

Supplementary Table S1. Total number of samples for tumor and control.

Type	RNA-seq	DNA-met	CNV
Tumour	371	377	371
Control	52	52	86

Supplementary Table S2. Different combination of omics data using linear and logistic regression models.

Regression Type	Coefficients	P-values	Derived Empirical Formula
Linear	$\alpha_0 : 0.607$ $\alpha_2 : 0.17$	$p_{\alpha_0} : 0.331$ $p_{\alpha_2} : 0.52$	Not statistically significant integration $y = 0.17 (RNA - seq) + 0.607 (CNV)$ $y = 0.17 (RNA - seq)$
Logistic	$\beta_0 : 0.887$ $\beta_2 : -2.607$	$p_{\beta_0} : 0.475$ $p_{\beta_2} : 0.219$	Not statistically significant integration $y = (1 + \exp(-0.8 (CNV)))^{-1}$ $y = (1 + \exp(2.6 (RNA - seq)))^{-1}$ $y = (1 + \exp(-0.8 (CNV) + 2.6 (RNA - seq)))^{-1}$
Linear	$\alpha_0 : 0.317$ $\alpha_1 : 3.34$	$p_{\alpha_0} : \mathbf{0.00161}$ $p_{\alpha_1} : \mathbf{0.00129}$	Statistically significant integration $y = 0.3(CNV) + 3.3(DNA - met)$ $y = 3.3(DNA - met)$
Logistic	$\beta_0 : -0.997$ $\beta_1 : -61.959$	$p_{\beta_0} : \mathbf{0.00456}$ $p_{\beta_1} : \mathbf{0.00482}$	Statistically significant integration $y = (1 + \exp(0.9(CNV) + 61.9(DNA - met)))^{-1}$ $y = (1 + \exp(61.9(DNA - met)))^{-1}$
Linear	$\alpha_2 : 0.379$ $\alpha_1 : 3.756$	$p_{\alpha_2} : 0.000379$ $p_{\alpha_1} : 0.001057$	Statistically significant integration $y = 0.3(RNA - seq) + 3.7(DNA - met)$ $y = 0.3(RNA - seq)$ $y = 3.7(DNA - met)$
Logistic	$\beta_2 : -40.8$ $\beta_1 : 154.2$	$p_{\beta_2} : 0.152$ $p_{\beta_1} : 0.152$	Not Statistically Significant integration $y = (1 + \exp(40.8(RNA - seq) - 154.2(DNA - met)))^{-1}$ $y = (1 + \exp(-154.2(DNA - met)))^{-1}$ $y = (1 + \exp(40.8(RNA - seq)))^{-1}$
Linear	$\alpha_0 : 0.317$ $\alpha_2 : -0.005$ $\alpha_1 : 4.081$	$p_{\alpha_0} : 0.1926$ $p_{\alpha_2} : 0.137$ $p_{\alpha_1} : 0.000507$	Not Statistically Significant integration $y = 0.317(CNV) - 0.005(RNA - seq) + 4.081(DNA - met)$ $y = 0.317(CNV) + 4.081(DNA - met)$ $y = -0.005(RNA_{seq}) + 4.081(DNA - met)$ $y = -0.005(RNA - seq)$ $y = 4.081(DNA - met)$
Logistic	$\beta_0 : 12$ $\beta_2 : -47.2$ $\beta_1 : 81.4$	$p_{\beta_0} : 0.29$ $p_{\beta_2} : 0.154$ $p_{\beta_1} : 0.152$	Not Statistically Significant integration $y = (1 + \exp(-12(CNV) + 47.2(RNA - seq) - 81.4(DNA - met)))^{-1}$ $y = 1/(1 + \exp(-12(CNV) + 47.2 (RNA - seq)))^{-1}$ $y = 1/(1 + \exp(47.2(RNA - seq) - 81.4(DNA - met)))$ $y = (1 + \exp(47.2(RNA - seq)))^{-1}$ $y = (1 + \exp(-81.4(DNA - met)))^{-1}$

Supplementary Table S3. Autoencoder architecture.

Encoder		Decoder	
Fully connected	(1209, 512)	Fully connected	(400, 512)
Fully connected	(512, 400)	Fully connected	(512, 1209)

Supplementary Table S4. Silhouette score and variance of Autoencoder and random stacking using regression analysis with different number of PCs.

<i>Autoencoder</i>		
Principal Component	Variance	Silhouette Score
PC = 2	0.6305	0.7602
PC = 4	0.7655	0.6643
PC = 20	0.9571	0.5664
PC = 100	0.9946	0.5576
PC = 300	0.9999	0.5554
<i>Random Stacking</i>		
PC=2	0.6040	0.7144
PC=4	0.7160	0.6311
PC=20	0.8128	0.5753
PC=100	0.9065	0.5326
PC=300	0.9838	0.5017