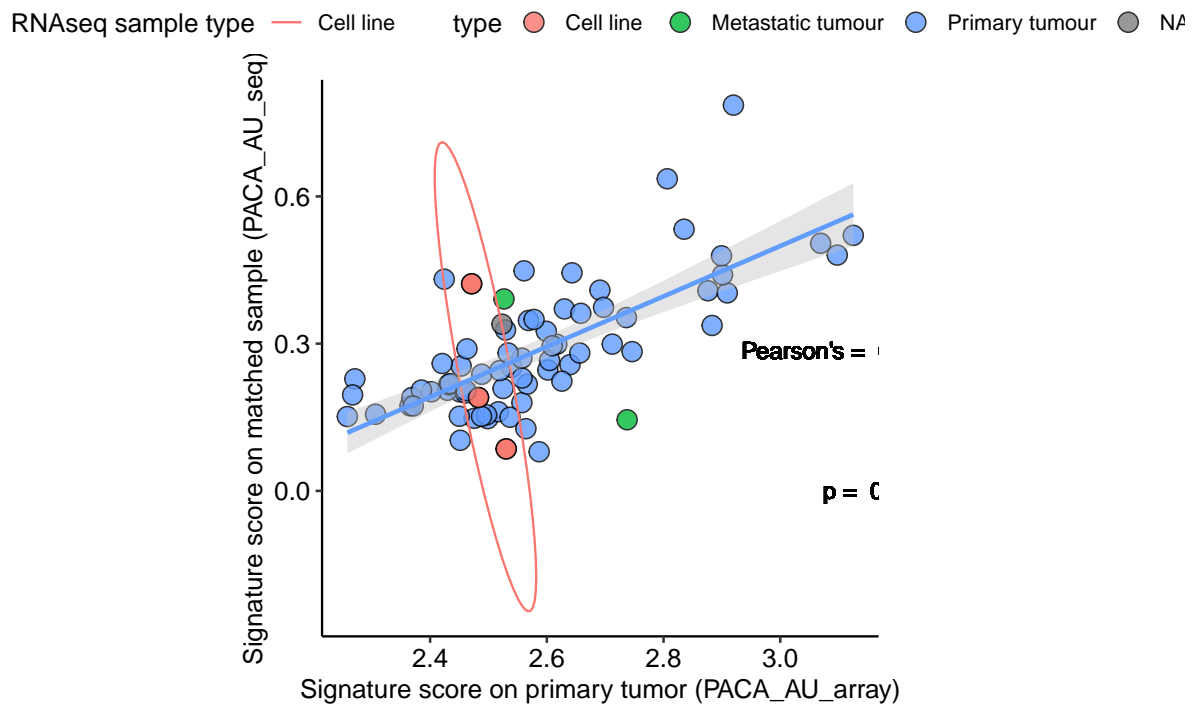
```
## 'geom_smooth()' using formula 'y ~ x'
```

Moffitt.F8_Classical.top100



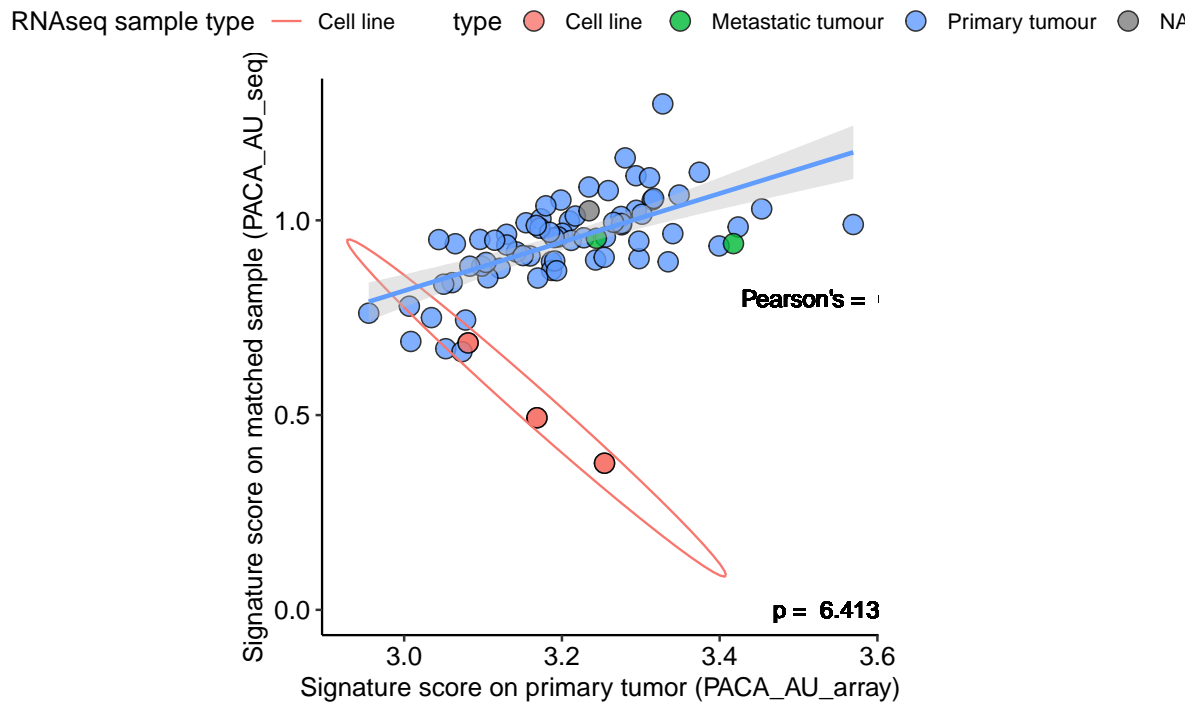
```
## 'geom_smooth()' using formula 'y ~ x'
```

Moffitt.F9_Lung.top25



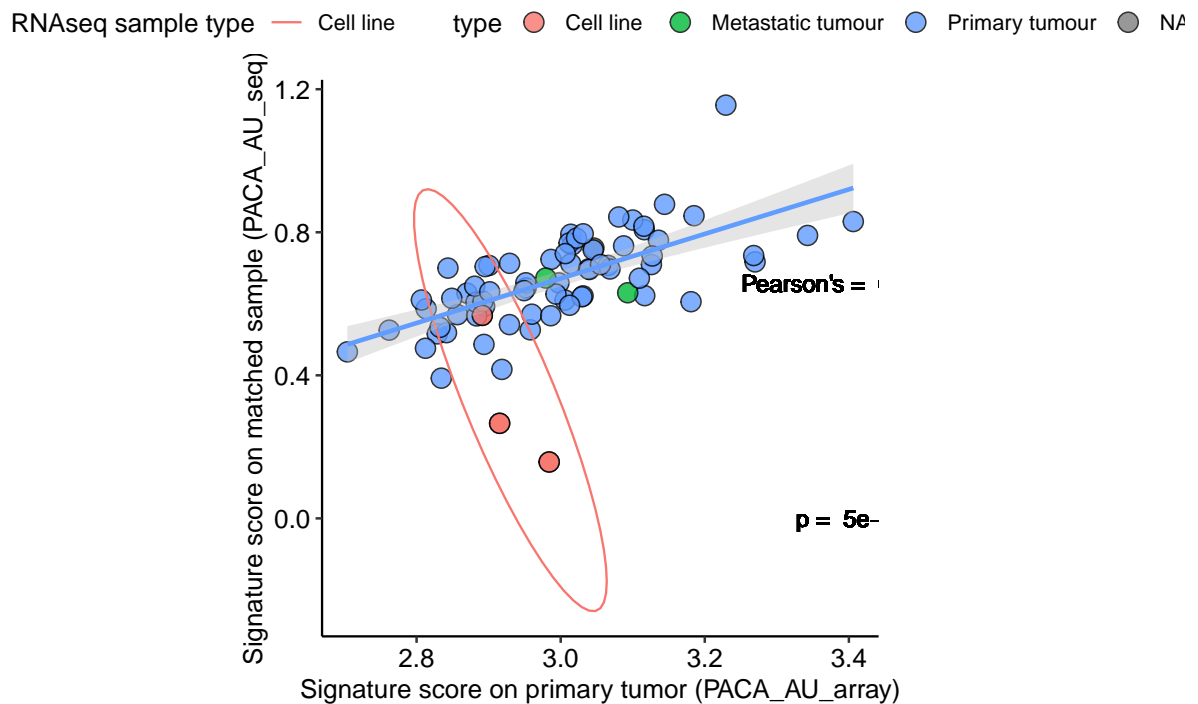
```
## 'geom_smooth()' using formula 'y ~ x'
```


Moffitt.F9_Lung.top250



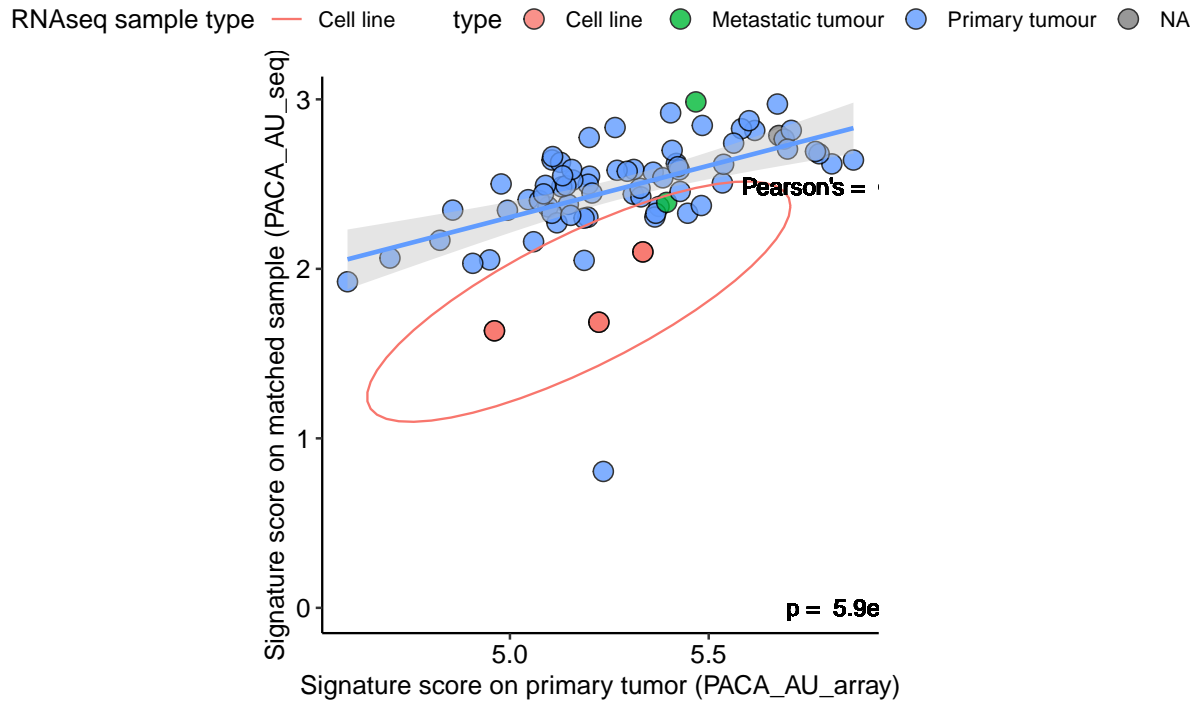
```
## 'geom_smooth()' using formula 'y ~ x'
```

Moffitt.F9_Lung.top100



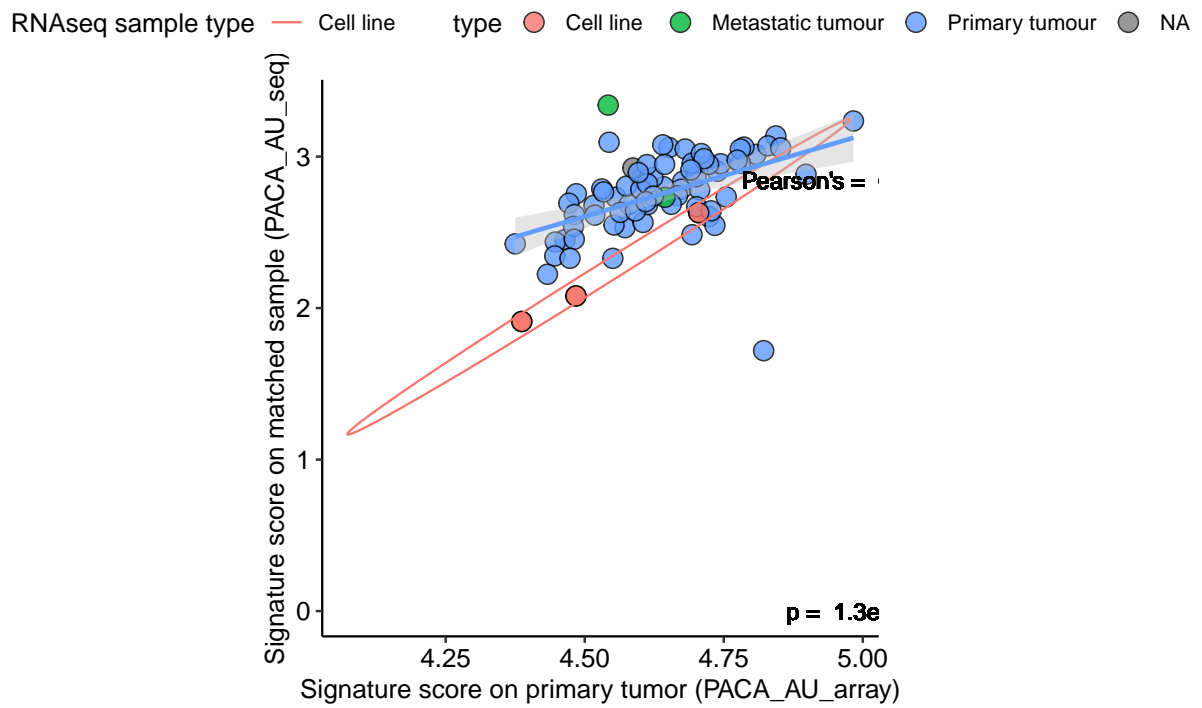
```
## 'geom_smooth()' using formula 'y ~ x'
```

Moffitt.F10.top25



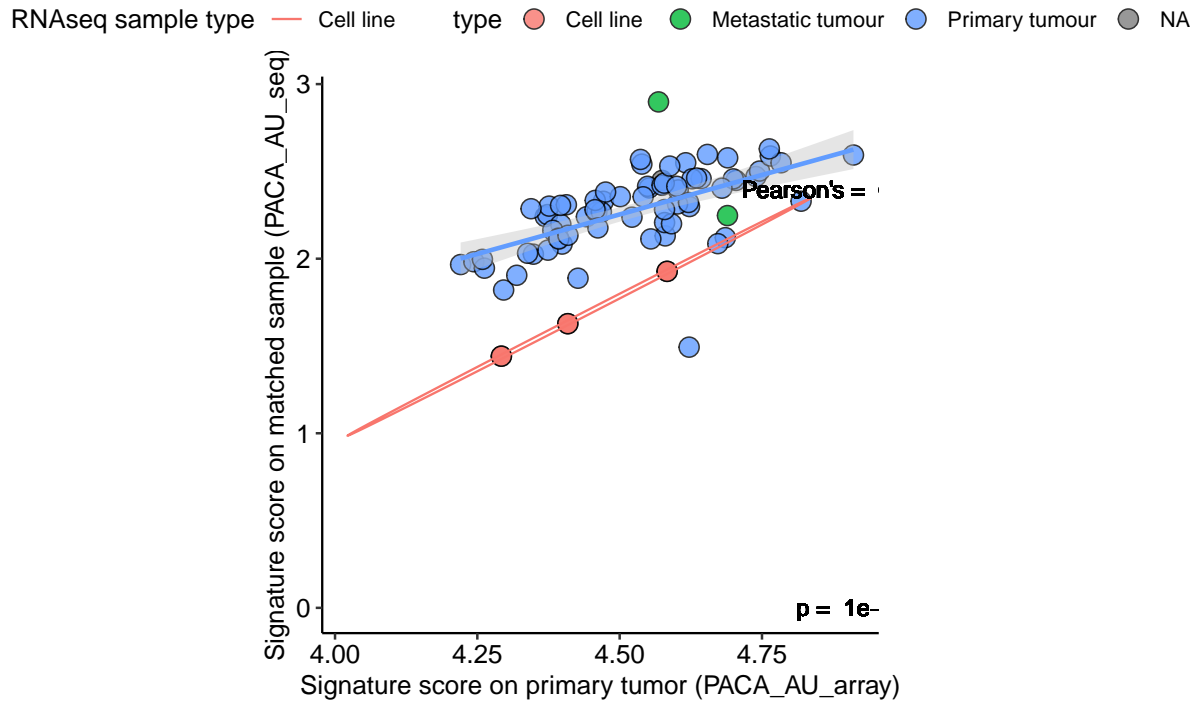
```
## 'geom_smooth()' using formula 'y ~ x'
```

Moffitt.F10.top250



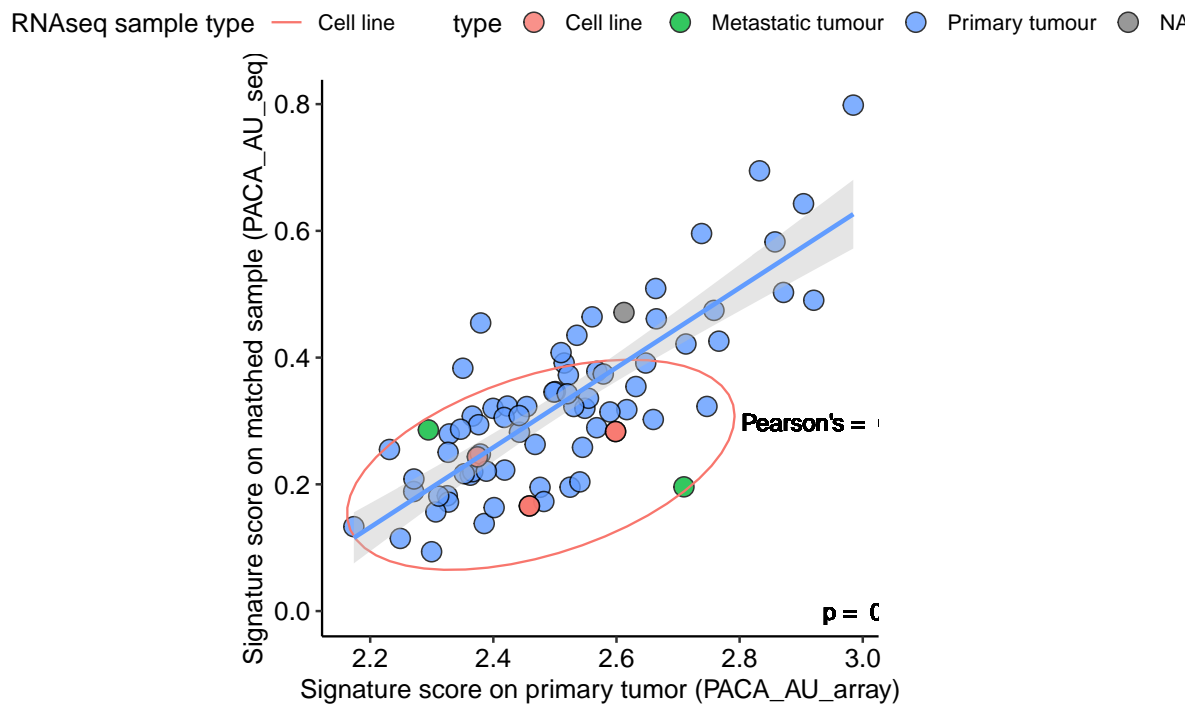
```
## 'geom_smooth()' using formula 'y ~ x'
```

Moffitt.F10.top100



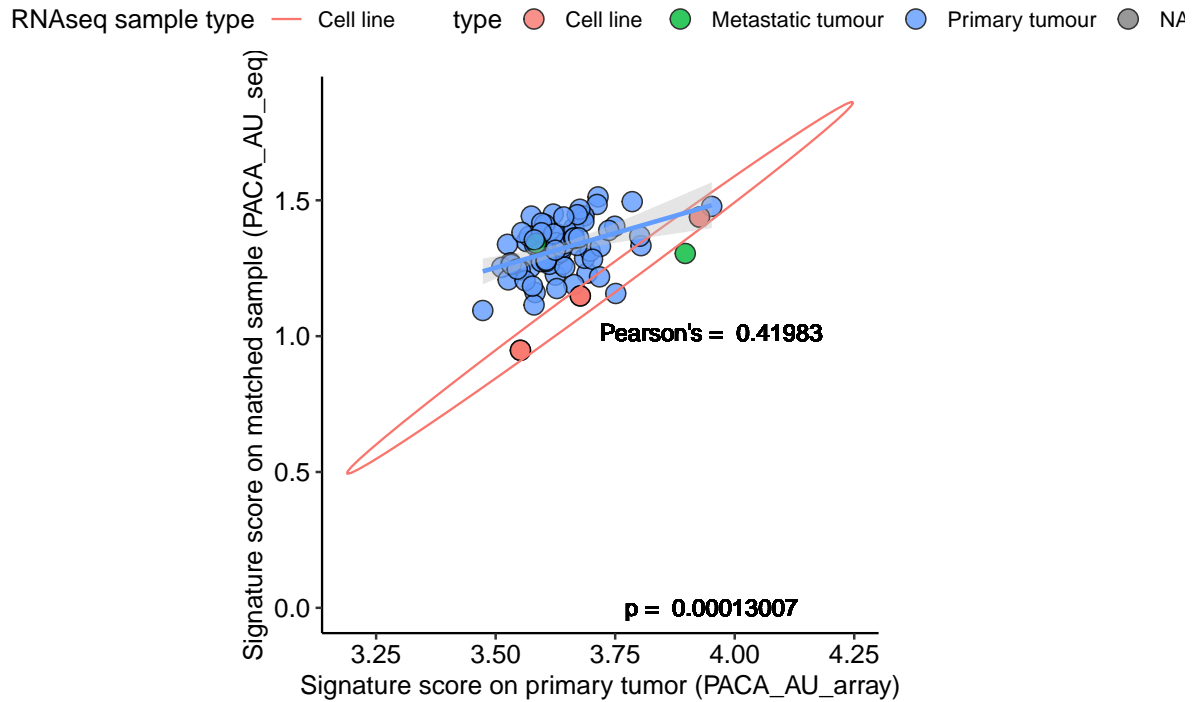
```
## 'geom_smooth()' using formula 'y ~ x'
```

Moffitt.F11_Muscle.top25



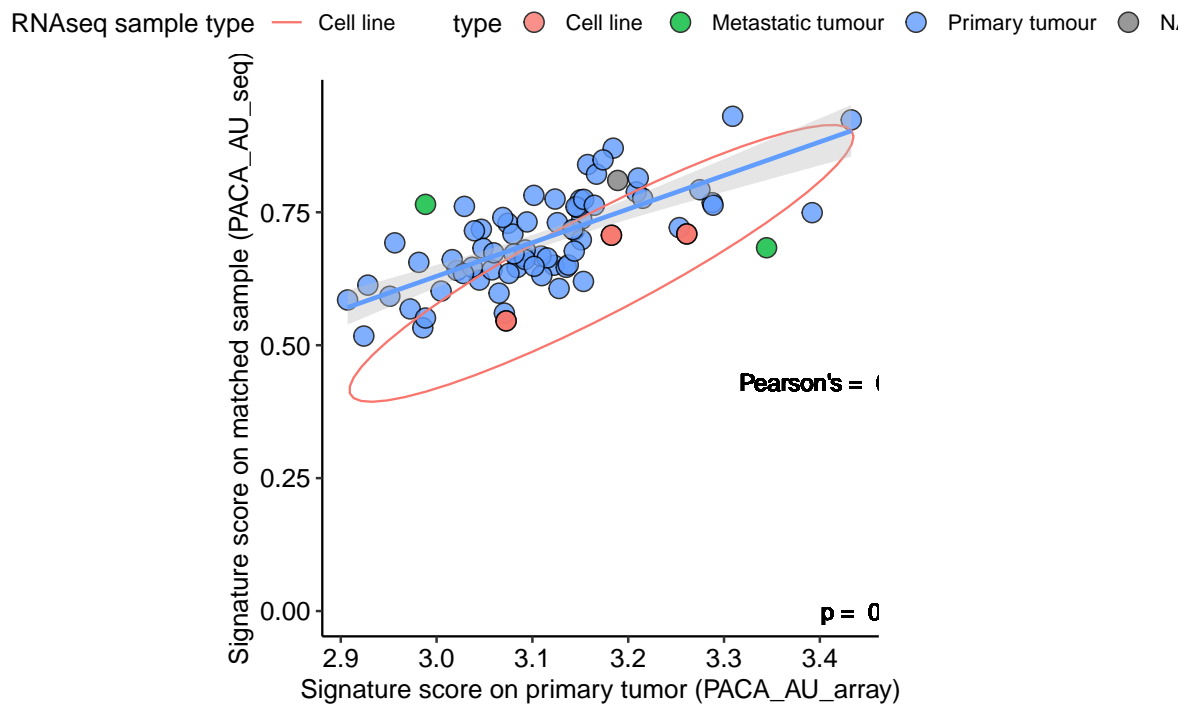
```
## 'geom_smooth()' using formula 'y ~ x'
```

Moffitt.F11_Muscle.top250



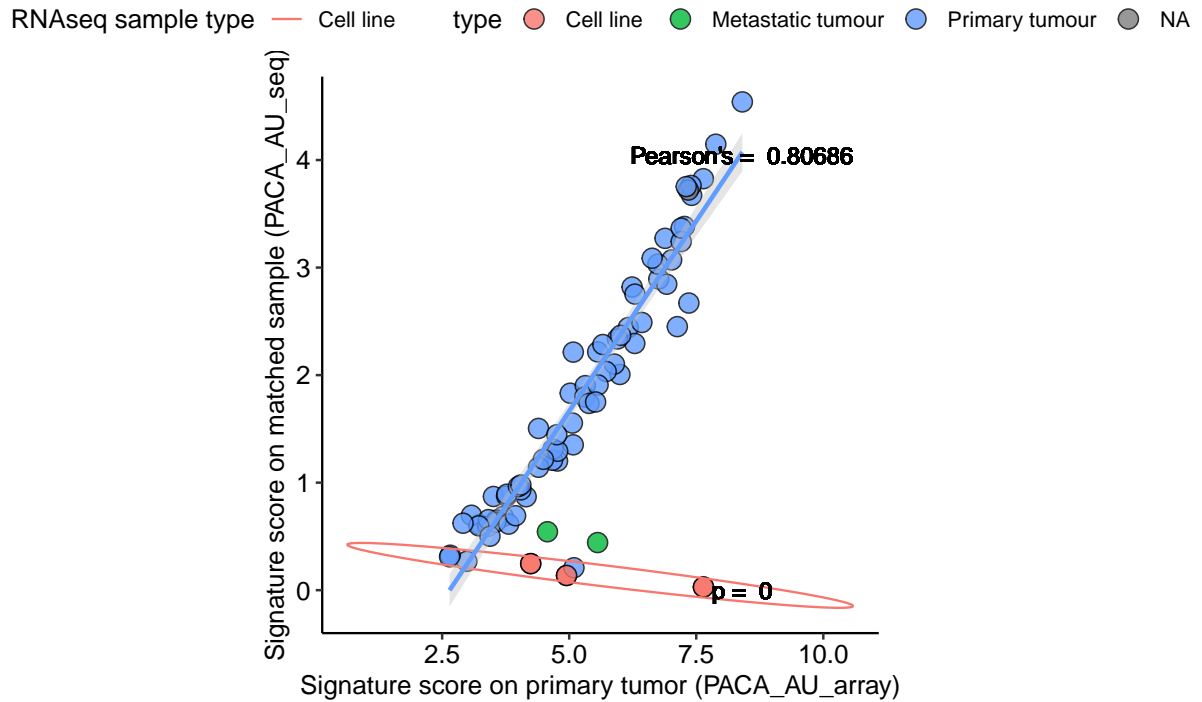
'geom_smooth()' using formula 'y ~ x'

Moffitt.F11_Muscle.top100



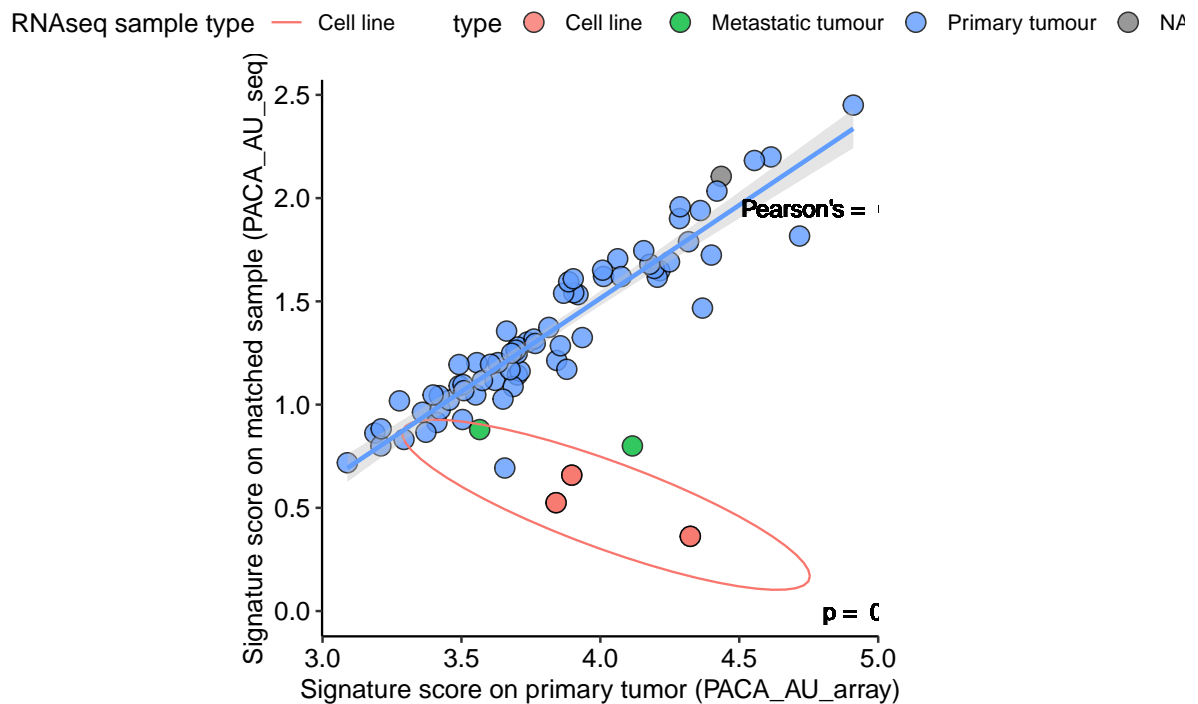
'geom_smooth()' using formula 'y ~ x'

Moffitt.F12_Endocrine.top25



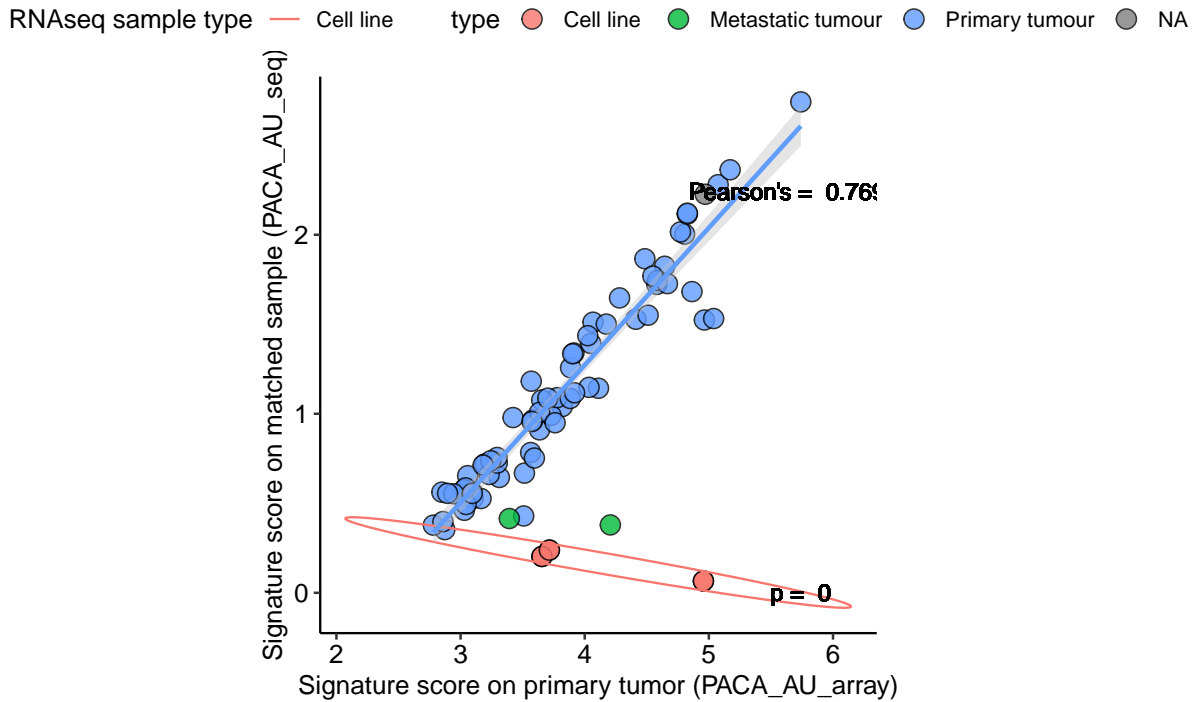
```
## 'geom_smooth()' using formula 'y ~ x'
```

Moffitt.F12_Endocrine.top250



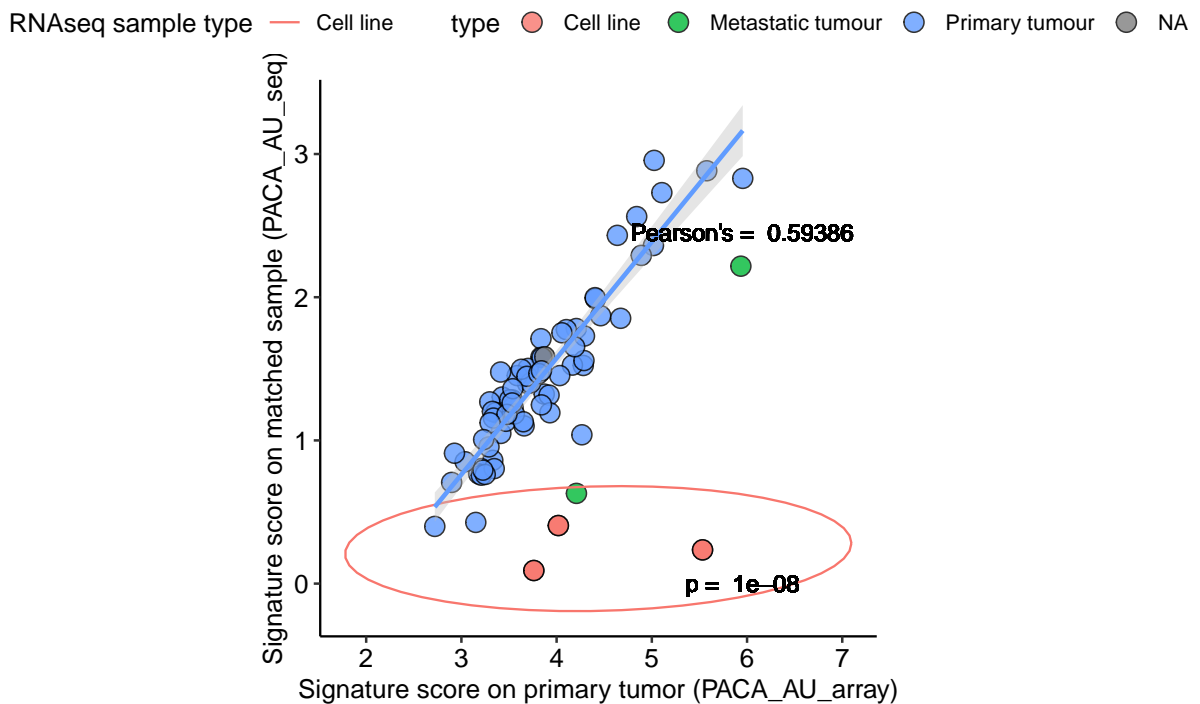
```
## 'geom_smooth()' using formula 'y ~ x'
```

Moffitt.F12_Endocrine.top100



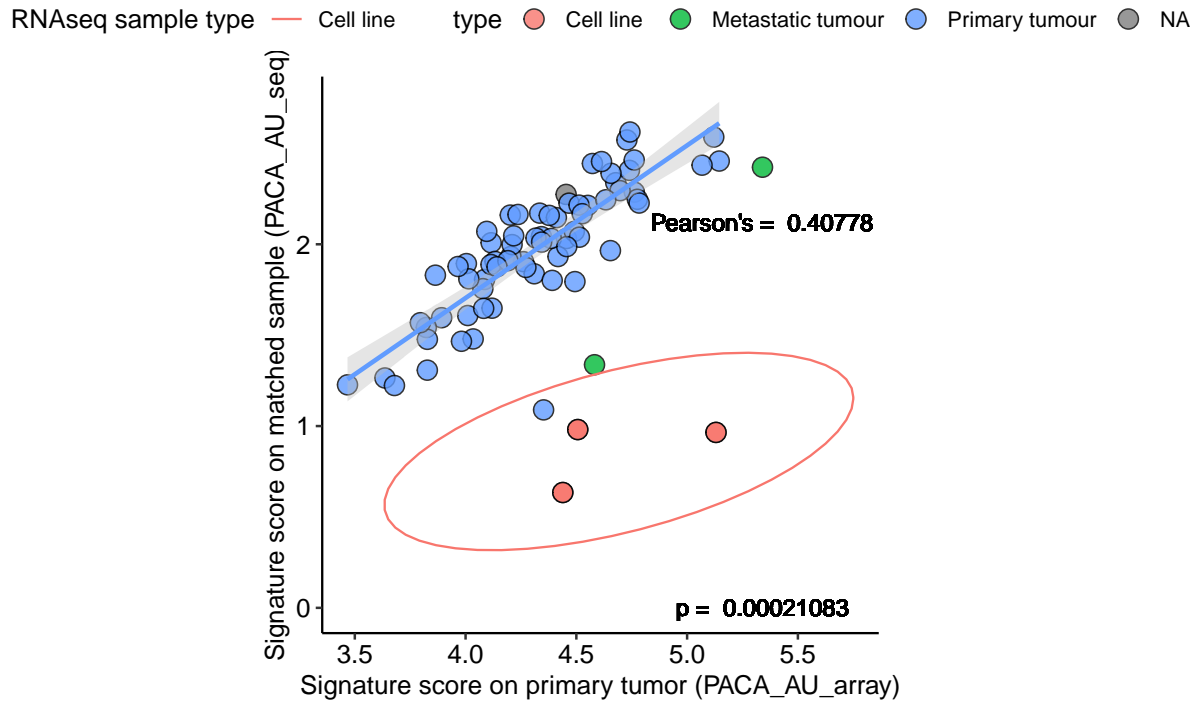
```
## 'geom_smooth()' using formula 'y ~ x'
```

Moffitt.F13_NormalStroma.top25



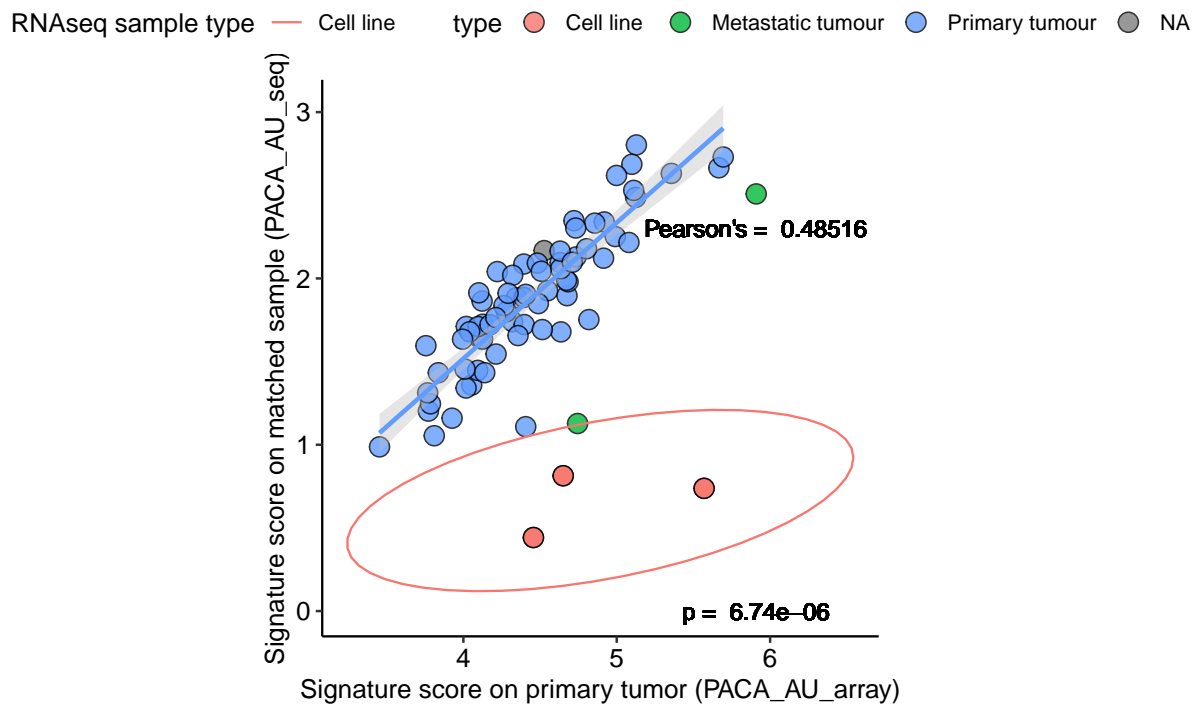
```
## 'geom_smooth()' using formula 'y ~ x'
```

Moffitt.F13_NormalStroma.top250



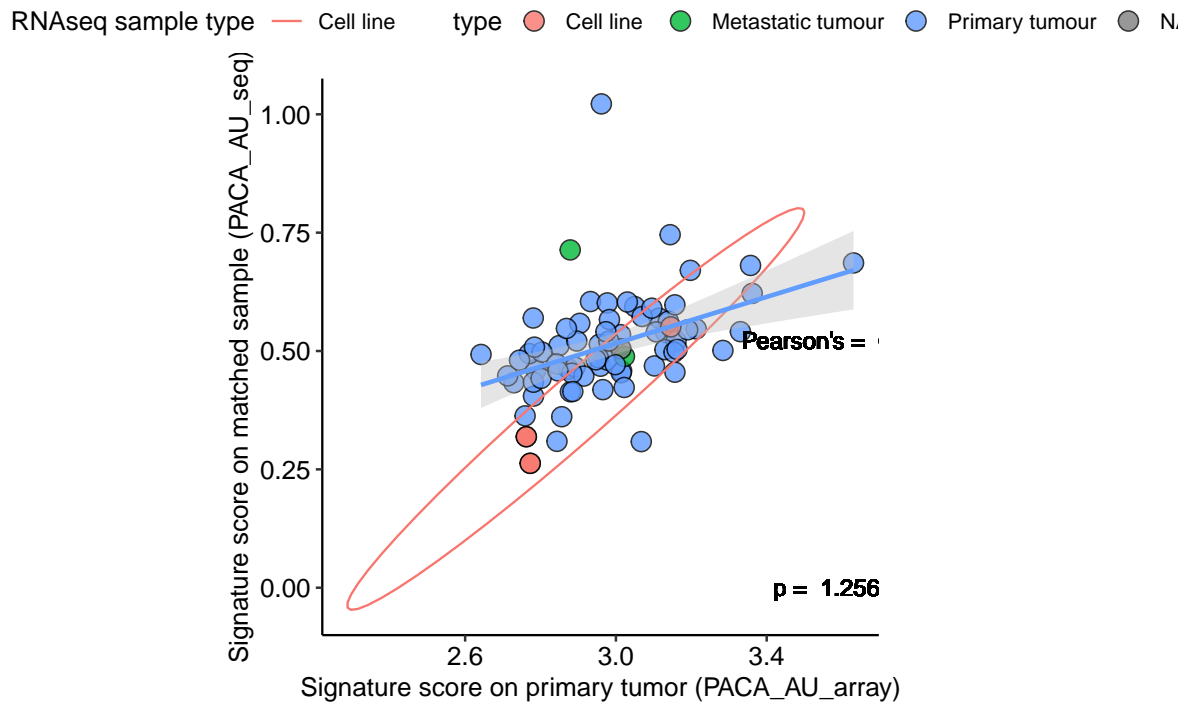
```
## 'geom_smooth()' using formula 'y ~ x'
```

Moffitt.F13_NormalStroma.top100



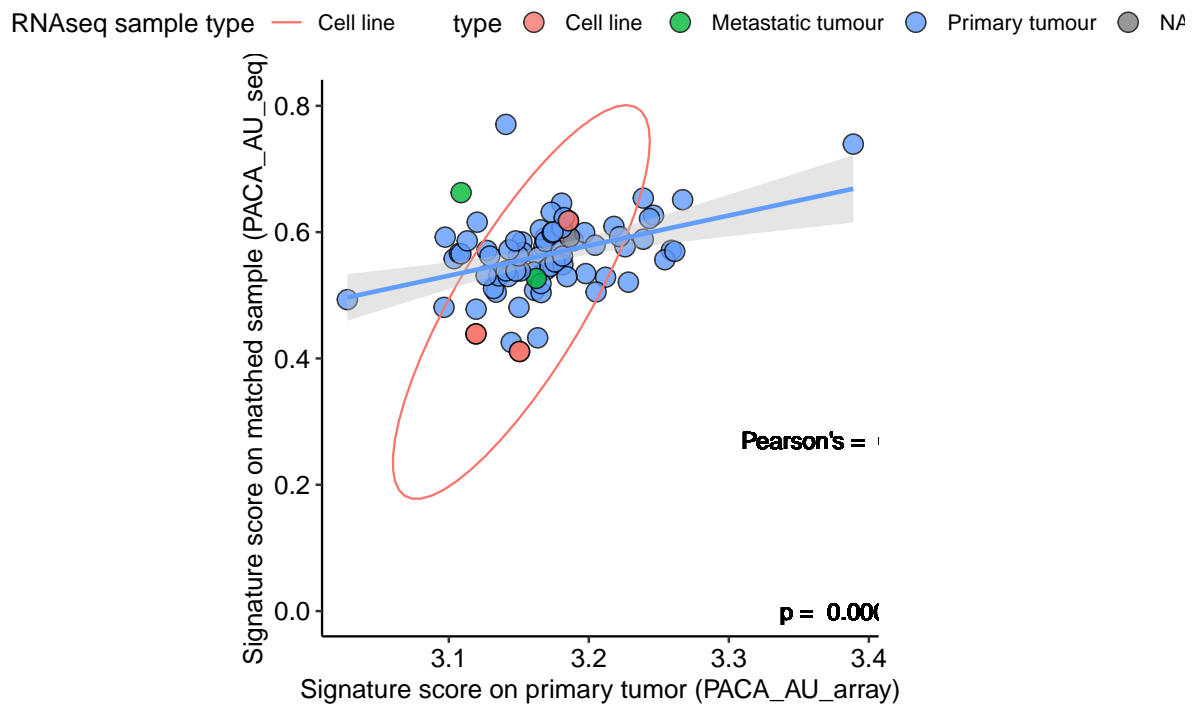
```
## 'geom_smooth()' using formula 'y ~ x'
```

Moffitt.F14.top25



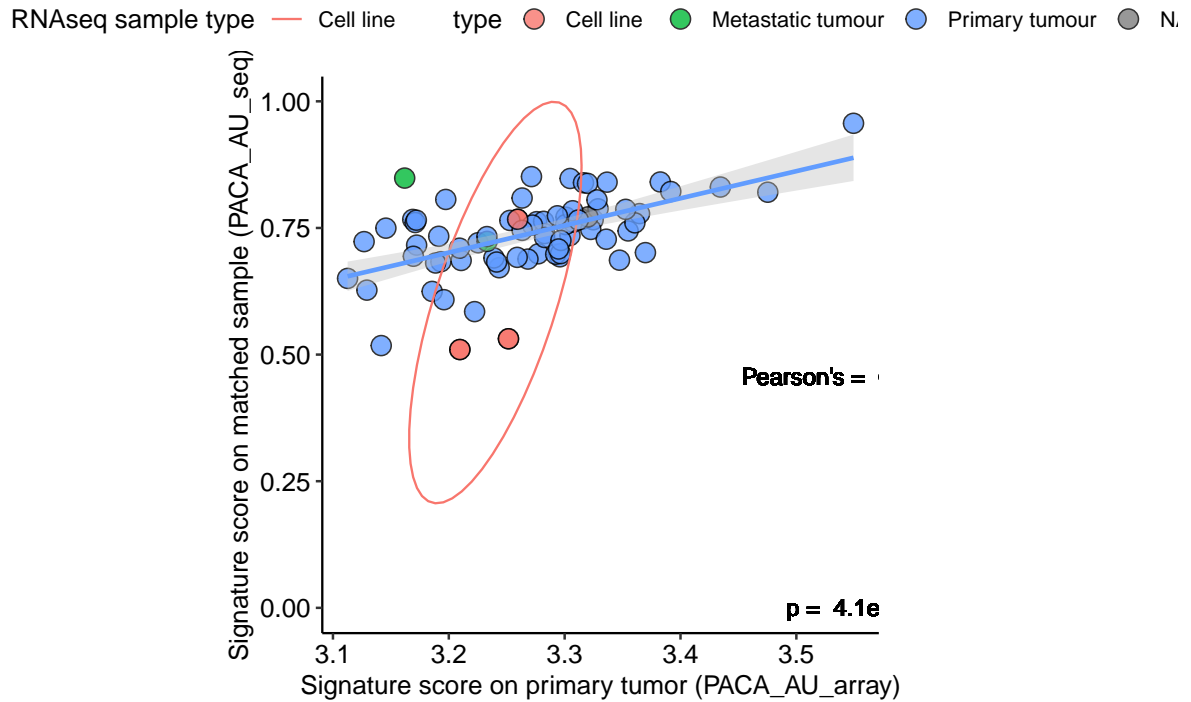
'geom_smooth()' using formula 'y ~ x'

Moffitt.F14.top250



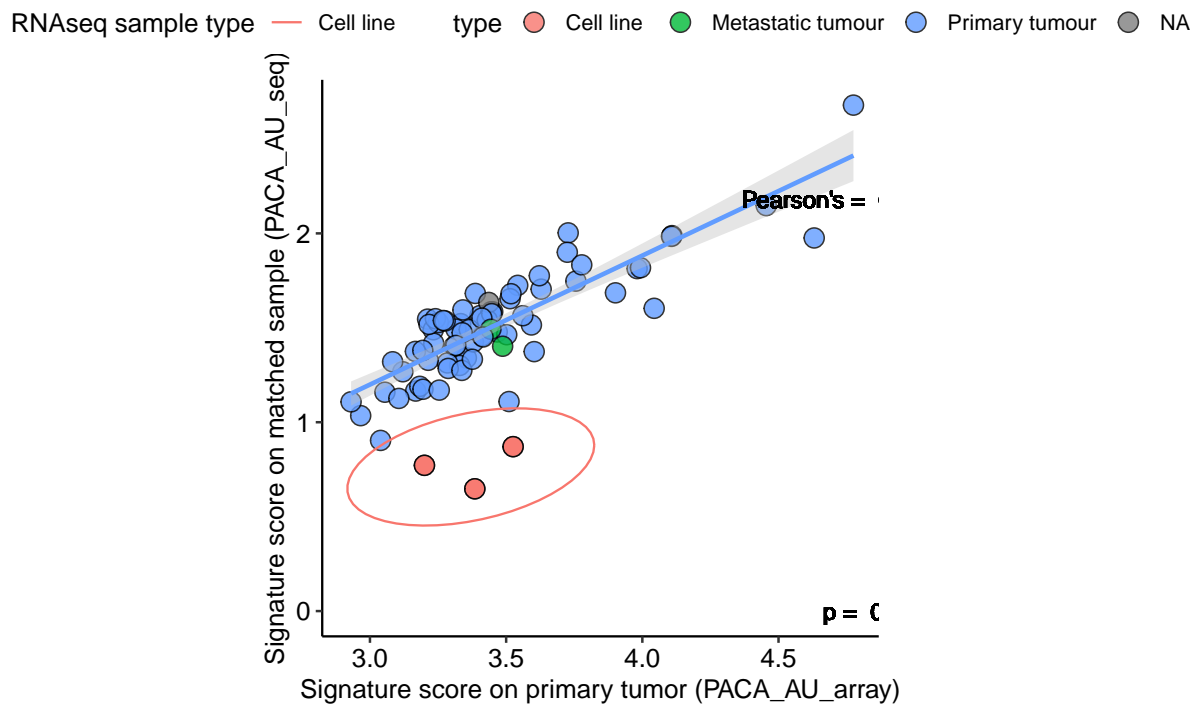
'geom_smooth()' using formula 'y ~ x'

Moffitt.F14.top100



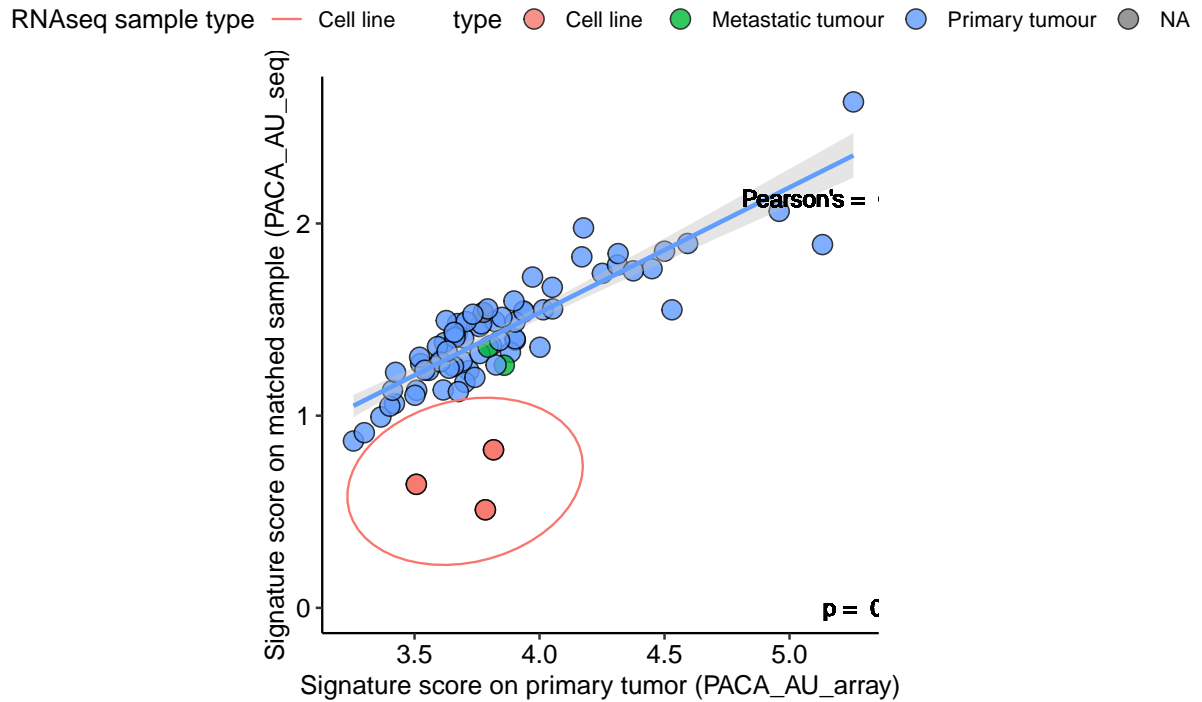
```
## 'geom_smooth()' using formula 'y ~ x'
```

CIBERSORT.B.cells.naive



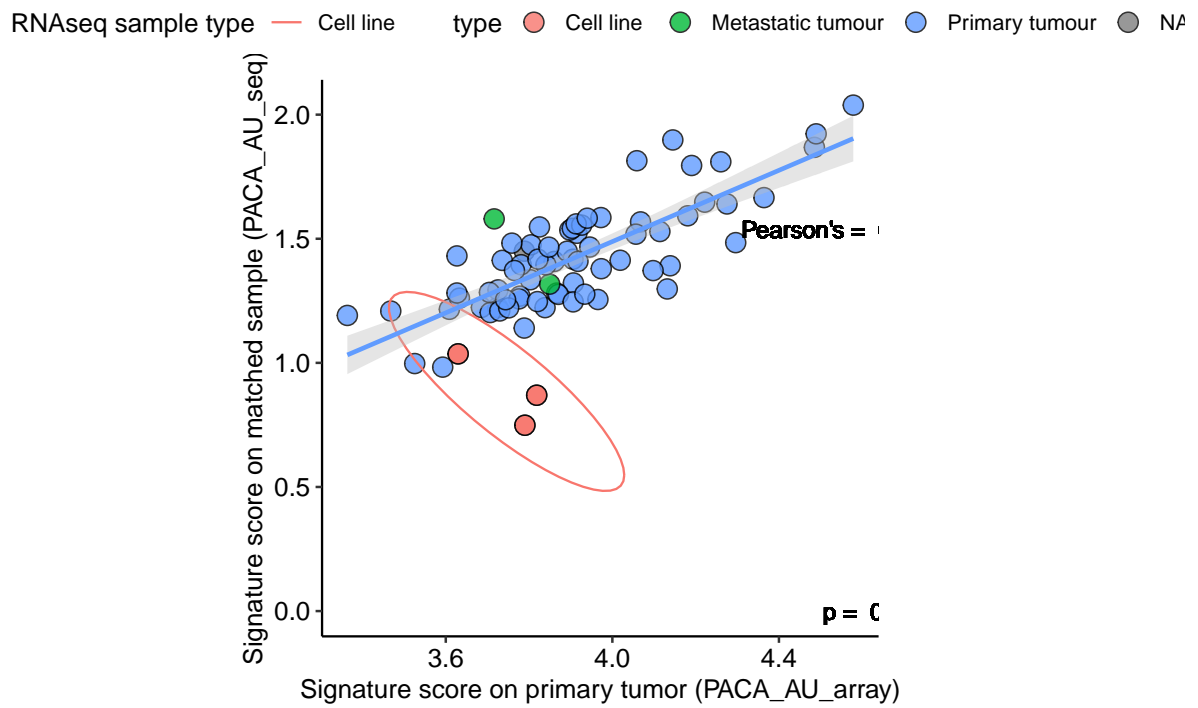
```
## 'geom_smooth()' using formula 'y ~ x'
```

CIBERSORT.B.cells.memory



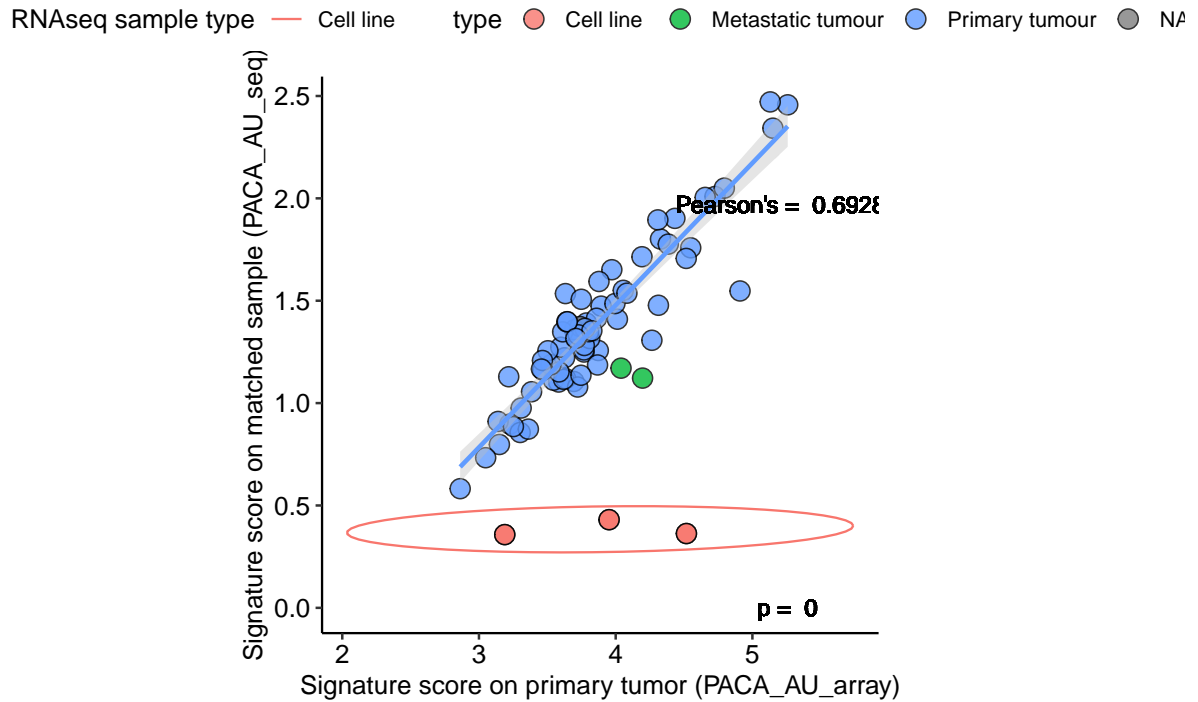
```
## 'geom_smooth()' using formula 'y ~ x'
```

CIBERSORT.Plasma.cells



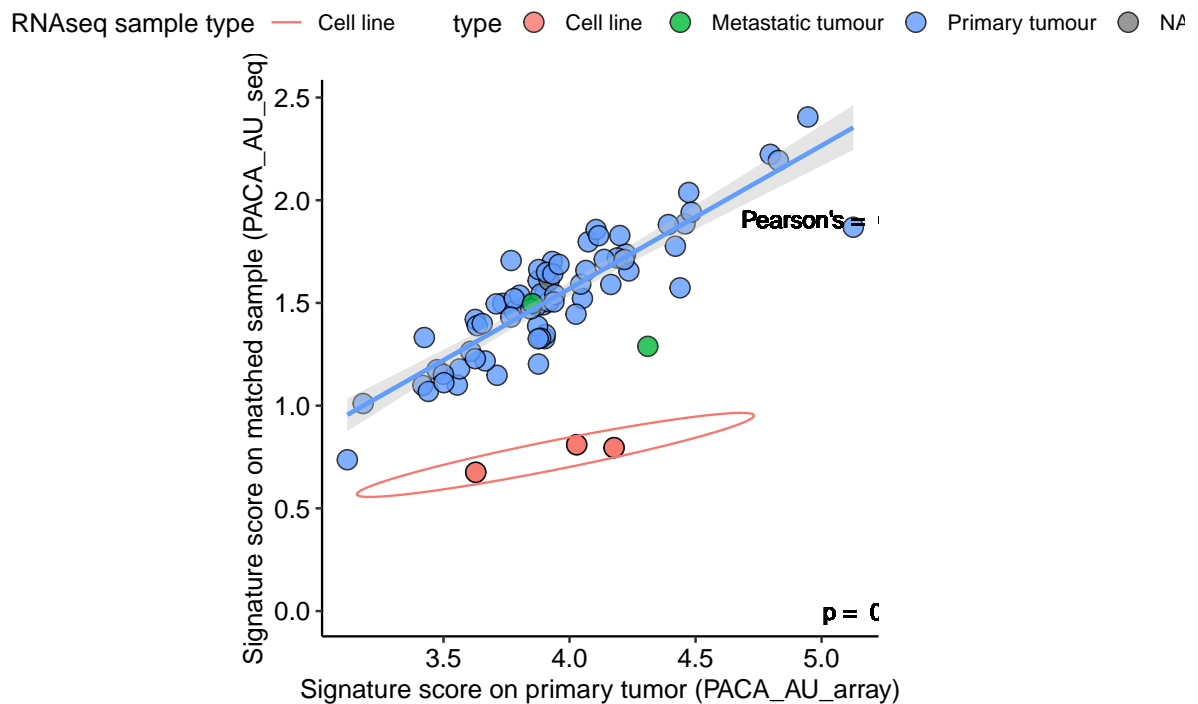
```
## 'geom_smooth()' using formula 'y ~ x'
```

CIBERSORT.T.cells.CD8



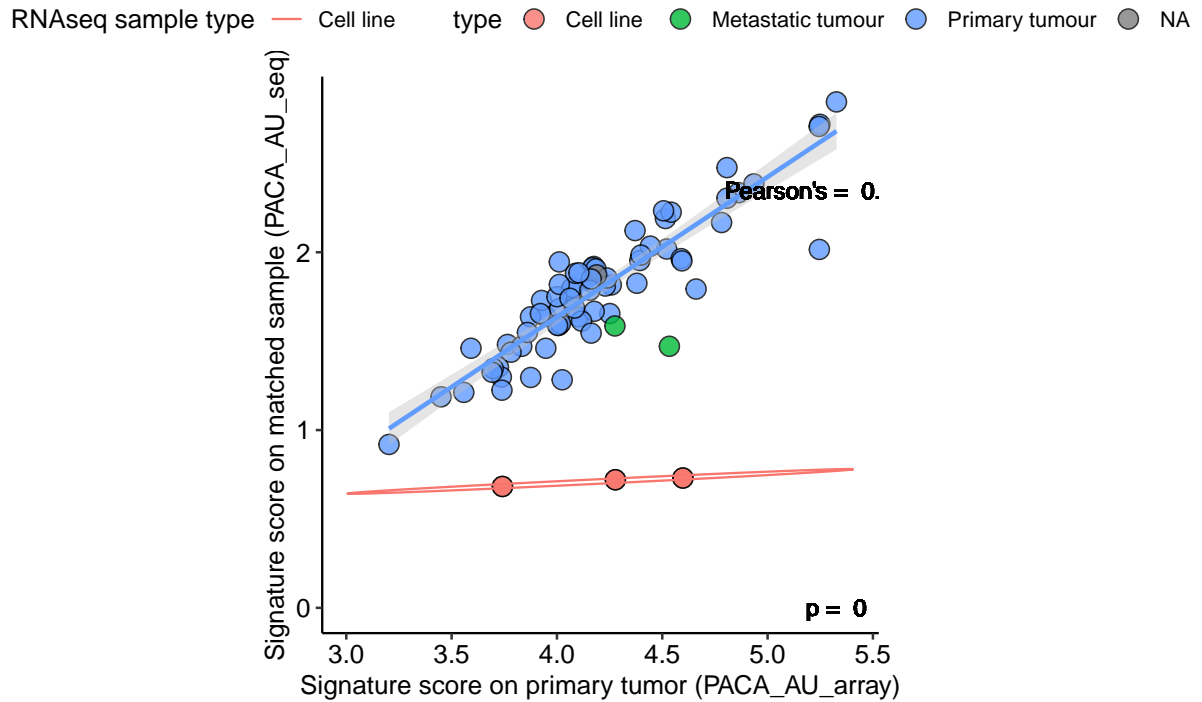
```
## 'geom_smooth()' using formula 'y ~ x'
```

CIBERSORT.T.cells.CD4.naive



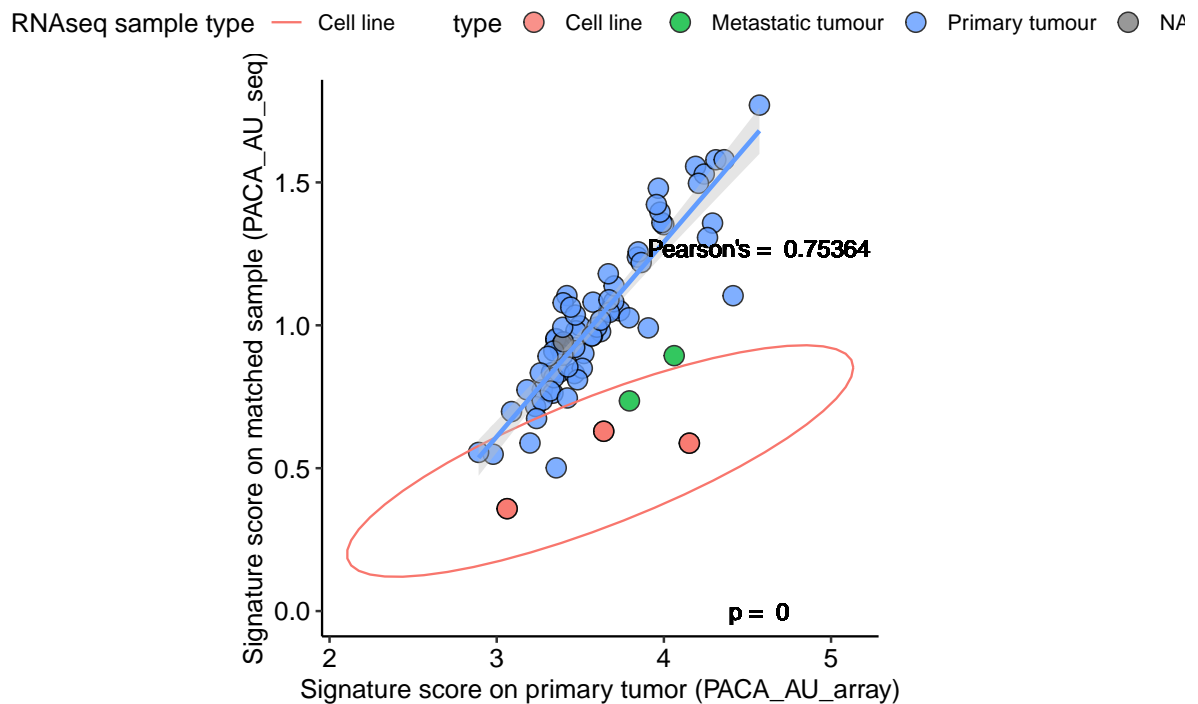
```
## 'geom_smooth()' using formula 'y ~ x'
```

CIBERSORT.T.cells.CD4.memory.resting



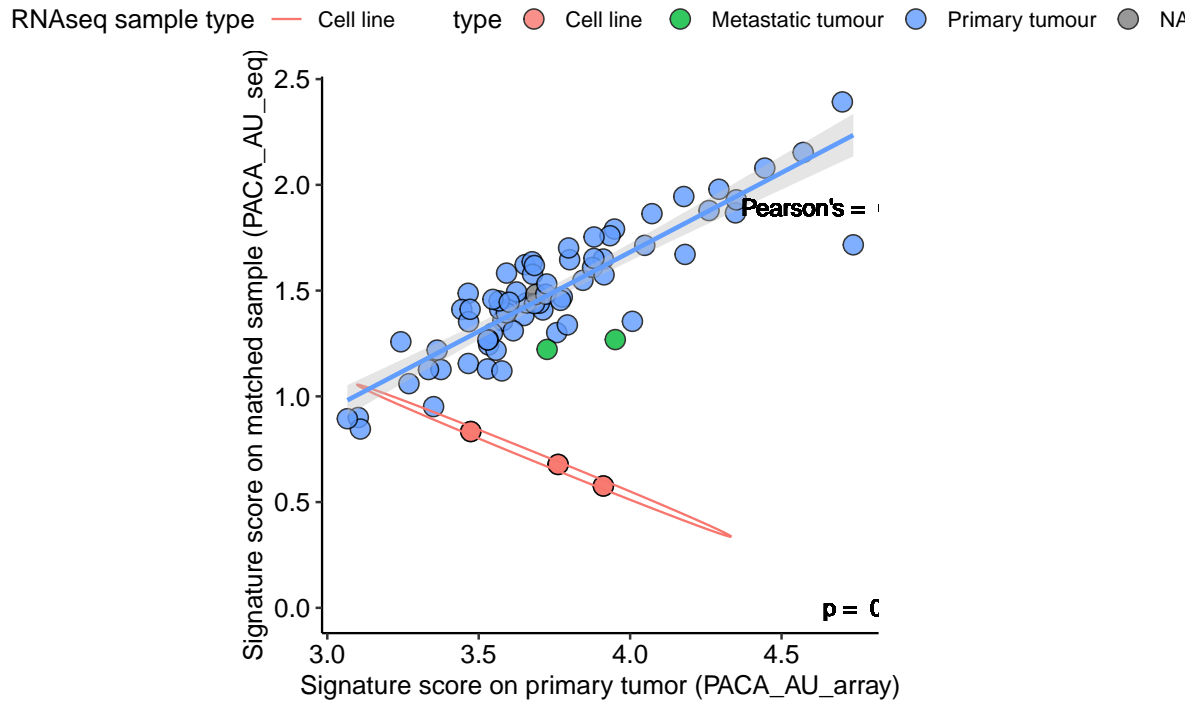
```
## 'geom_smooth()' using formula 'y ~ x'
```

CIBERSORT.T.cells.CD4.memory.activated



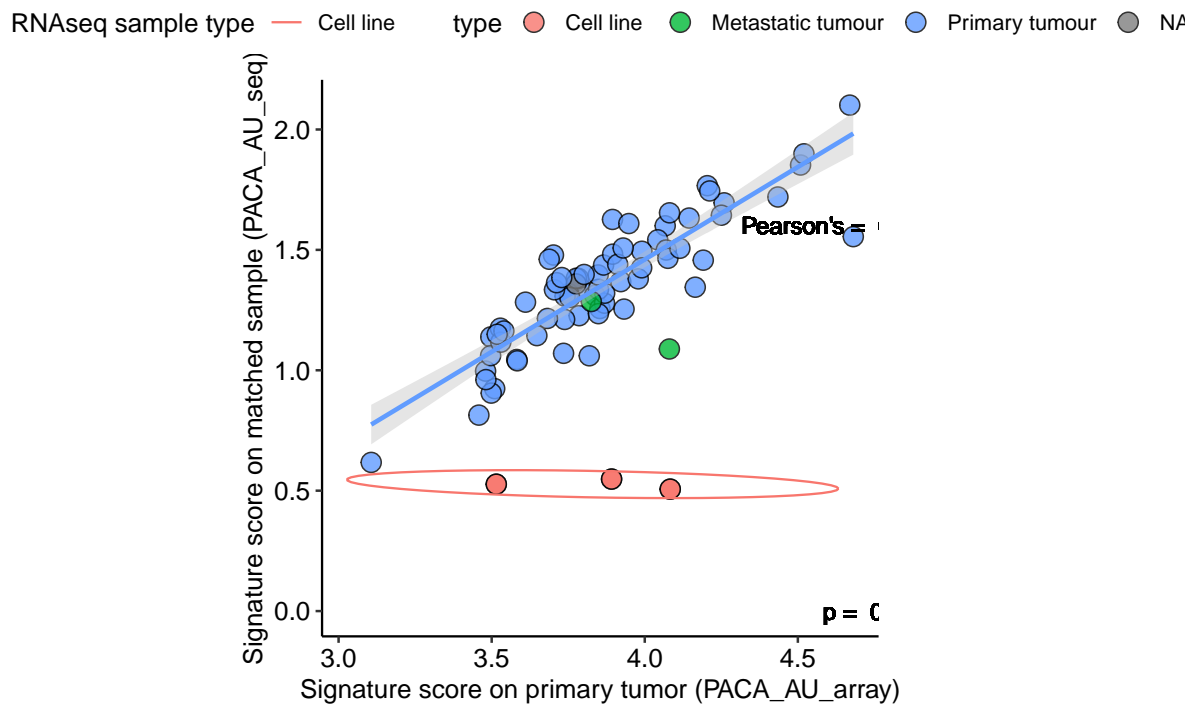
```
## 'geom_smooth()' using formula 'y ~ x'
```

CIBERSORT.T.cells.follicular.helper



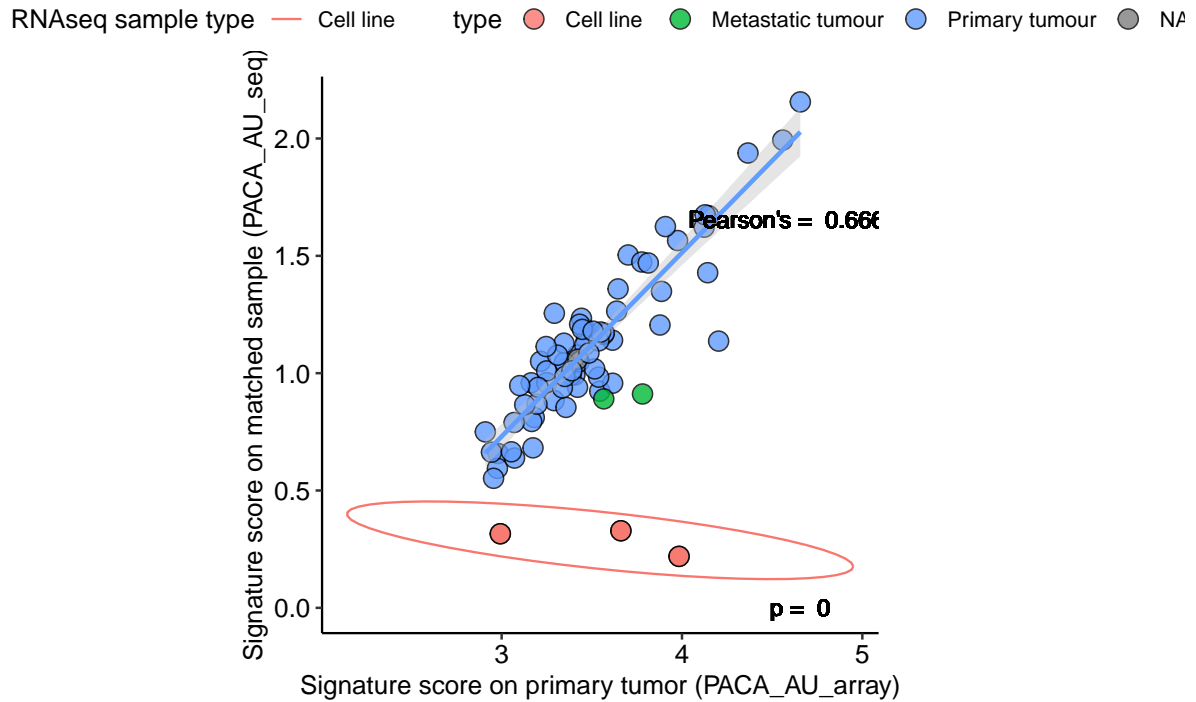
```
## 'geom_smooth()' using formula 'y ~ x'
```

CIBERSORT.T.cells.regulatory..Tregs.



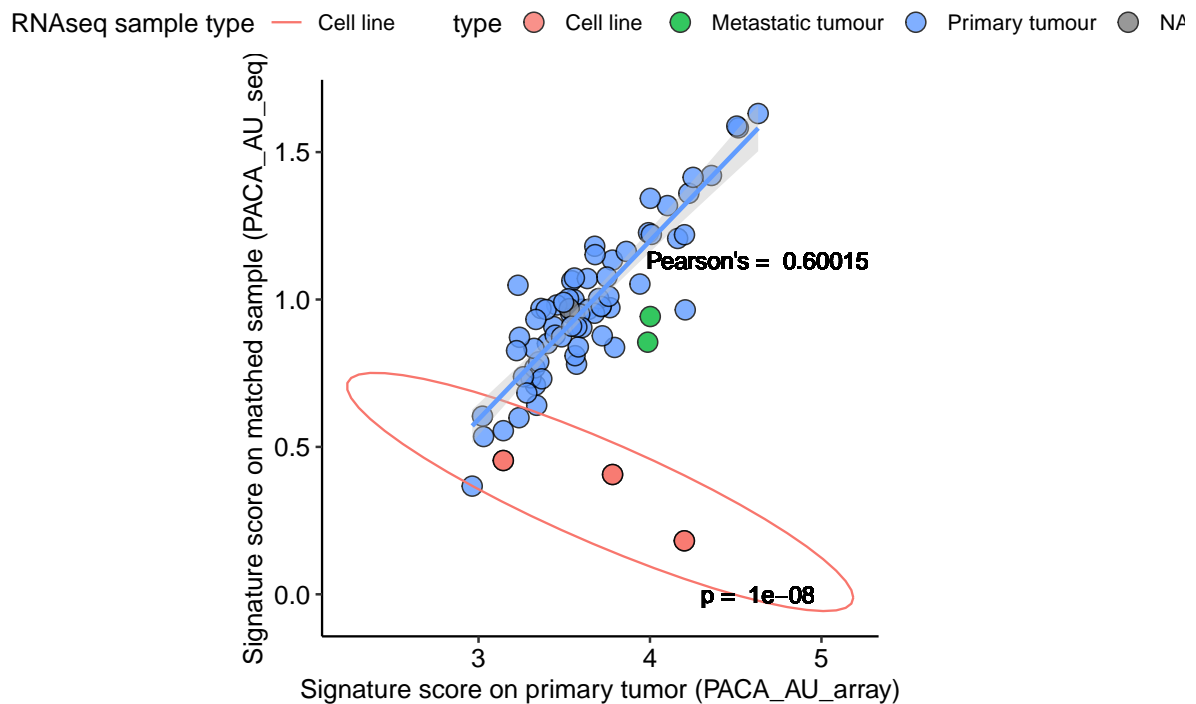
```
## 'geom_smooth()' using formula 'y ~ x'
```

CIBERSORT.T.cells.gamma.delta



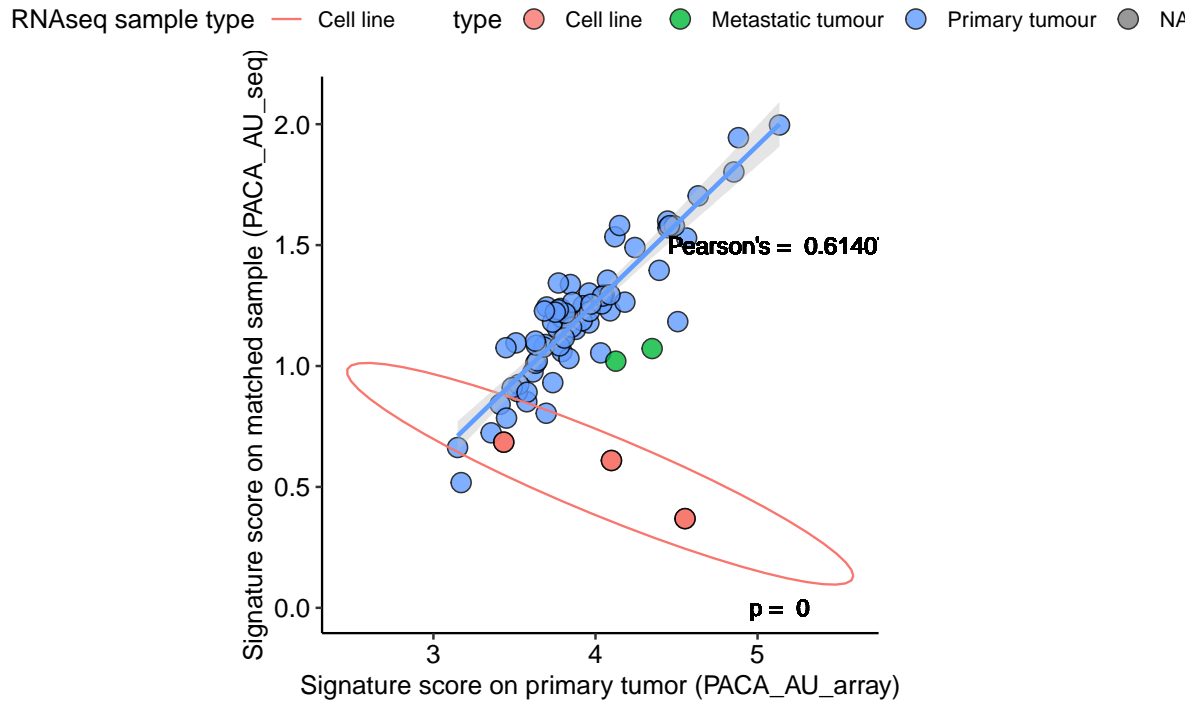
```
## 'geom_smooth()' using formula 'y ~ x'
```

CIBERSORT.NK.cells.resting



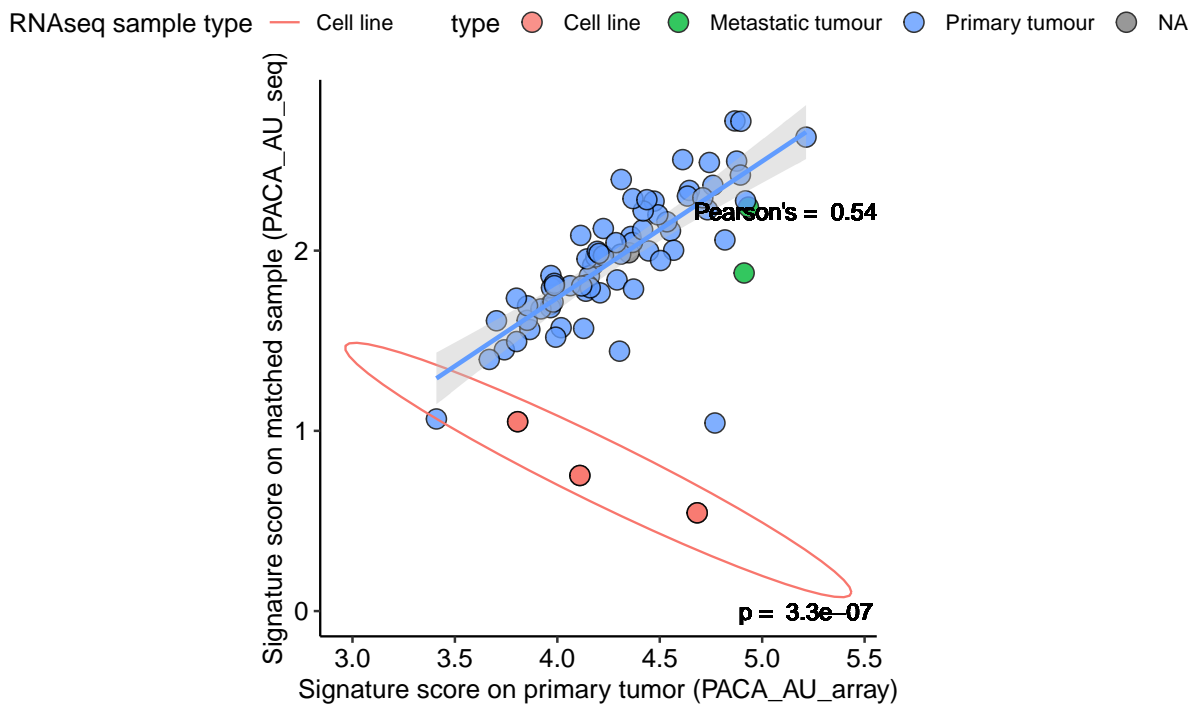
```
## 'geom_smooth()' using formula 'y ~ x'
```

CIBERSORT.NK.cells.activated



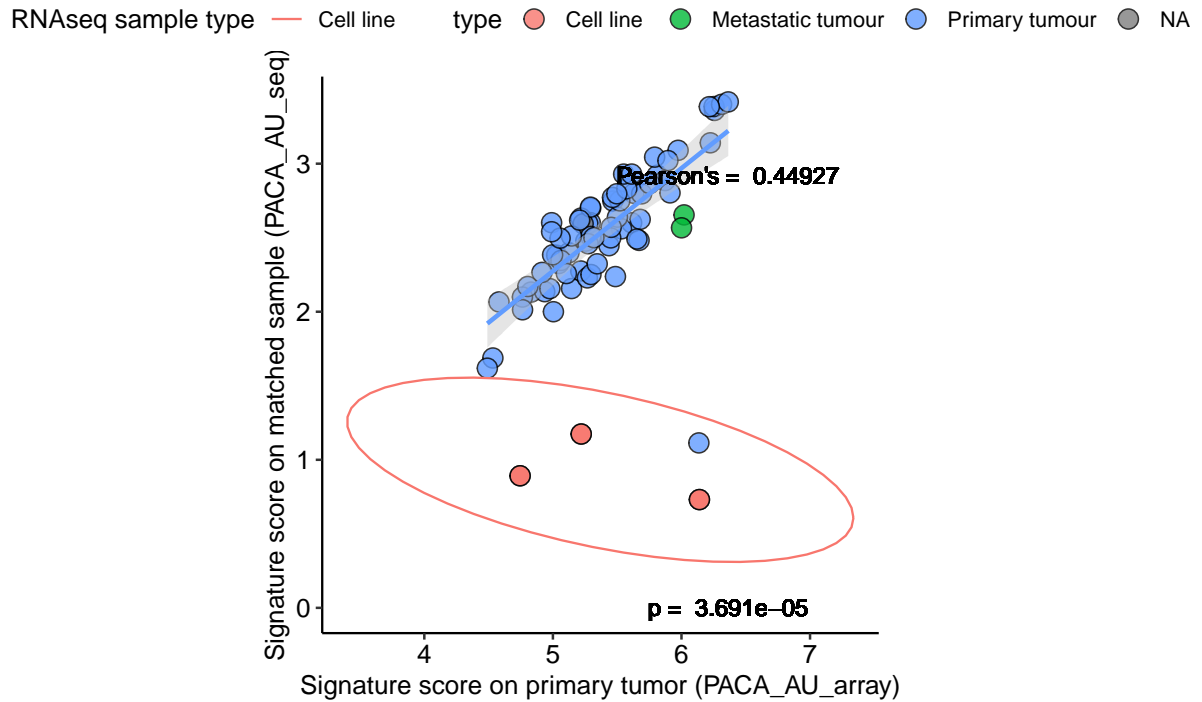
```
## 'geom_smooth()' using formula 'y ~ x'
```

CIBERSORT.Monocytes



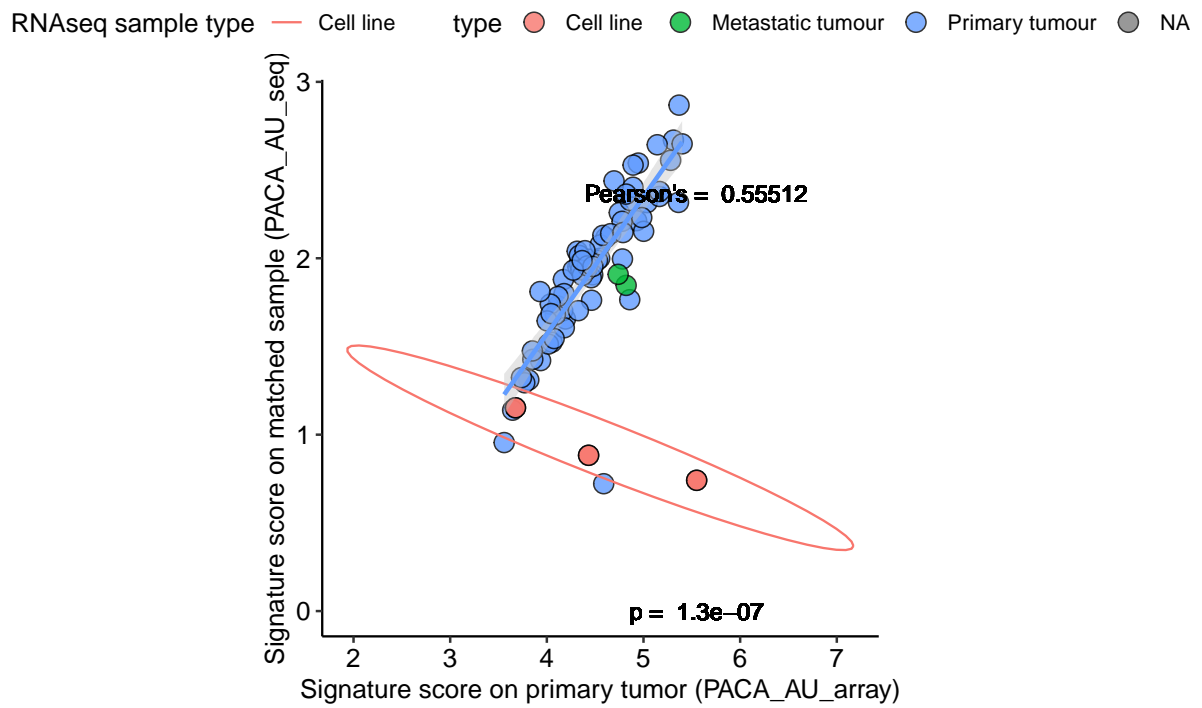
```
## 'geom_smooth()' using formula 'y ~ x'
```

CIBERSORT.Macrophages.M0



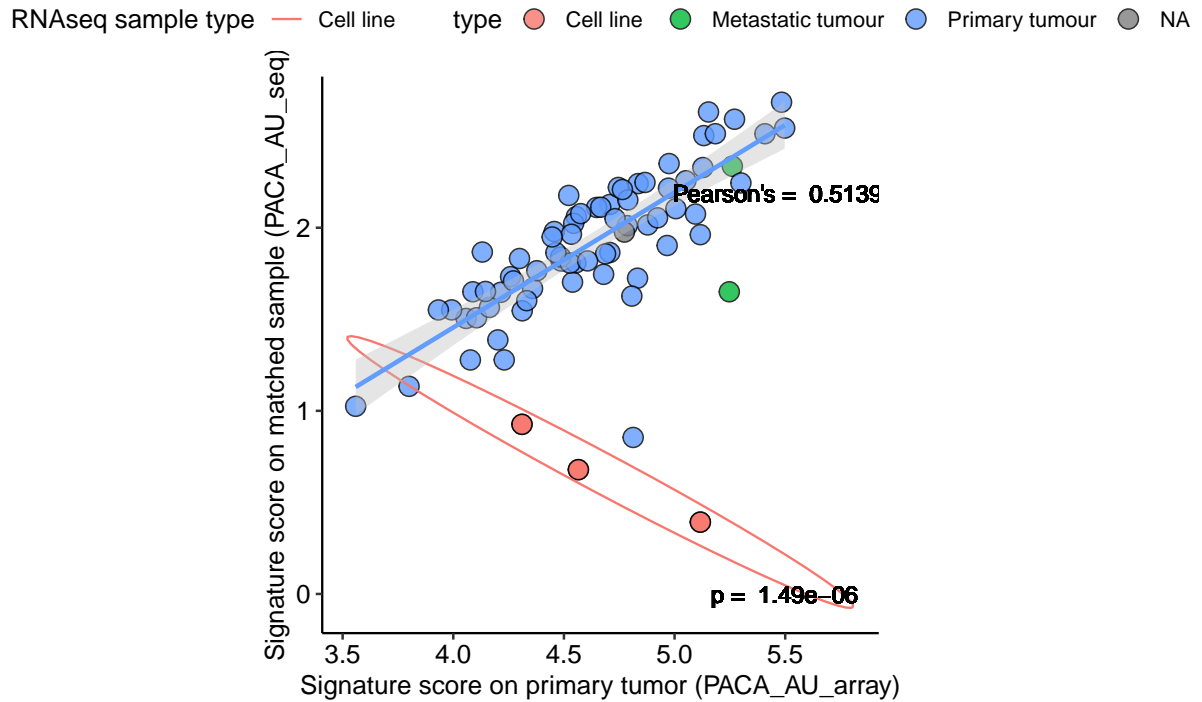
'geom_smooth()' using formula 'y ~ x'

CIBERSORT.Macrophages.M1



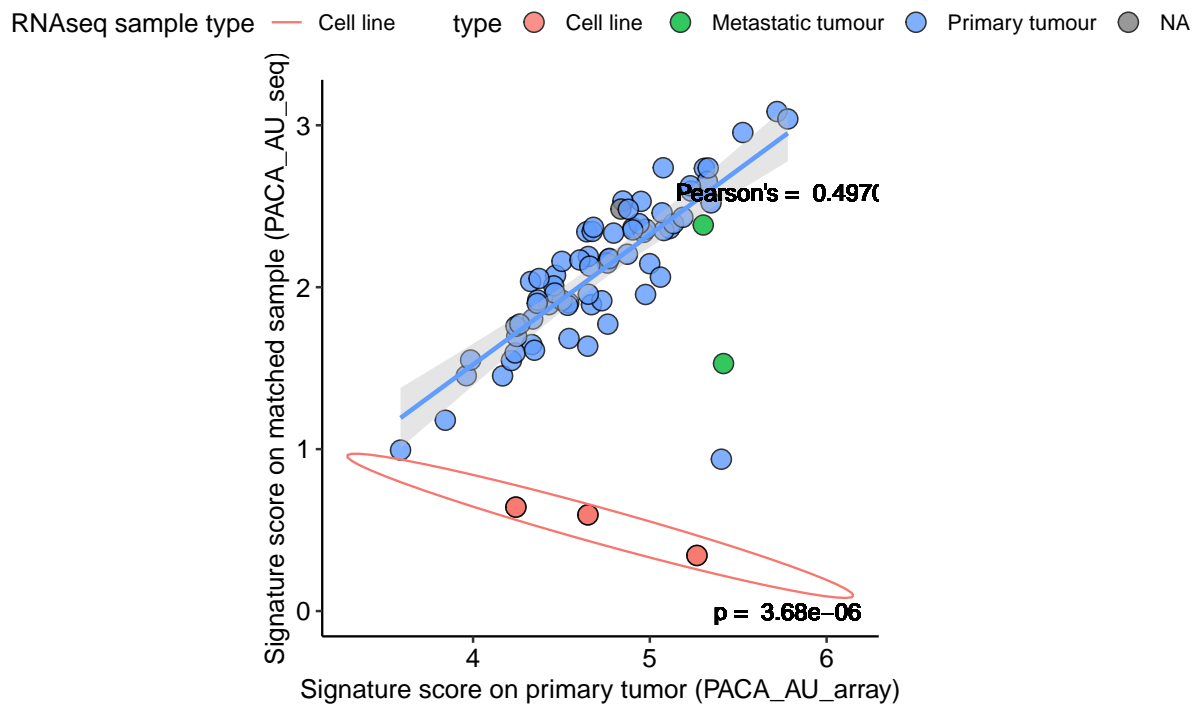
'geom_smooth()' using formula 'y ~ x'

CIBERSORT.Macrophages.M2



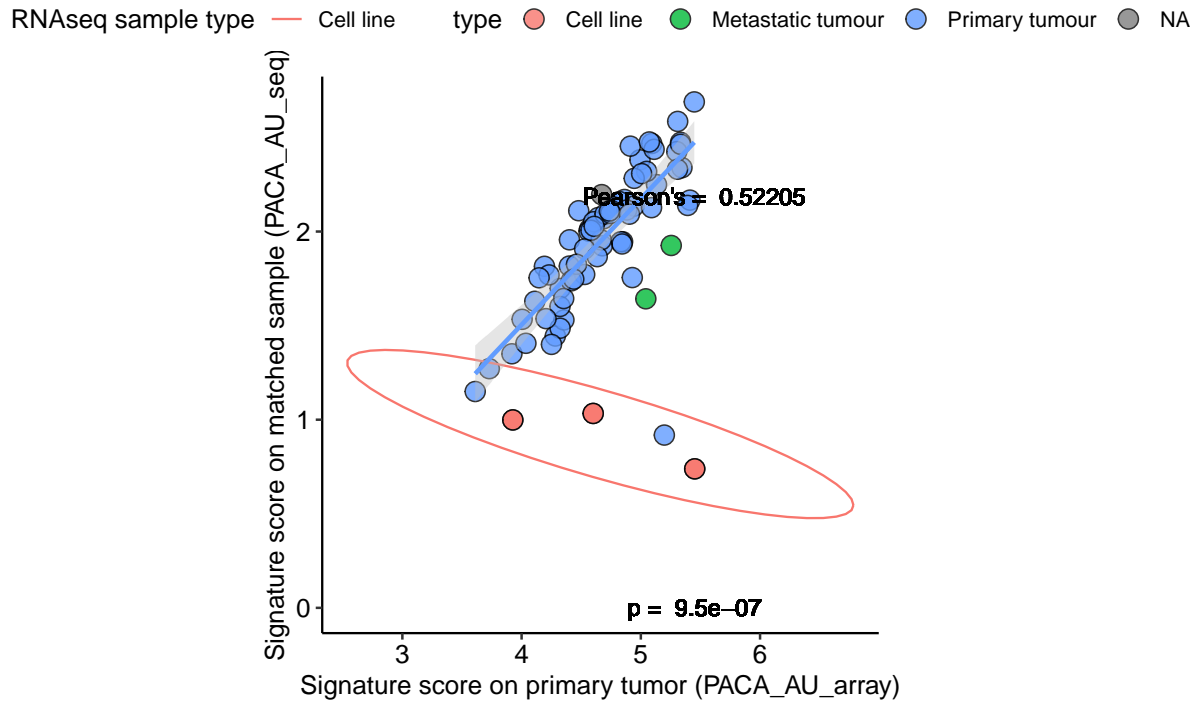
```
## 'geom_smooth()' using formula 'y ~ x'
```

CIBERSORT.Dendritic.cells.resting



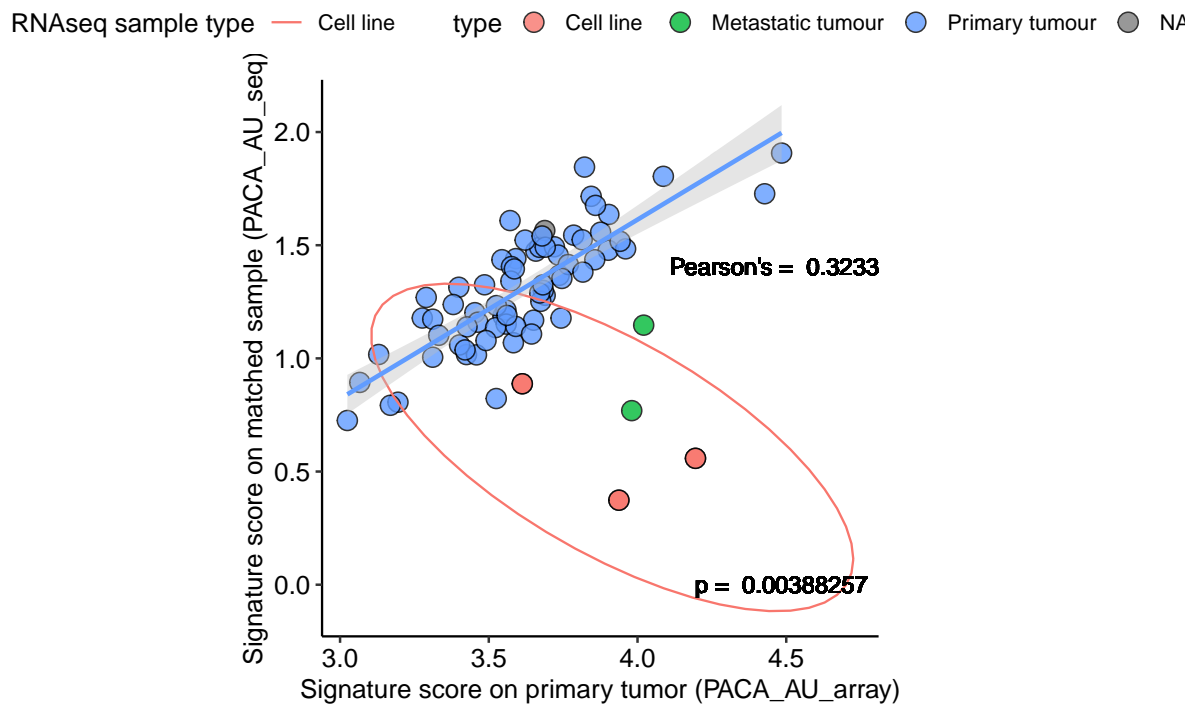
```
## 'geom_smooth()' using formula 'y ~ x'
```

CIBERSORT.Dendritic.cells.activated



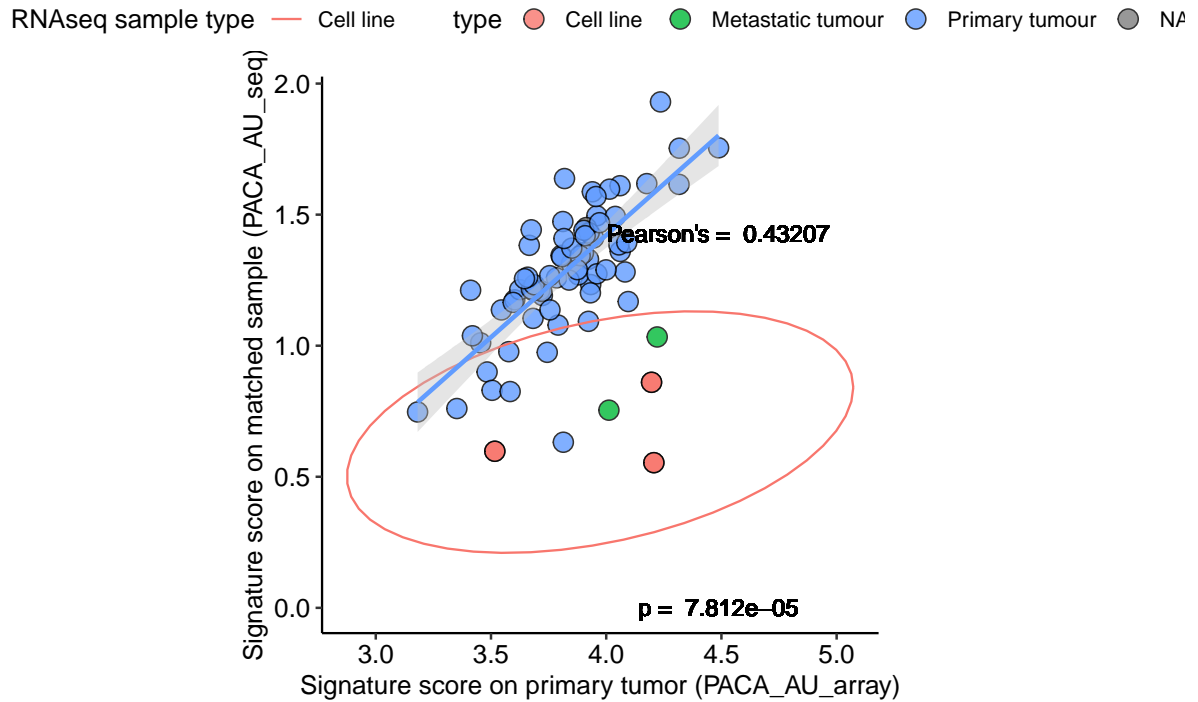
```
## 'geom_smooth()' using formula 'y ~ x'
```

CIBERSORT.Mast.cells.resting



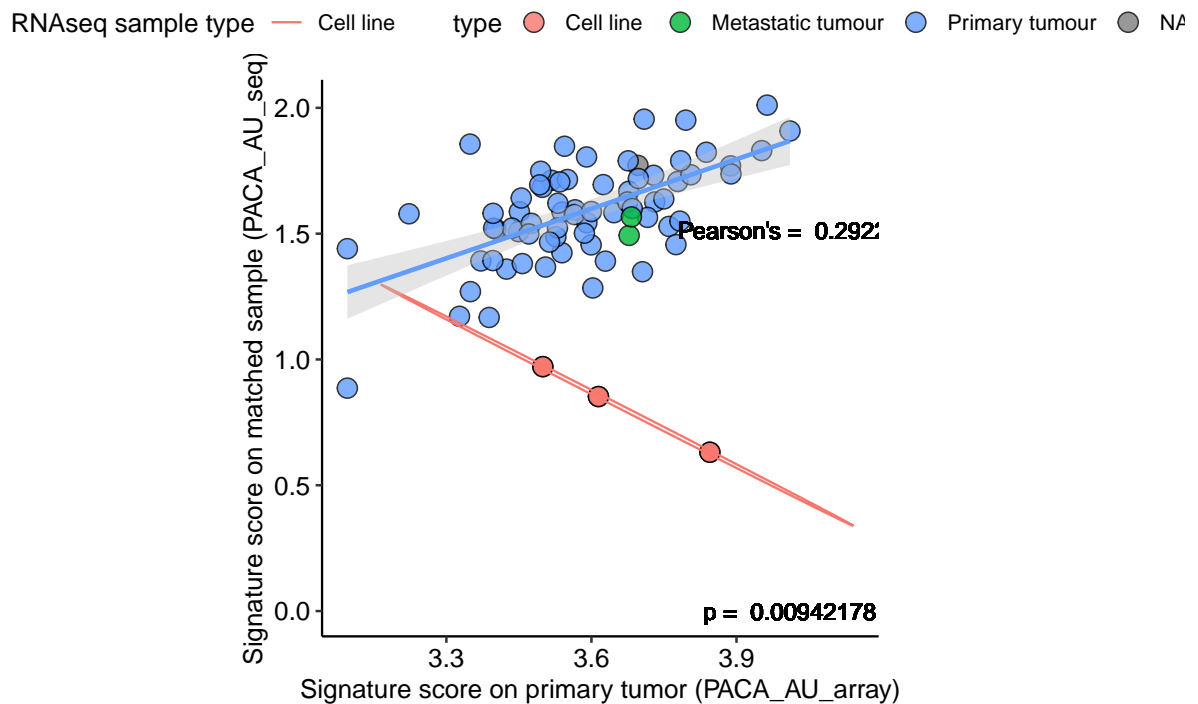
```
## 'geom_smooth()' using formula 'y ~ x'
```

CIBERSORT.Mast.cells.activated



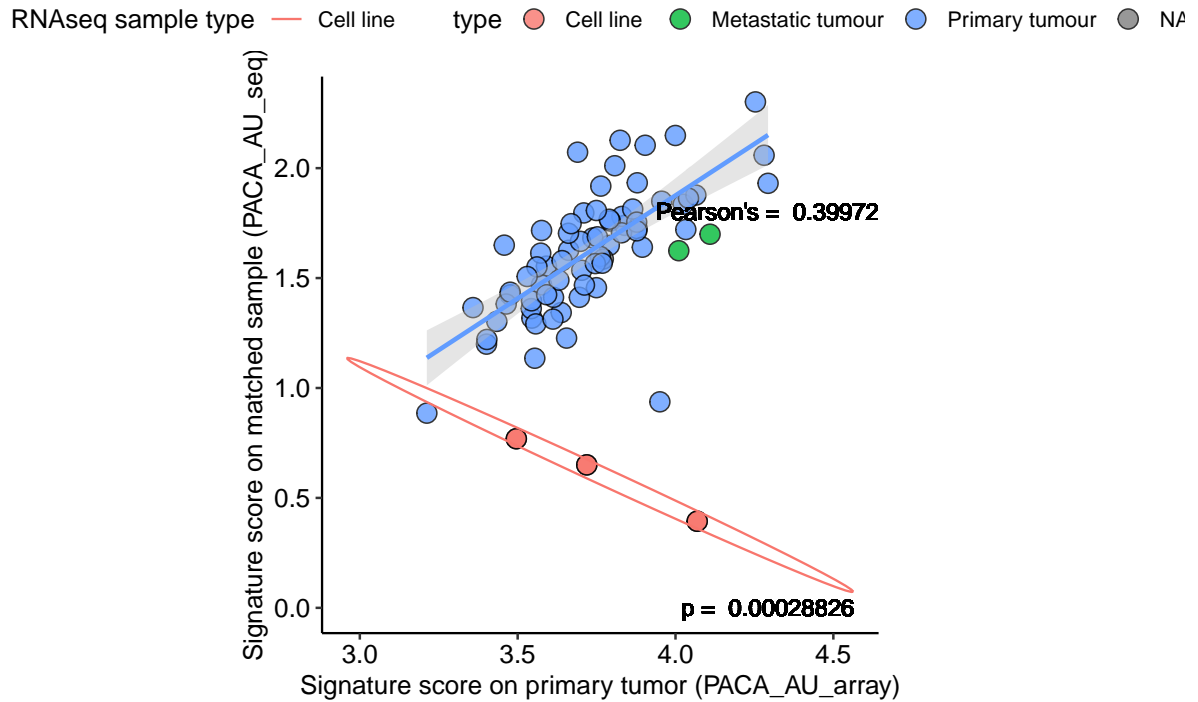
```
## 'geom_smooth()' using formula 'y ~ x'
```

CIBERSORT.Eosinophils



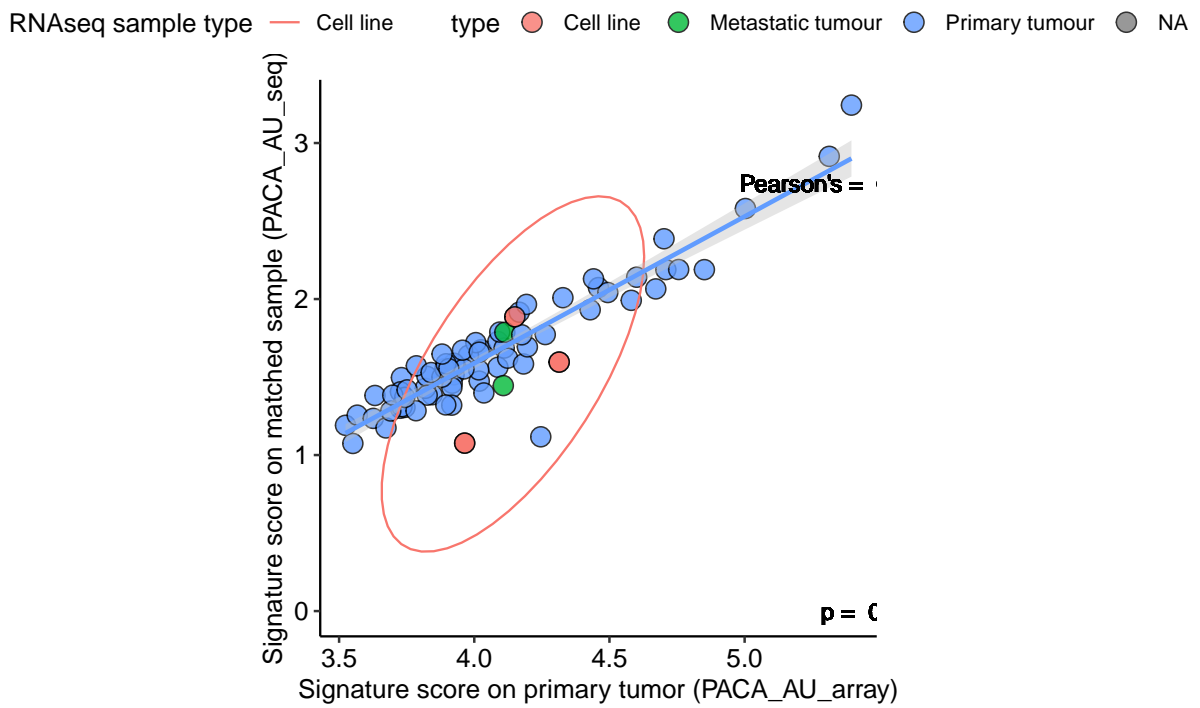
```
## 'geom_smooth()' using formula 'y ~ x'
```

CIBERSORT.Neutrophils



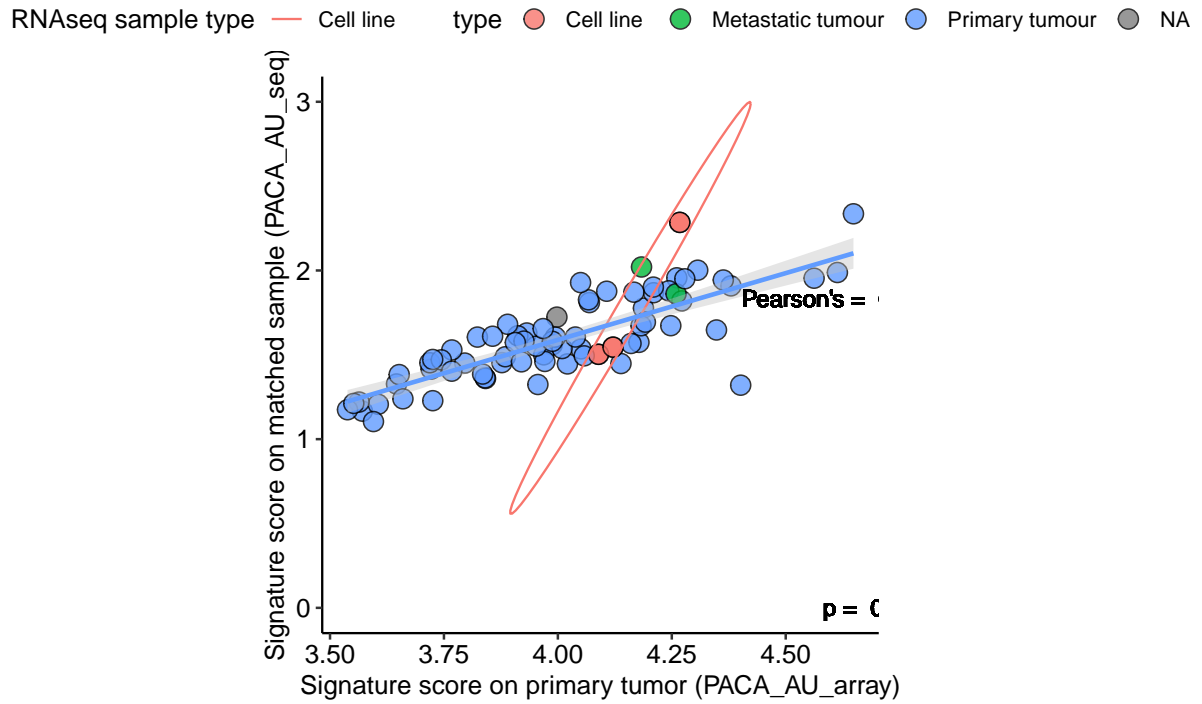
'geom_smooth()' using formula 'y ~ x'

Notta.BasalA



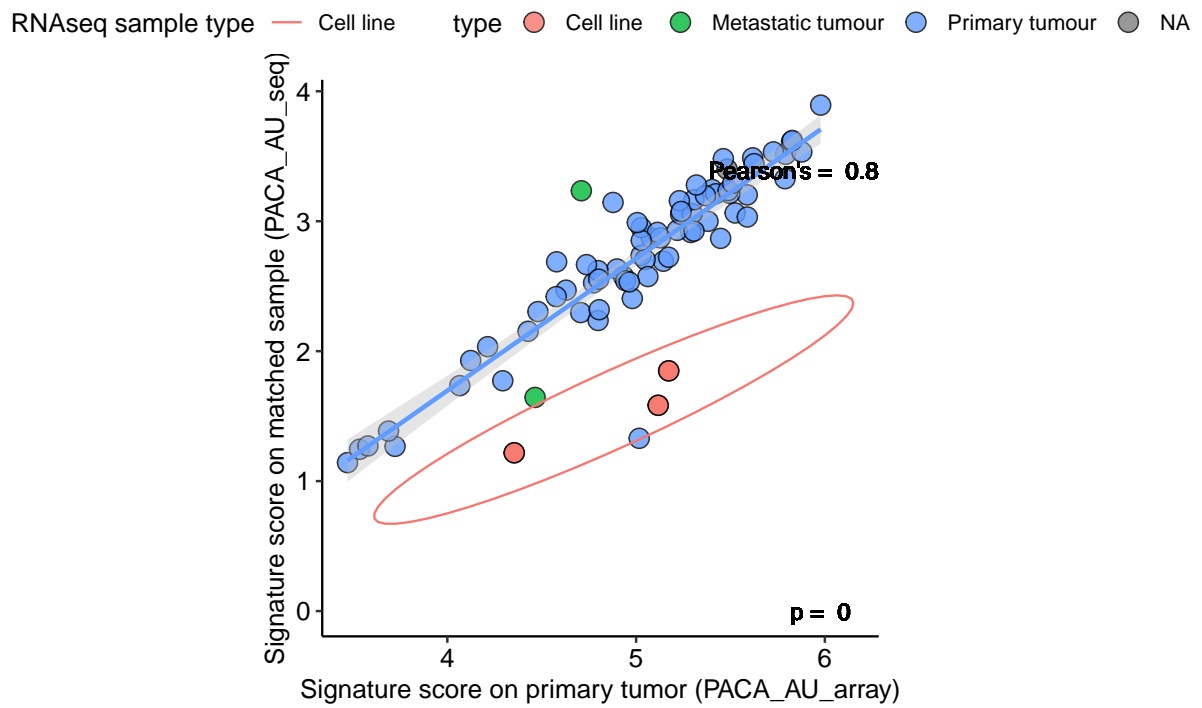
'geom_smooth()' using formula 'y ~ x'

Notta.BasalB



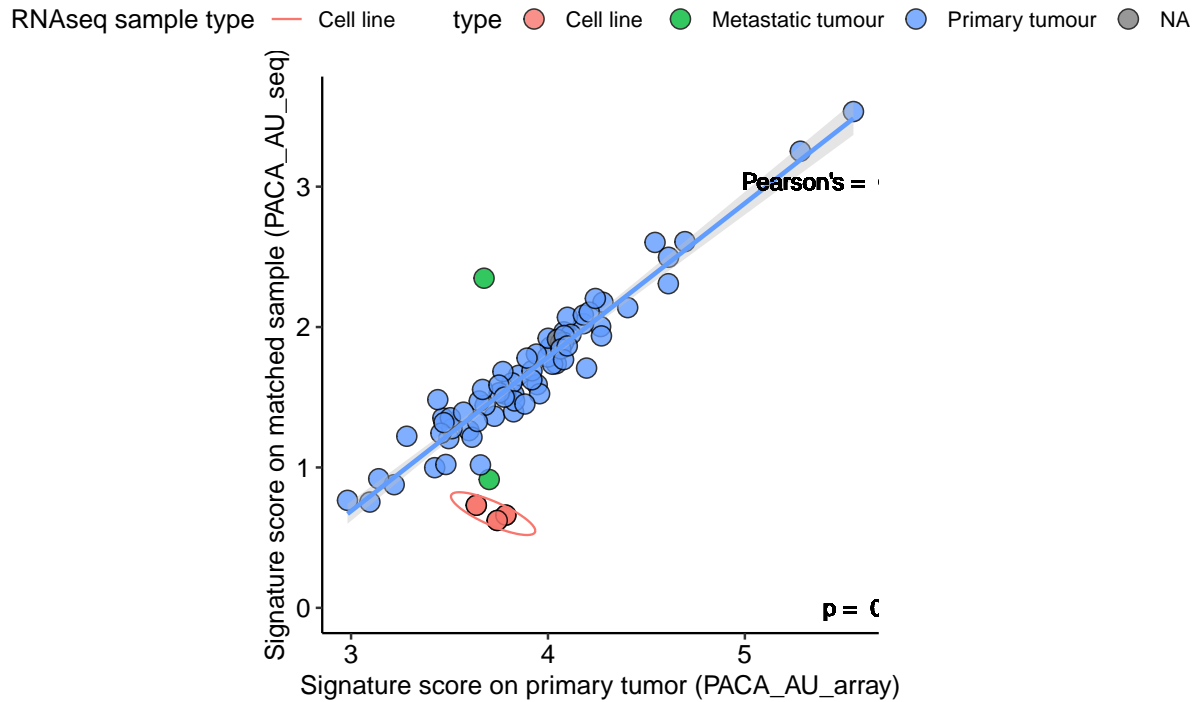
```
## 'geom_smooth()' using formula 'y ~ x'
```

Notta.ClassicalA



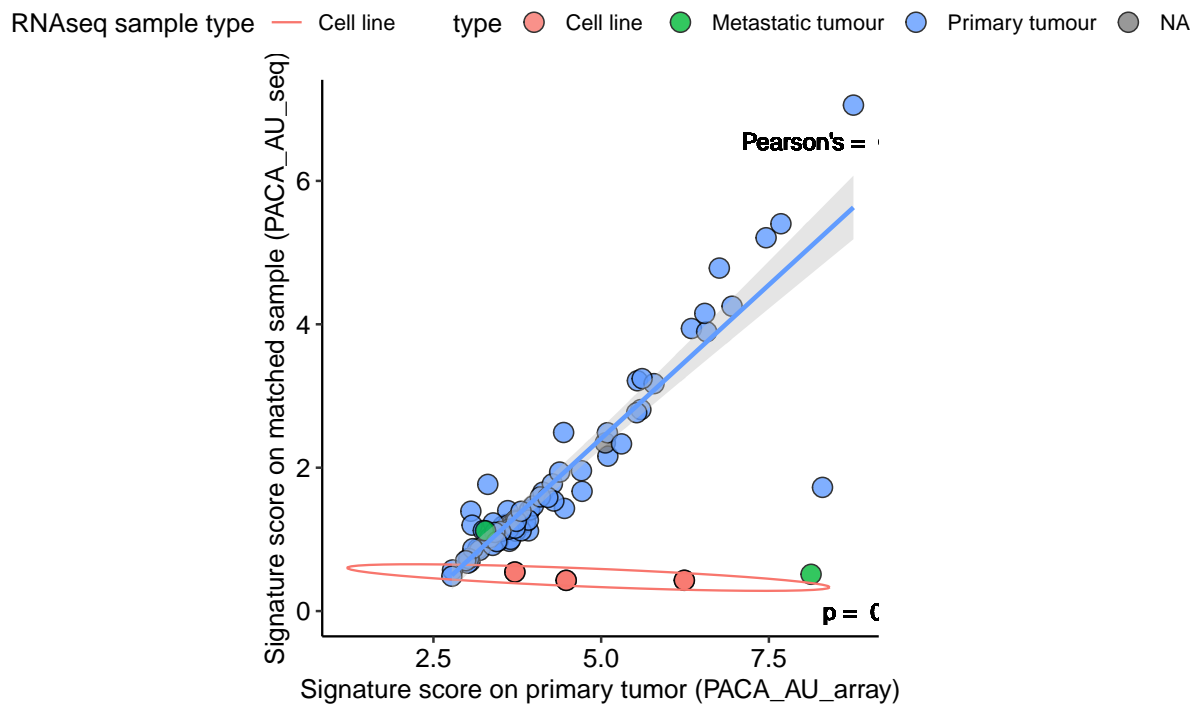
```
## 'geom_smooth()' using formula 'y ~ x'
```

Notta.ClassicalB



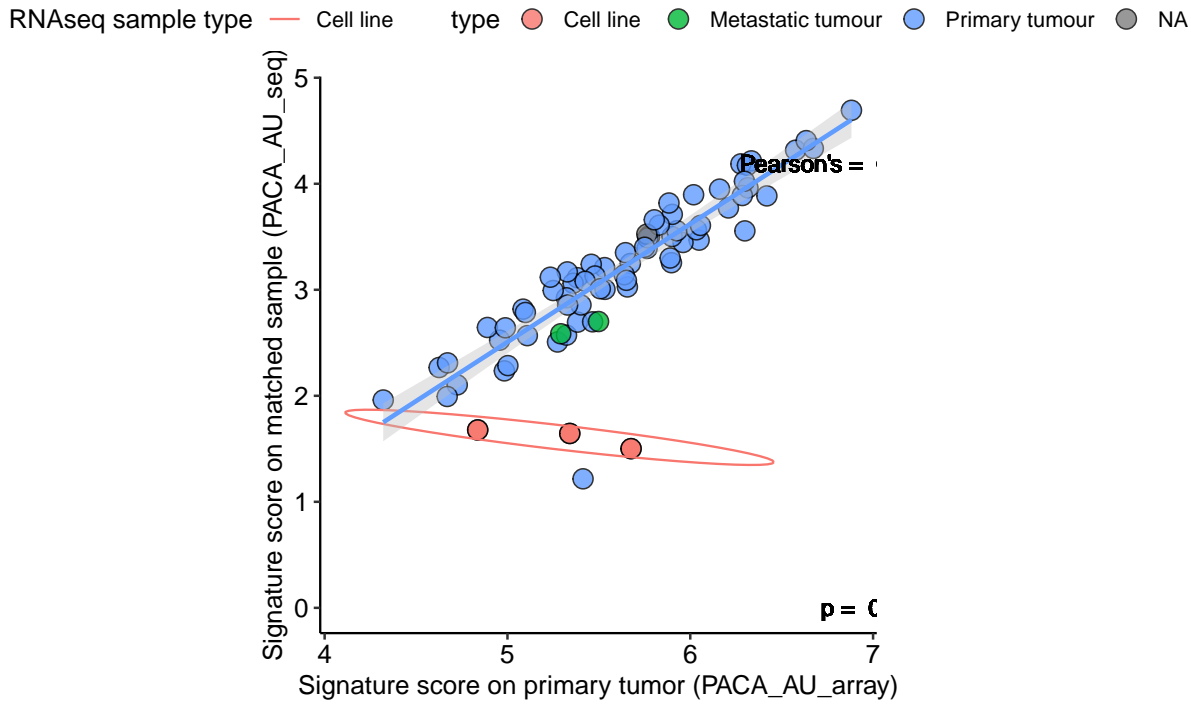
```
## 'geom_smooth()' using formula 'y ~ x'
```

ADEX_unique



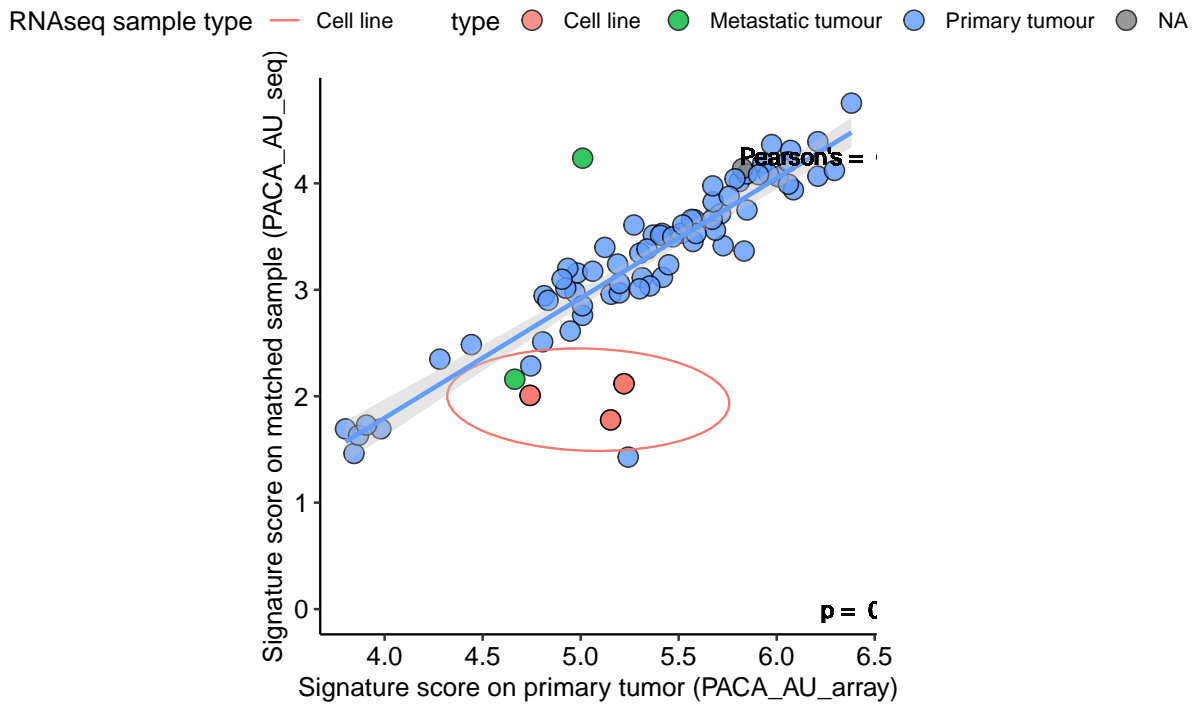
```
## 'geom_smooth()' using formula 'y ~ x'
```

Immunogenic_unique



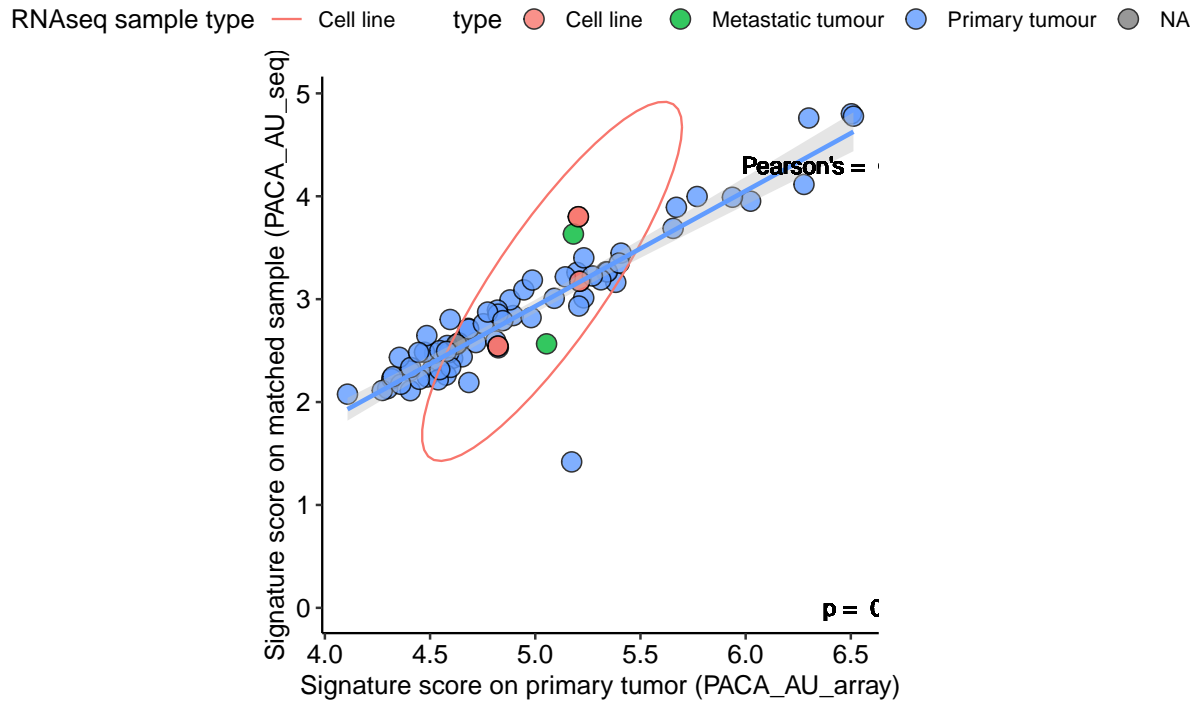
```
## 'geom_smooth()' using formula 'y ~ x'
```

Progenitor_unique



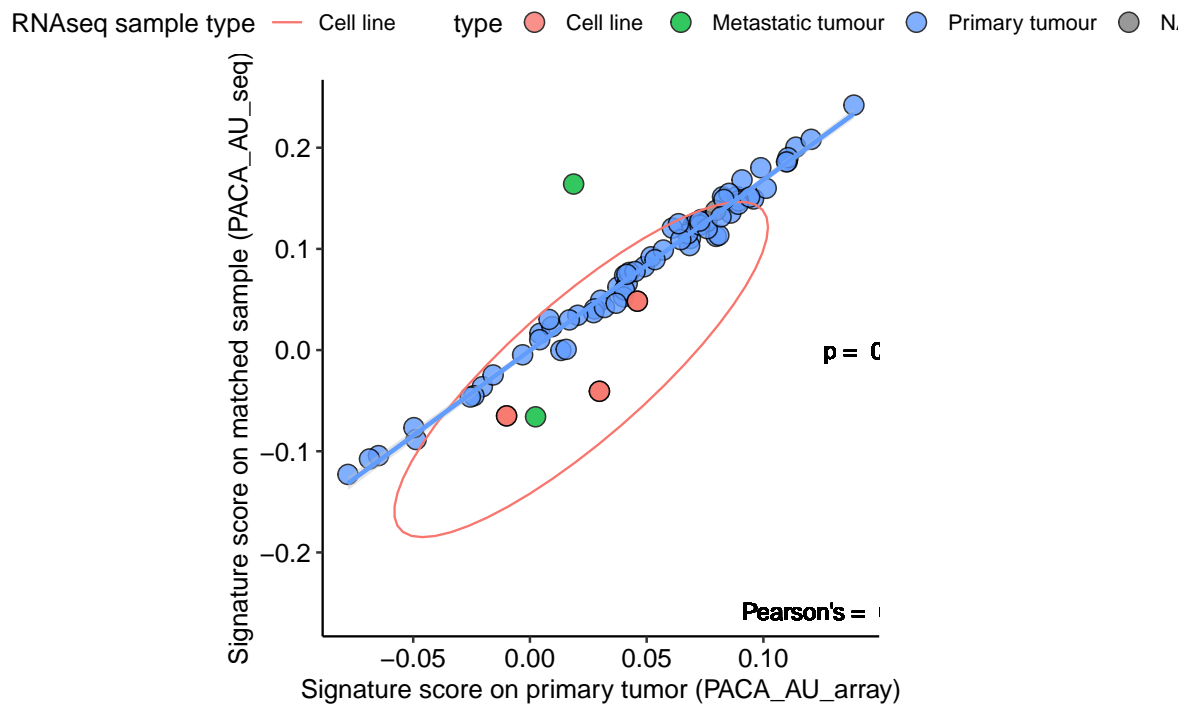
```
## 'geom_smooth()' using formula 'y ~ x'
```

Squamous_unique

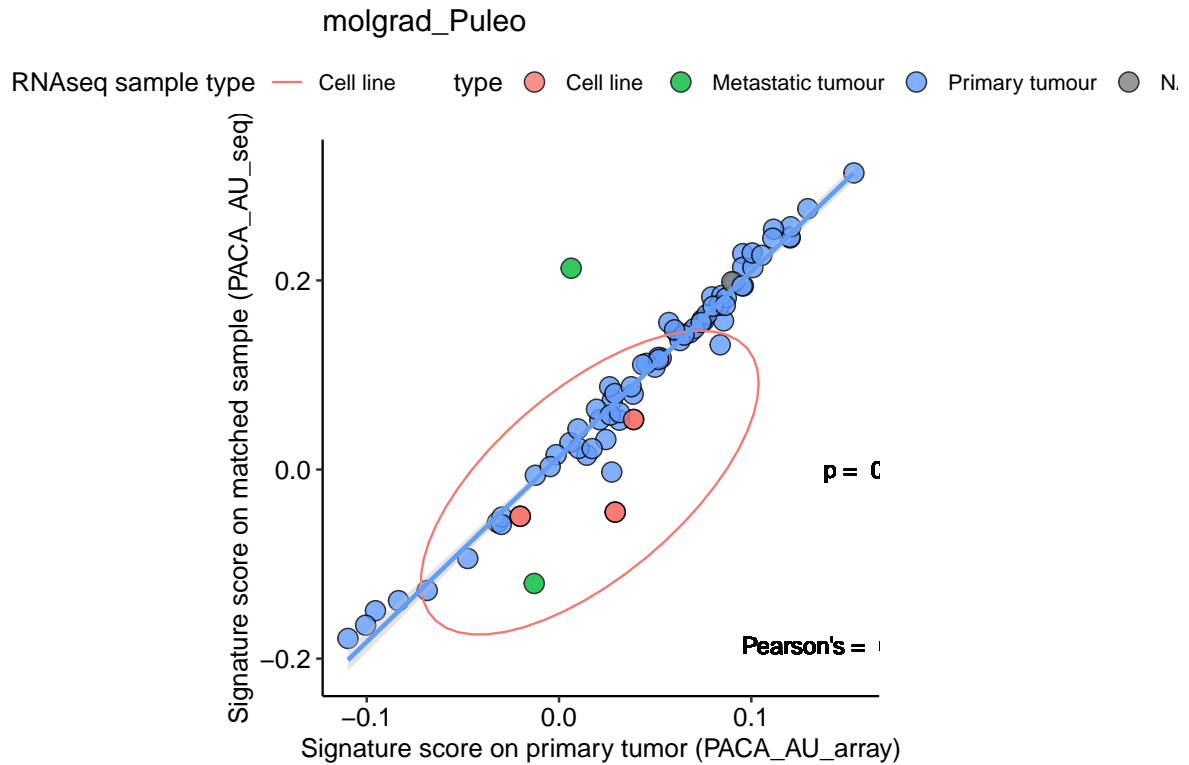


```
## 'geom_smooth()' using formula 'y ~ x'
```

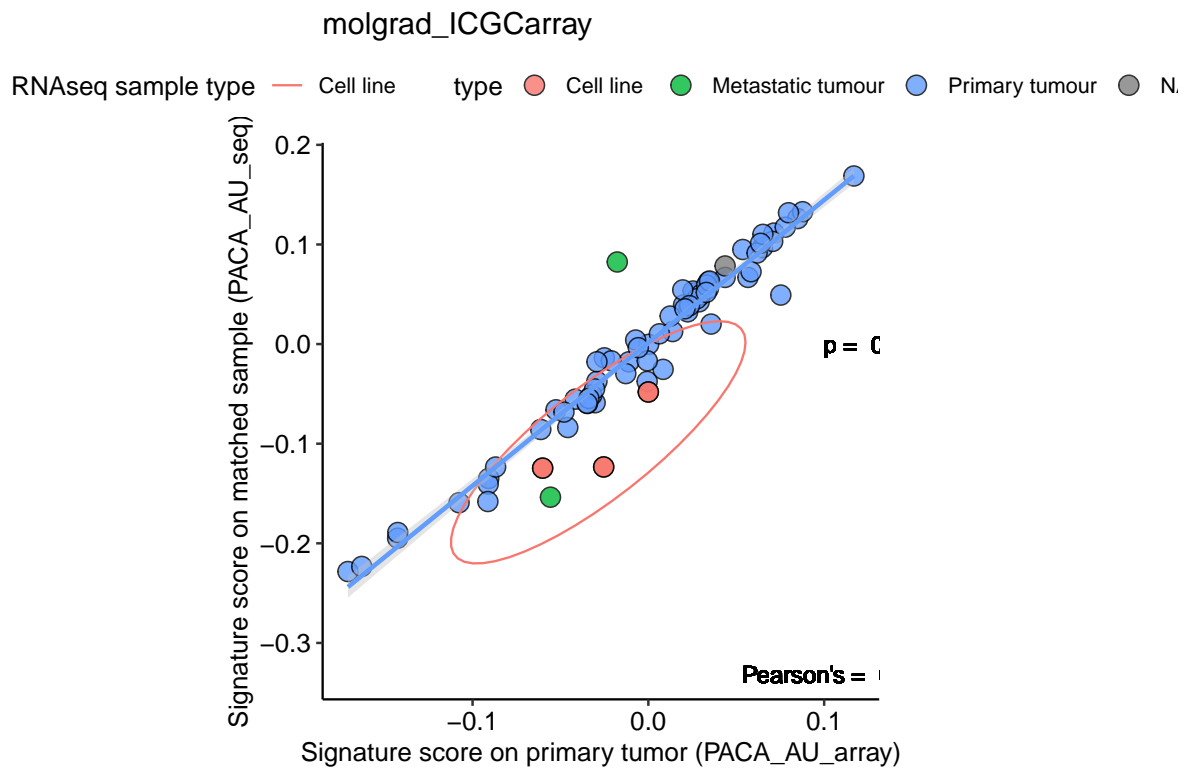
molgrad_PDX



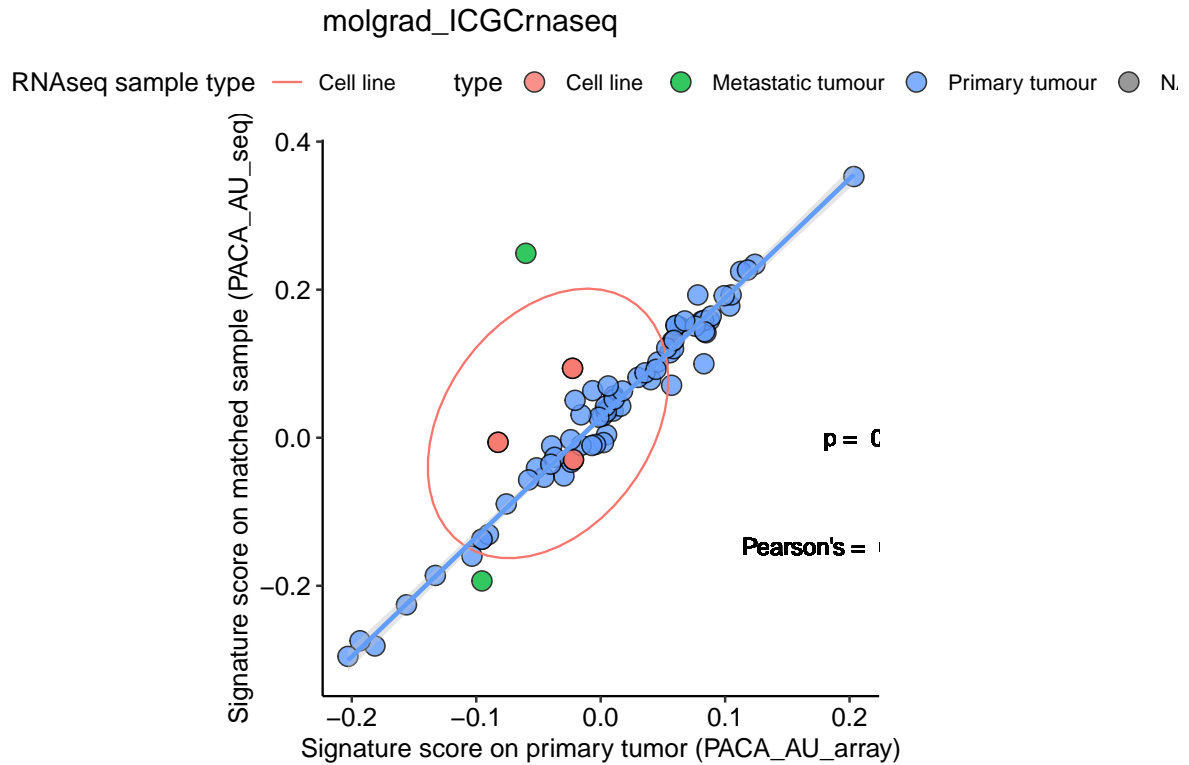
```
## 'geom_smooth()' using formula 'y ~ x'
```

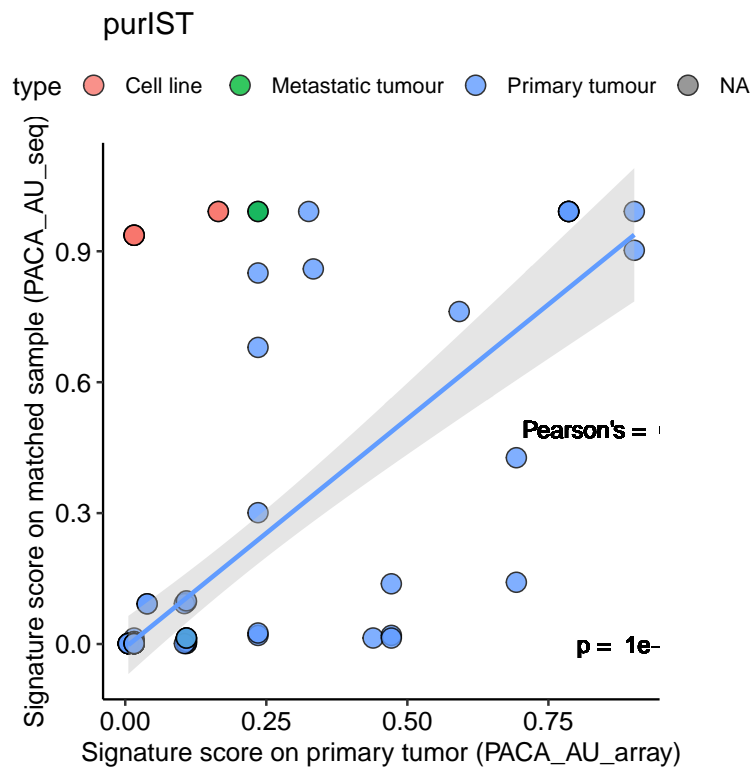
```
## 'geom_smooth()' using formula 'y ~ x'
```



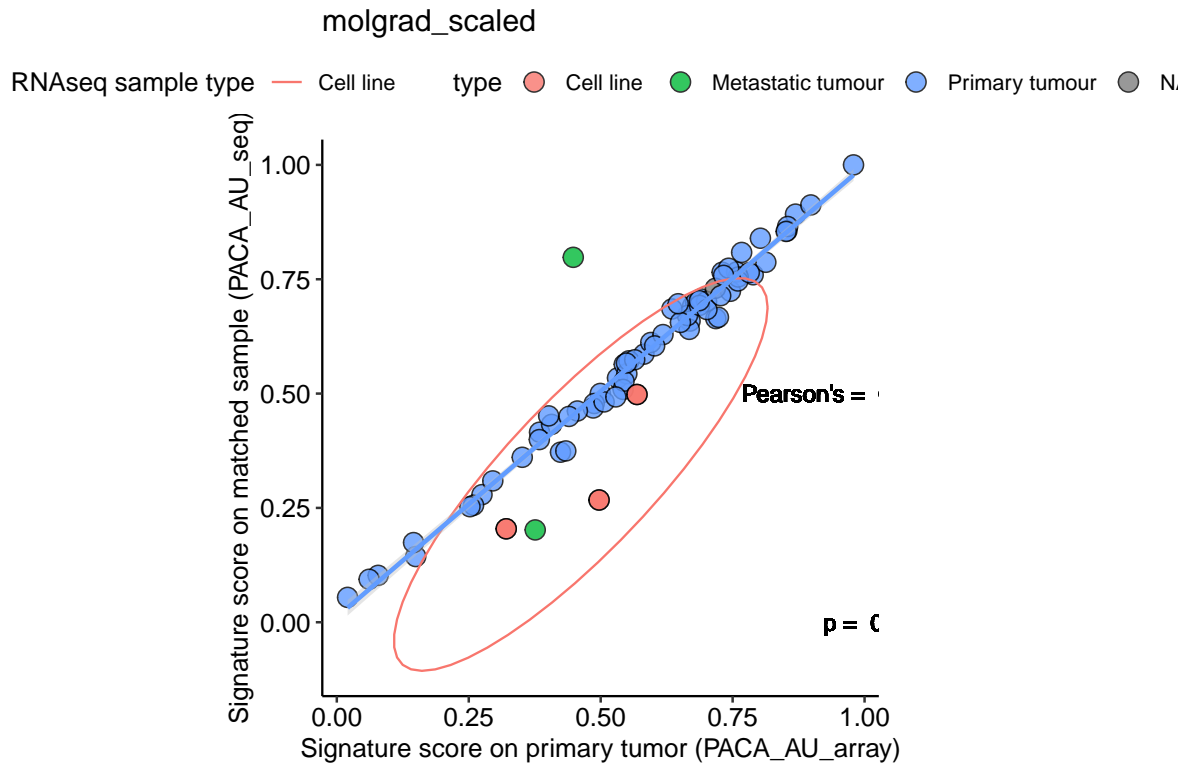
```
## 'geom_smooth()' using formula 'y ~ x'
```



```
## 'geom_smooth()' using formula 'y ~ x'
```



```
## 'geom_smooth()' using formula 'y ~ x'
```

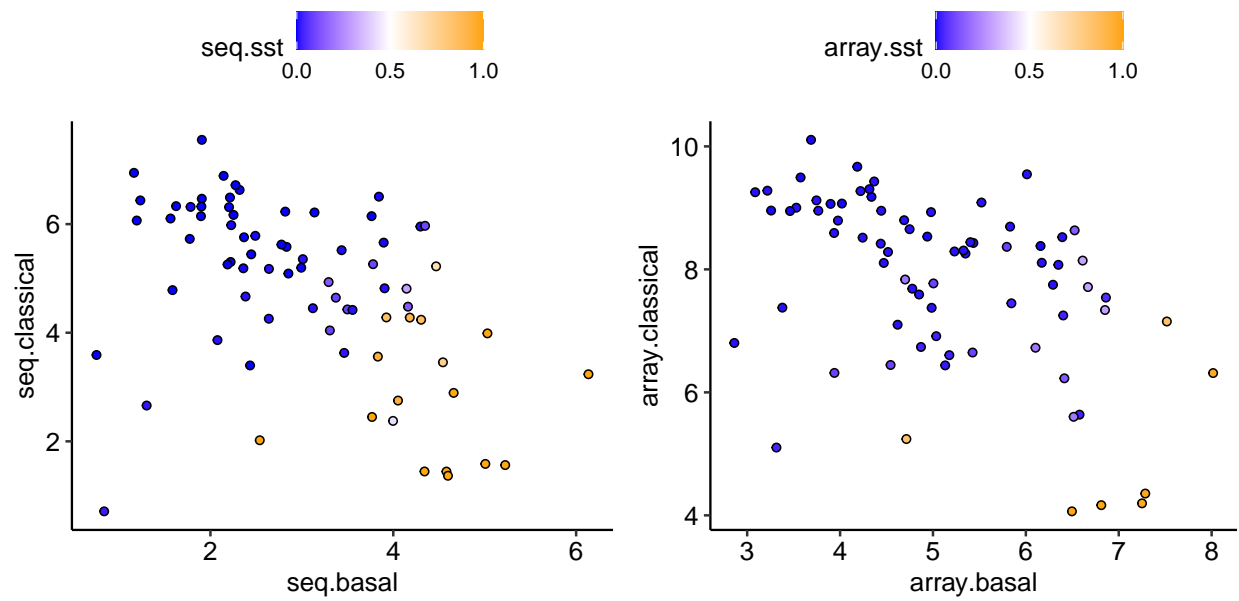


Add classifier geneset to dataset

Popular signatures and classifier score

```
## [1] 23
```

```
## [1] 23
```



```
## 'geom_smooth()' using formula 'y ~ x'
```

