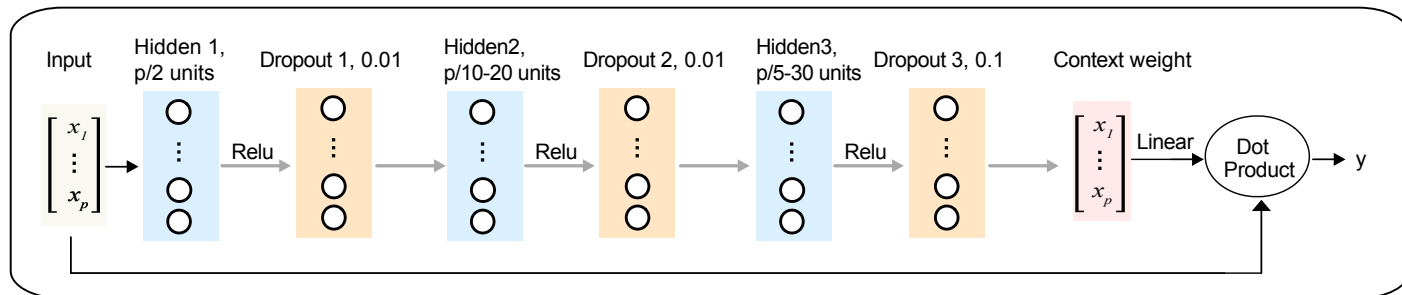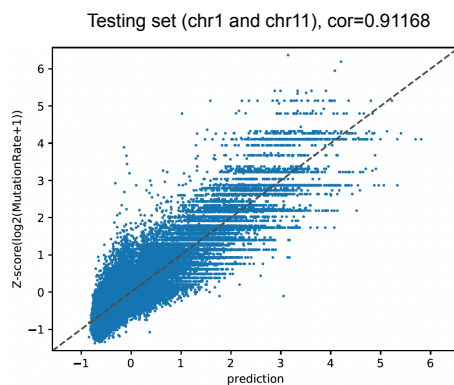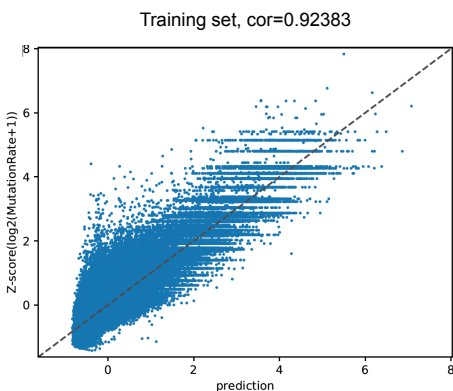**a   The structure of the contextual regression model**

b   The prediction performance of the contextual regression model

Cancer type	Training accuracy	Testing accuracy	Included for retraining	Testing accuracy of the retrained model	Testing accuracy after removing overlapping regions
Bone-Osteosarc	0.944218	0.910314	Yes	0.93221	NA
Breast-AdenoCA	0.927085	0.879672		0.87191	0.89364
CNS-Medullo	0.955174	0.924729	Yes	0.94388	NA
Eso-AdenoCA	0.898108	0.820361		0.76146	0.83817
Kidney-RCC	0.947068	0.907047	Yes	0.92032	NA
Liver-HCC	0.791536	0.664126		0.54613	0.74837
Lymph-BNHL	0.907874	0.813415		0.79035	0.81249
Lymph-CLL	0.943216	0.898522		0.90963	0.91113
Ovary-AdenoCA	0.939376	0.89834		0.89556	0.90591
Panc-AdenoCA	0.896348	0.825653		0.78616	0.85249
Panc-Endocrine	0.939561	0.905864	Yes	0.92968	NA
Prost-AdenoCA	0.938862	0.8928		0.90796	0.90151
Stomach-AdenoCA	0.95121	0.91713	Yes	0.95109	NA
Average	**0.92151**	**0.86600**		**0.85741**	**0.85796**

c   Cross validation performance

d   Re-trained model performance