| LncRNA | Gene Name | Clinseq | | | | TCGA | | | |
|---|---|---|---|---|---|---|---|---|---|
| | | p−value | p−value(adj.) | HR(95% CI) | | p−value | p−value(adj.) | HR(95% CI) | |
| G011836 | | 3.3864E−06 | 0.01026 | 1.71(1.36−2.14) | | 1.7589E−01 | 0.39598 | 1.05(0.98−1.14) | |
| G083070 | | 2.7656E−05 | 0.02095 | 0.68(0.57−0.82) | | 2.5987E−01 | 0.50537 | 0.94(0.83−1.05) | |
| G054155 | | 2.1648E−05 | 0.02095 | 1.61(1.29−2.01) | | | | | |
| G070568 | | 1.9204E−05 | 0.02095 | 1.48(1.23−1.76) | | | | | |
| G083740 | LACAT12 | 5.3785E−05 | 0.03259 | 1.48(1.22−1.78) | | 3.6139E−01 | 0.60564 | 1.17(0.83−1.66) | |
| G066126 | CAT672 | 7.4225E−05 | 0.03748 | 1.43(1.20−1.71) | | | | | |
| G033492 | | 8.9613E−05 | 0.03879 | 1.53(1.23−1.88) | | 2.2062E−01 | 0.46097 | 1.28(0.86−1.89) | |
| G009787 | CAT1264 | 3.6613E−04 | 0.04290 | 1.55(1.22−1.97) | | 4.4609E−01 | 0.67847 | 1.02(0.96−1.09) | |
| G057584 | | 3.6546E−04 | 0.04290 | 0.67(0.53−0.83) | | 9.0933E−03 | 0.09080 | 0.91(0.85−0.98) | |
| G043947 | HICLINC53 | 2.2457E−04 | 0.04290 | 1.88(1.35−2.64) | | 5.5962E−01 | 0.76408 | 1.02(0.95−1.10) | |
| G004936 | | 3.0590E−04 | 0.04290 | 1.41(1.17−1.70) | | 2.5718E−01 | 0.50209 | 1.04(0.97−1.12) | |
| G063211 | | 2.9597E−04 | 0.04290 | 0.69(0.56−0.84) | | 2.2844E−03 | 0.05108 | 0.88(0.81−0.96) | |
| G078456 | | 1.7228E−04 | 0.04290 | 0.66(0.53−0.82) | | 9.1911E−01 | 0.96523 | 1.00(0.91−1.09) | |
| G034197 | | 3.4161E−04 | 0.04290 | 0.72(0.60−0.86) | | 6.1390E−01 | 0.79965 | 0.96(0.84−1.11) | |
| G016839 | A2M−AS1 | 1.8619E−04 | 0.04290 | 1.55(1.23−1.94) | | 5.0582E−01 | 0.72054 | 0.96(0.84−1.09) | |
| G070048 | | 1.5876E−04 | 0.04290 | 1.48(1.21−1.81) | | 2.8736E−01 | 0.53259 | 0.93(0.81−1.06) | |
| G072219 | BLCAT4 | 3.1442E−04 | 0.04290 | 1.47(1.19−1.81) | | 4.3620E−01 | 0.67281 | 0.93(0.78−1.12) | |
| G042800 | | 2.7443E−04 | 0.04290 | 1.44(1.18−1.75) | | 6.2183E−01 | 0.80450 | 0.95(0.79−1.15) | |
| G055385 | | 2.8026E−04 | 0.04290 | 1.42(1.18−1.72) | | 2.3754E−01 | 0.48098 | 1.13(0.92−1.38) | |
| G074303 | PSMG3−AS1 | 1.6398E−04 | 0.04290 | 1.48(1.21−1.82) | | 4.7346E−01 | 0.69660 | 1.08(0.87−1.34) | |
| G052428 | | 2.7789E−04 | 0.04290 | 1.37(1.16−1.63) | | 3.3796E−01 | 0.58905 | 1.11(0.90−1.37) | |
| G052918 | | 3.6808E−04 | 0.04290 | 1.41(1.17−1.71) | | 5.9859E−01 | 0.79383 | 0.94(0.75−1.18) | |
| G042911 | CAT222 | 1.8542E−04 | 0.04290 | 1.45(1.19−1.77) | | 3.8836E−02 | 0.18842 | 0.73(0.55−0.98) | |
| G055391 | ENTPD3−AS1 | 1.5346E−04 | 0.04290 | 1.45(1.20−1.77) | | 2.8395E−01 | 0.53063 | 0.86(0.65−1.13) | |
| G034420 | | 2.4073E−04 | 0.04290 | 1.41(1.17−1.69) | | 9.7564E−01 | 0.99014 | 1.00(0.74−1.37) | |
| G081611 | | 2.1312E−04 | 0.04290 | 1.50(1.21−1.85) | | 9.7772E−01 | 0.99014 | 1.00(0.76−1.32) | |
| G021874 | | 3.8407E−04 | 0.04310 | 1.49(1.20−1.86) | | 4.3776E−01 | 0.67323 | 1.08(0.89−1.31) | |
| G075058 | CAT914 | 4.4712E−04 | 0.04455 | 1.56(1.22−1.99) | | 9.3378E−01 | 0.97221 | 1.00(0.92−1.10) | |
| G036051 | | 4.3743E−04 | 0.04455 | 0.74(0.62−0.87) | | 2.3815E−01 | 0.48183 | 0.93(0.82−1.05) | |
| G030631 | | 4.6824E−04 | 0.04455 | 0.70(0.57−0.85) | | 2.2072E−03 | 0.05065 | 0.87(0.79−0.95) | |
| G054140 | | 4.1567E−04 | 0.04455 | 1.56(1.22−1.99) | | 9.1180E−01 | 0.96214 | 1.01(0.88−1.16) | |
| G005197 | | 4.7046E−04 | 0.04455 | 1.42(1.17−1.73) | | 4.0772E−02 | 0.19253 | 0.75(0.57−0.99) | |
| G047323 | | 5.2911E−04 | 0.04858 | 1.41(1.16−1.72) | | 5.0772E−02 | 0.21238 | 0.69(0.48−1.00) | |

Hazard ratio

Hazard ratio

Figure S1: Multivariate time-to-event analysis (overall survival) of individual lncRNA (adjusting for established risk factors) in the Clinseq-AML (red) and TCGA-AML cohort (blue)

(a) K=2

(b) K=3

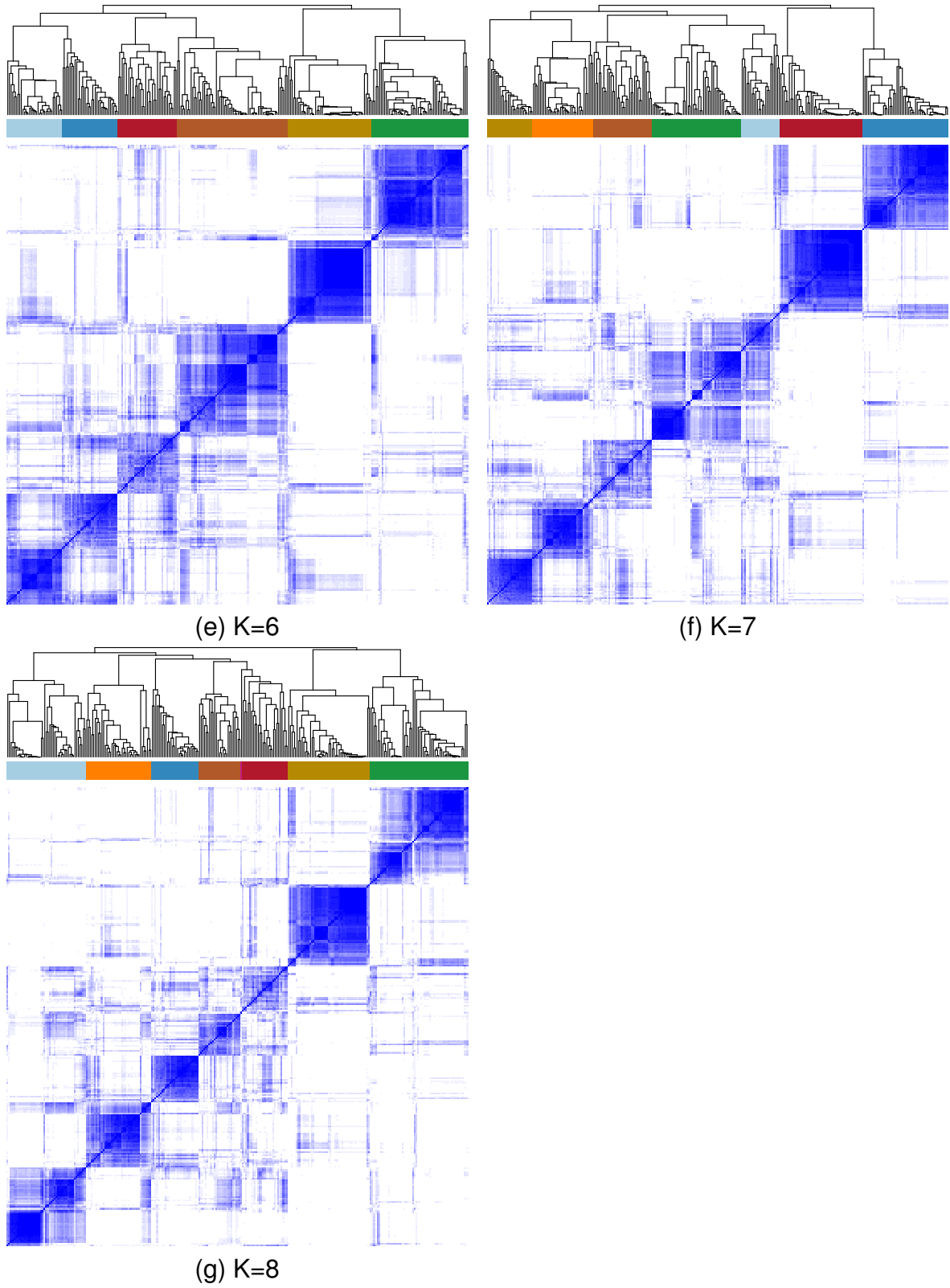(c) K=4

(d) K=5

(e) K=6


(f) K=7


(g) K=8
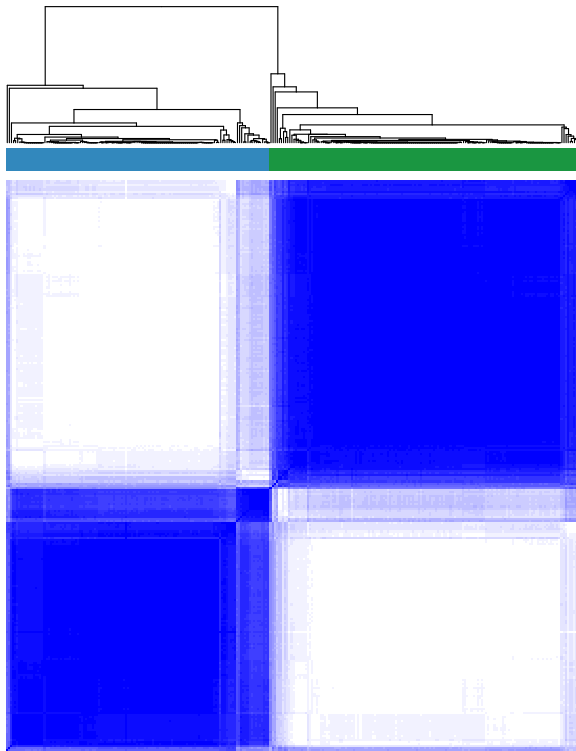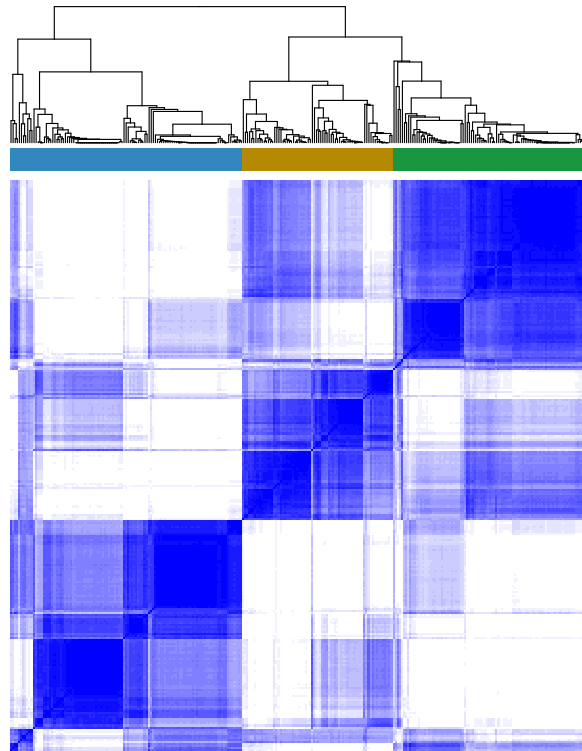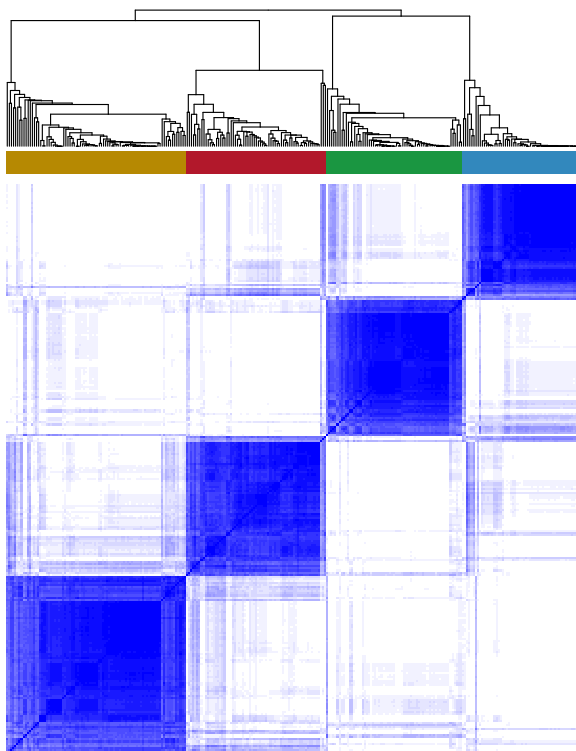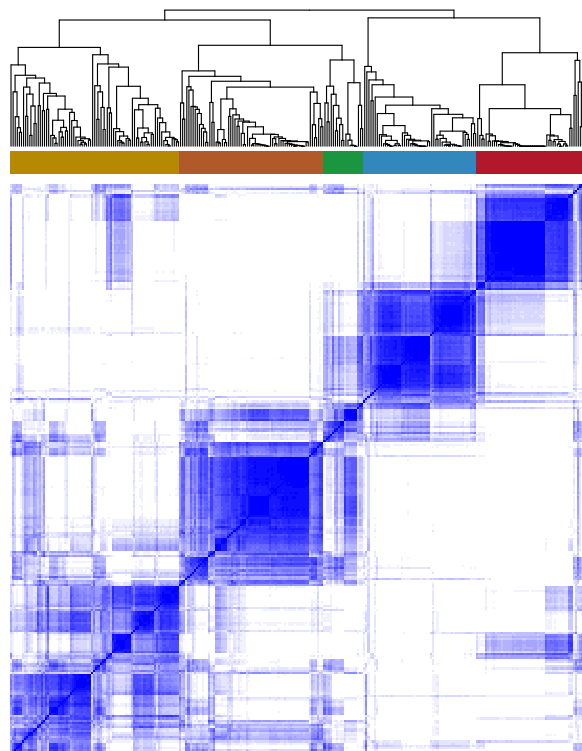
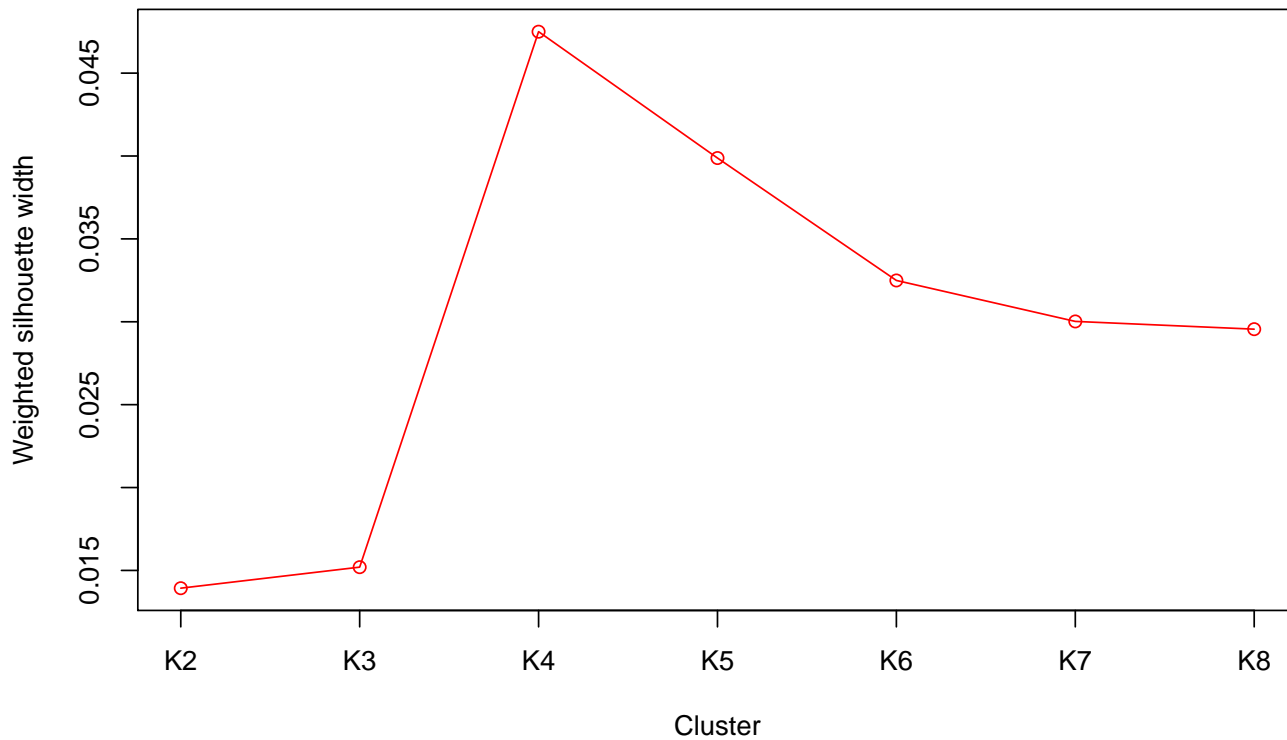Figure S2: Consensus matrix for clustering

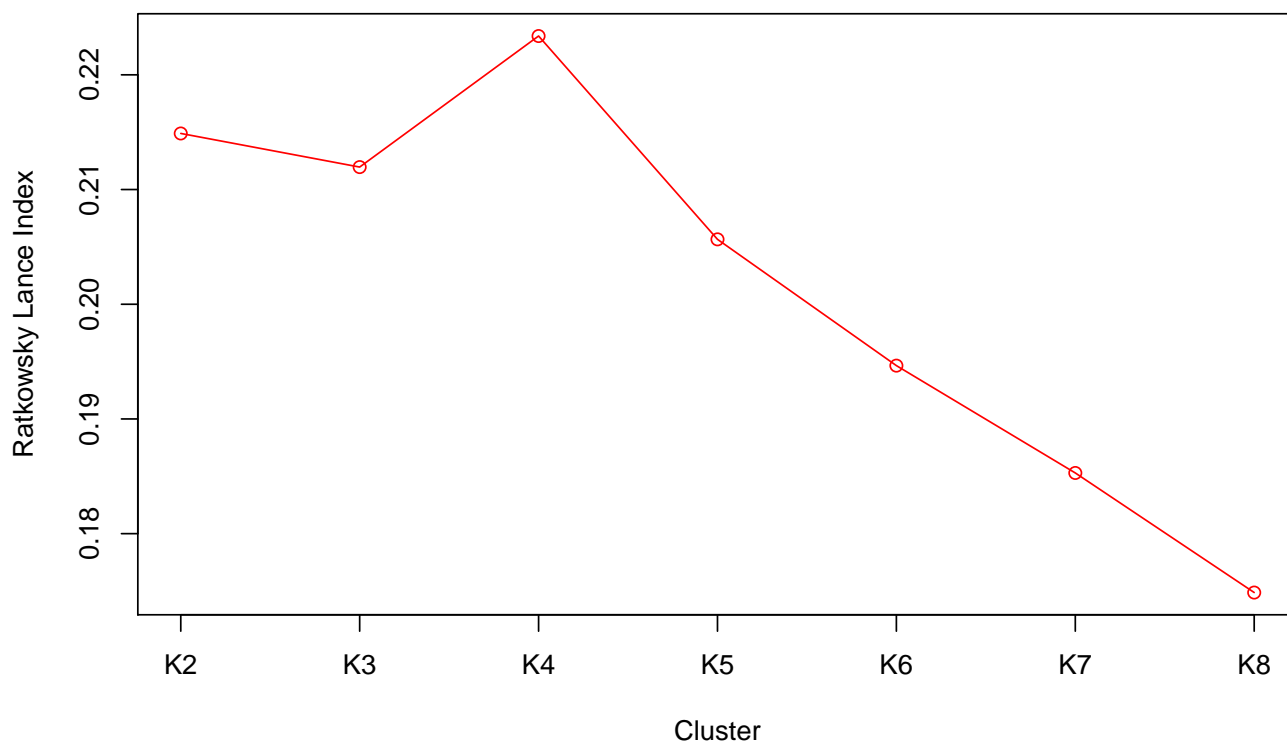Figure S3: Weighted silhouette width for different number of clusters in lncRNA expression dataset



Figure S4: Clustering performance as a function of Ratkowsky Lance Index for different number of clusters in lncRNA expression dataset
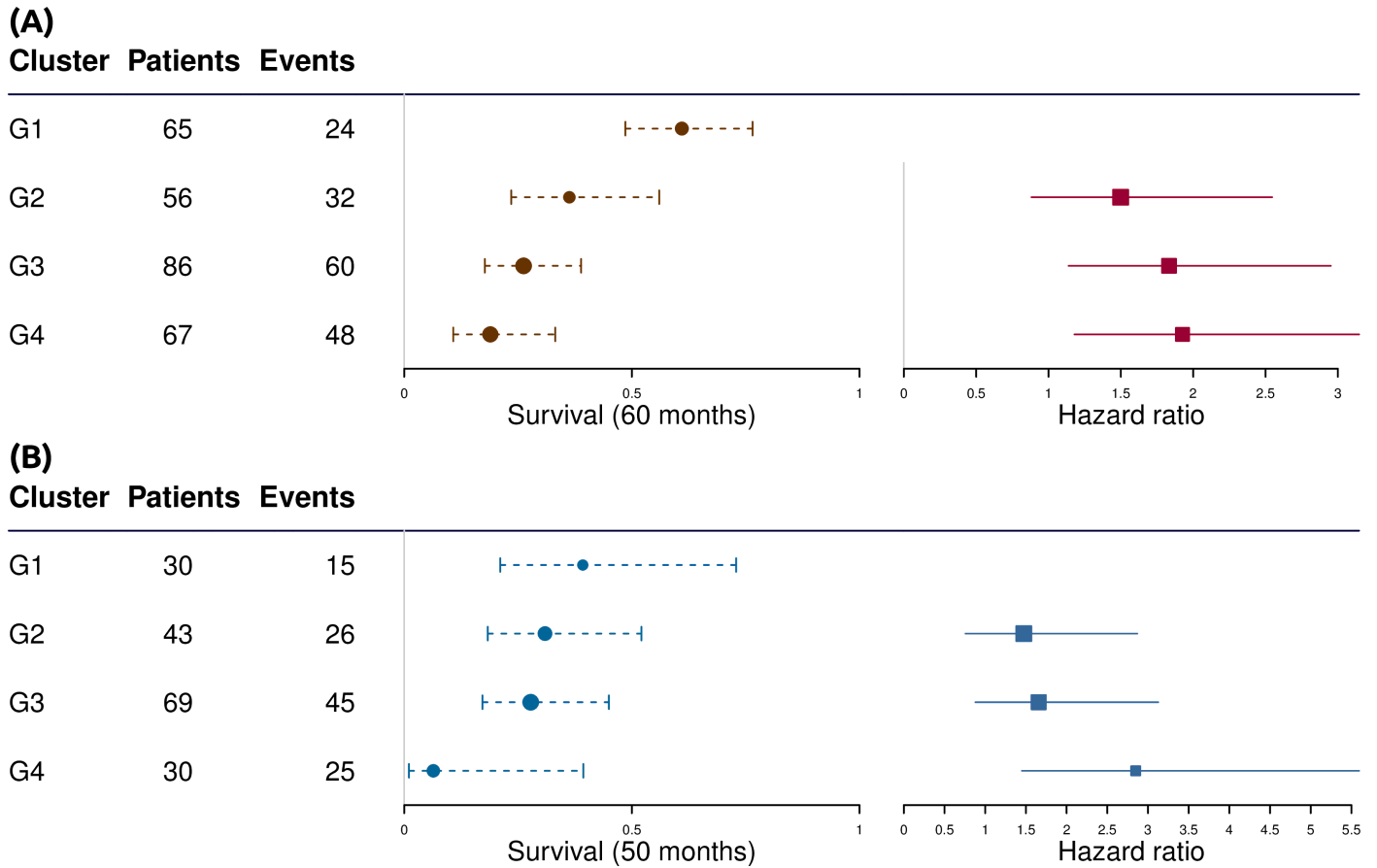
**(A)**

| Cluster | Patients | Events |
|---------|----------|--------|
| G1 | 65 | 24 |
| G2 | 56 | 32 |
| G3 | 86 | 60 |
| G4 | 67 | 48 |

Survival (60 months)    Hazard ratio

**(B)**

| Cluster | Patients | Events |
|---------|----------|--------|
| G1 | 30 | 15 |
| G2 | 43 | 26 |
| G3 | 69 | 45 |
| G4 | 30 | 25 |

Survival (50 months)    Hazard ratio

Figure S5: Hazard ratio and survival probability at 60 months in 4 different groups for (A) Clinseq AML cohort and (B) TCGA AML cohort. Barplot represent 95% confidence interval.
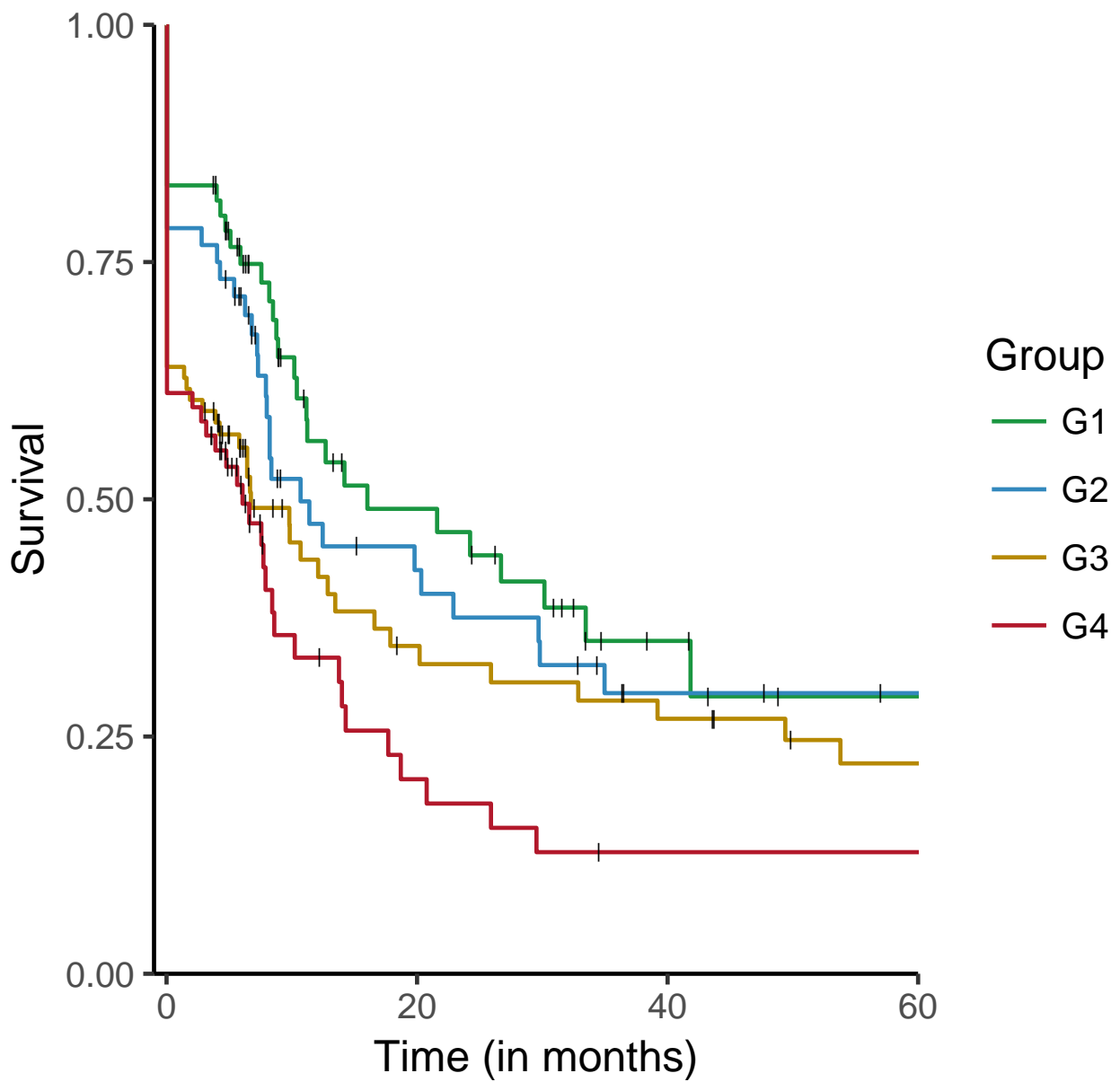
Figure S6: LncRNA expression subtypes and event free survival (Kaplan-Meier) in Clinseq AML cohort (p-value = 0.0159, Log-rank test).
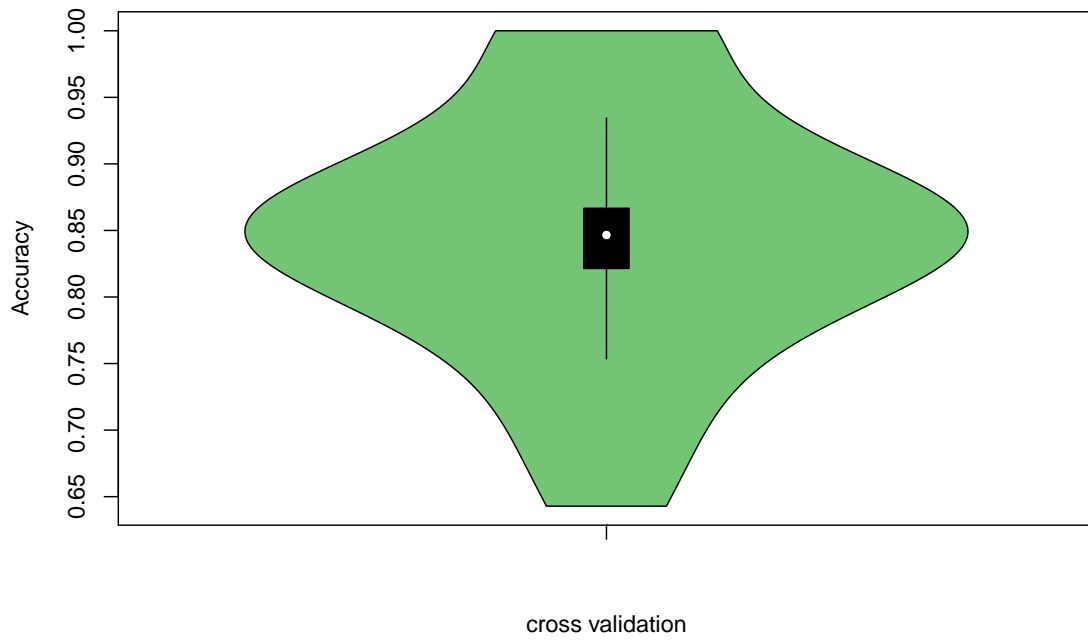
Figure S7: Violin plot visualisation for 100-fold cross-validation of lncRNA based AML subtype
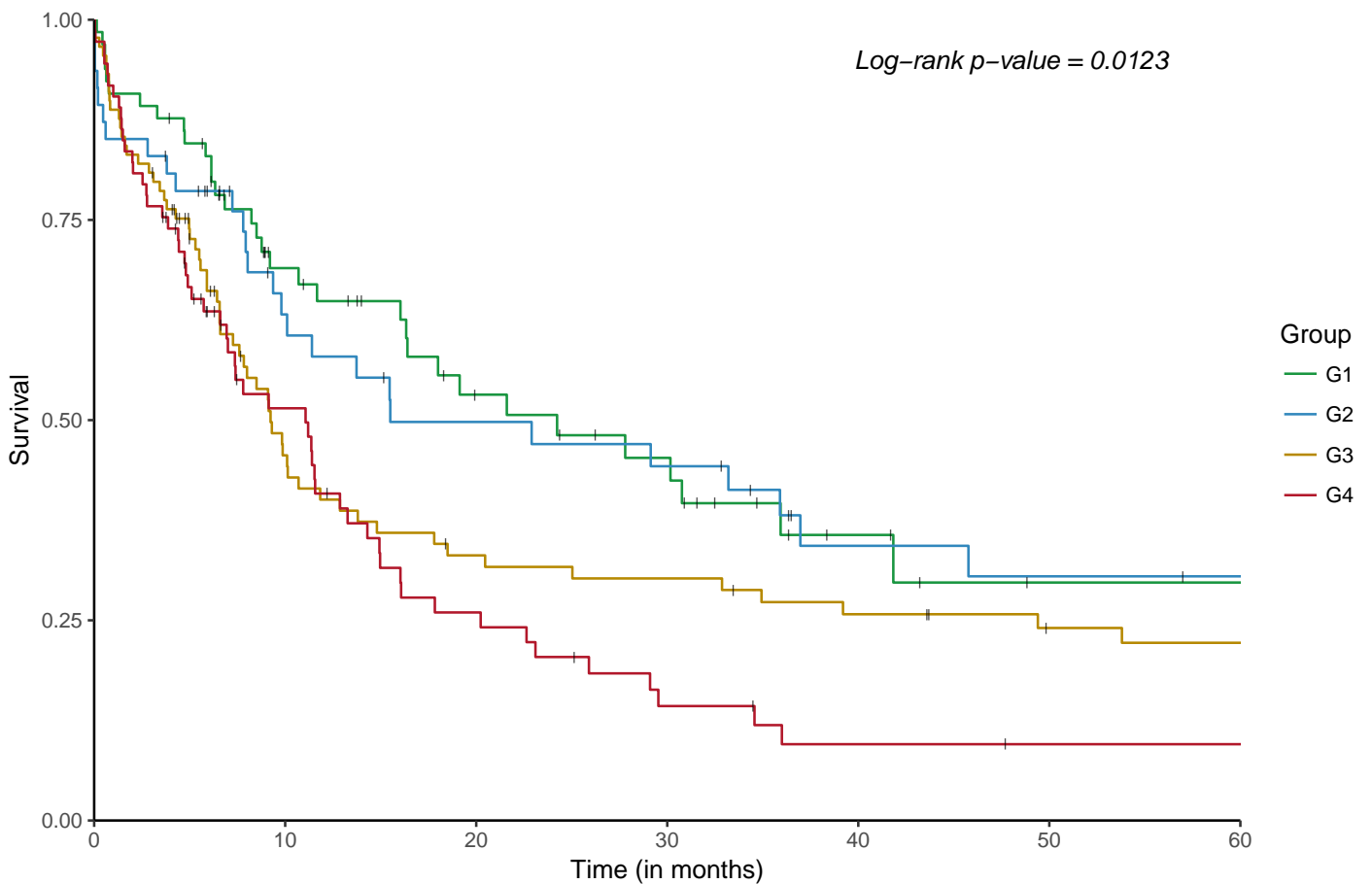


Figure S8: Overall survival (Kaplan-Meier) using predicted labels using 100-fold cross-validation in the complete Clinseq AML cohort
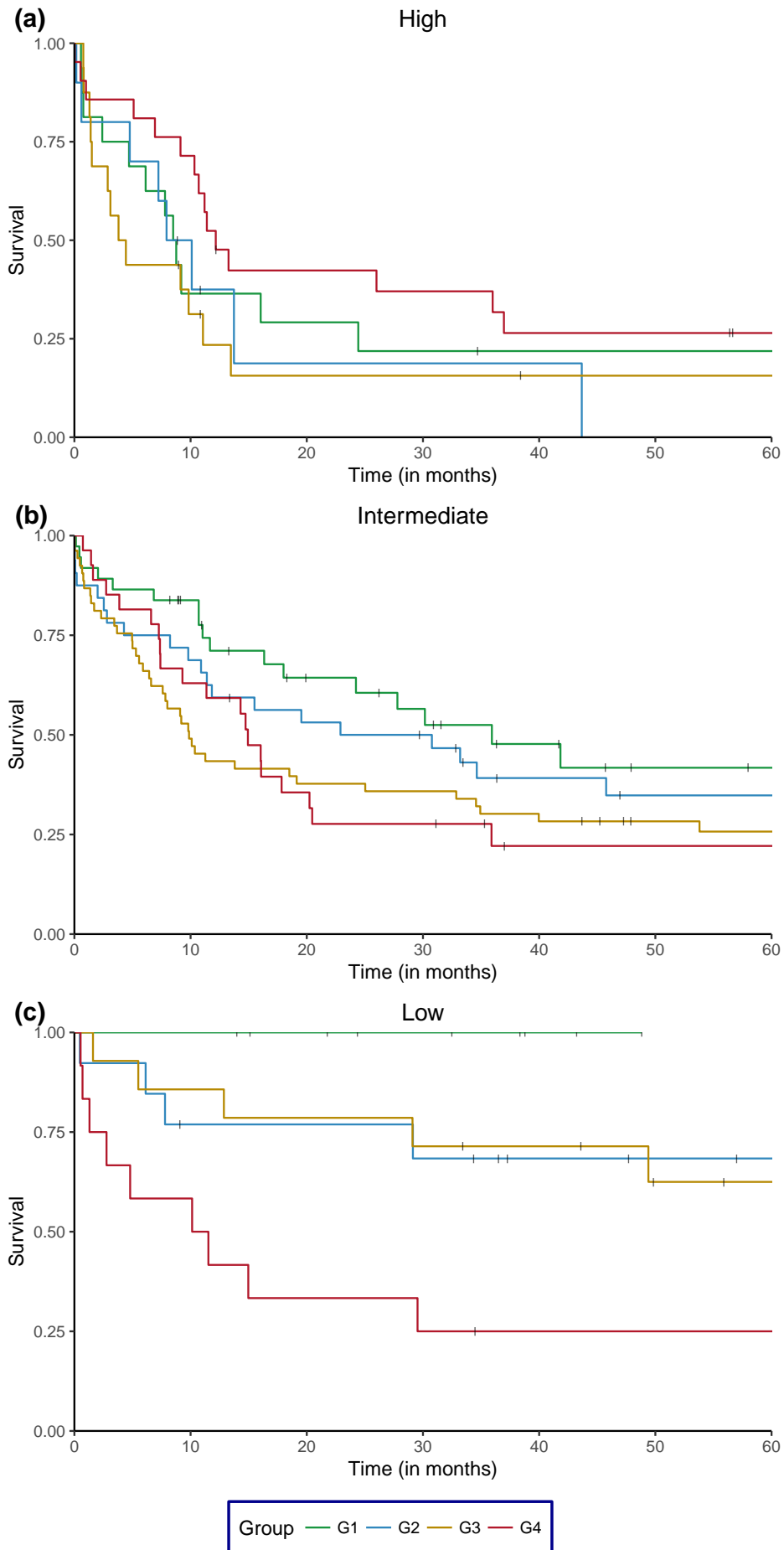
Figure S9: Overall survival (Kaplan-Meier) for 3 ELN risk groups, (a) high, (b) intermediate and (c) low further stratified by lncRNA based subtype

Table 1: CEBPA (p-value = 5.3242E-01)

|    | No mutation (in %) | Mutation (in %) | Double mutation (in %) |
|----|--------------------|-----------------|------------------------|
| G1 | 19.71              | 2.56            | 1.46                   |
| G2 | 18.25              | 1.82            | 0.36                   |
| G3 | 25.91              | 2.56            | 2.92                   |
| G4 | 21.90              | 1.09            | 1.46                   |

Table 2: NPM1 (p-value = 1.0924E-05)

|    | No mutation (in %) | Mutation (in %) |
|----|--------------------|-----------------|
| G1 | 17.15              | 6.57            |
| G2 | 13.50              | 6.93            |
| G3 | 16.79              | 14.60           |
| G4 | 22.26              | 2.19            |

Table 3: TP53 (p-value = 3.9498E-03)

|    | No mutation (in %) | Mutation (in %) |
|----|--------------------|-----------------|
| G1 | 21.90              | 1.82            |
| G2 | 19.34              | 1.09            |
| G3 | 30.29              | 1.09            |
| G4 | 19.71              | 4.75            |

Table 4: DNMT3A (p-value = 8.5920E-01)

|    | No mutation (in %) | Mutation (in %) |
|----|--------------------|-----------------|
| G1 | 17.88              | 5.84            |
| G2 | 15.33              | 5.11            |
| G3 | 25.18              | 6.20            |
| G4 | 18.61              | 5.84            |

Table 5: KRAS (p-value = 4.9475E-02)

|    | No mutation (in %) | Mutation (in %) |
|----|--------------------|-----------------|
| G1 | 22.63              | 1.09            |
| G2 | 18.61              | 1.82            |
| G3 | 31.39              | 0.00            |
| G4 | 23.36              | 1.09            |

Table 6: RUNX1 (p-value = 1.1877E-01)

|    | No mutation (in %) | Mutation (in %) |
|----|--------------------|-----------------|
| G1 | 18.61              | 5.11            |
| G2 | 17.88              | 2.56            |
| G3 | 28.83              | 2.56            |
| G4 | 20.44              | 4.01            |

Table 7: TET2 (p-value = 4.2230E-01)

|    | No mutation (in %) | Mutation (in %) |
|----|--------------------|-----------------|
| G1 | 18.61              | 5.11            |
| G2 | 14.60              | 5.84            |
| G3 | 23.72              | 7.66            |
| G4 | 20.44              | 4.01            |

Table 8: FLT3 mutation (p-value = 1.9160E-06)

|    | No mutation (in %) | Mutation (in %) |
|----|--------------------|-----------------|
| G1 | 18.25              | 5.47            |
| G2 | 14.96              | 5.47            |
| G3 | 16.42              | 14.96           |
| G4 | 22.26              | 2.19            |

Table 9: FLT3-ITD (p-value = 2.8758E-06)

|    | No duplication (in %) | Duplication (in %) |
|----|-----------------------|--------------------|
| G1 | 18.25                 | 5.47               |
| G2 | 16.06                 | 4.38               |
| G3 | 17.88                 | 13.50              |
| G4 | 22.99                 | 1.46               |

Table 10: Karyotype (p-value = 3.9627E-03)

|     | Abnormal (in %) | Normal (in %) |
| --- | --- | --- |
| G1 | 9.96 | 13.79 |
| G2 | 9.20 | 11.88 |
| G3 | 14.56 | 17.24 |
| G4 | 16.48 | 6.90 |

Table 11: t(8;21) (p-value = 2.3159E-01)

|     | Abnormal (in %) | Normal (in %) |
| --- | --- | --- |
| G1 | 0.00 | 23.75 |
| G2 | 0.38 | 20.69 |
| G3 | 0.38 | 31.42 |
| G4 | 1.15 | 22.22 |

Table 12: inv(16)/t(16;16) (p-value = 9.0495E-03)

|     | Abnormal (in %) | Normal (in %) |
| --- | --- | --- |
| G1 | 0.00 | 23.75 |
| G2 | 0.77 | 20.31 |
| G3 | 0.38 | 31.42 |
| G4 | 2.30 | 21.07 |

Table 13: t(15;17) (p-value = 6.5962E-01)

|     | Abnormal (in %) | Normal (in %) |
| --- | --- | --- |
| G1 | 1.15 | 22.61 |
| G2 | 0.38 | 20.69 |
| G3 | 1.53 | 30.27 |
| G4 | 0.38 | 22.99 |

Table 14: inv(3)/t(3;3) (p-value = 8.6716E-01)

|     | Abnormal (in %) | Normal (in %) |
| --- | --- | --- |
| G1 | 0.38 | 23.37 |
| G2 | 0.38 | 20.69 |
| G3 | 0.38 | 31.42 |
| G4 | 0.77 | 22.61 |

Table 15: t(11q23) (p-value = 2.9389E-01)

|     | Abnormal (in %) | Normal (in %) |
| --- | --- | --- |
| G1 | 0.00 | 23.75 |
| G2 | 1.15 | 19.92 |
| G3 | 0.77 | 31.03 |
| G4 | 0.77 | 22.61 |

Table 16: del5 (p-value = 7.8496E-03)

|    | Abnormal (in %) | Normal (in %) |
|----|-----------------|---------------|
| G1 | 1.92            | 21.84         |
| G2 | 0.77            | 20.31         |
| G3 | 0.38            | 31.42         |
| G4 | 3.45            | 19.92         |

Table 17: del7 (p-value = 1.5314E-02)

|    | Abnormal (in %) | Normal (in %) |
|----|-----------------|---------------|
| G1 | 2.68            | 21.07         |
| G2 | 0.38            | 20.69         |
| G3 | 2.68            | 29.12         |
| G4 | 4.60            | 18.77         |

Table 18: +8 (p-value = 2.4024E-01)

|    | Abnormal (in %) | Normal (in %) |
|----|-----------------|---------------|
| G1 | 0.77            | 22.99         |
| G2 | 1.92            | 19.16         |
| G3 | 1.53            | 30.27         |
| G4 | 2.68            | 20.69         |

Table 19: ELN Risk (p-value = 2.1069E-01)

|    | High (in %) | Intermediate (in %) | Low (in %) |
|----|-------------|---------------------|------------|
| G1 | 6.15        | 14.23               | 3.46       |
| G2 | 3.85        | 12.31               | 5.00       |
| G3 | 6.15        | 20.39               | 5.38       |
| G4 | 8.08        | 10.38               | 4.62       |

Table 20: Etiology (p-value = 1.5194E-01)

|    | de-novo (in %) | s-AML (in %) | t-AML (in %) |
|----|----------------|--------------|--------------|
| G1 | 17.65          | 1.47         | 4.04         |
| G2 | 16.54          | 1.47         | 2.57         |
| G3 | 26.84          | 2.94         | 1.84         |
| G4 | 20.59          | 2.94         | 1.10         |

Table 21: lncRNA vs. mRNA clusters (p-value = 2.5615E-68)

| | C1 (in %) | C2 (in %) | C3 (in %) | C4 (in %) | C5 (in %) | C6 (in %) | C7 (in %) |
|---|---|---|---|---|---|---|---|
| G1 | 0.00 | 13.87 | 1.46 | 5.84 | 0.36 | 1.46 | 0.73 |
| G2 | 0.00 | 1.09 | 0.00 | 9.49 | 4.38 | 0.36 | 5.11 |
| G3 | 8.76 | 0.00 | 5.11 | 0.00 | 1.46 | 16.06 | 0.00 |
| G4 | 0.36 | 0.00 | 9.12 | 0.00 | 5.84 | 1.82 | 7.30 |