Summary table of the Top gene features identified by each ML model (RF, XGB, SVM, LASSO and NN), highlighting overlaps and consistently selected biomarkers. The "Intersection" column lists genes identified across multiple models, suggesting potential robustness and biological relevance in classifying FLT3-ITD mutation status in AML.

RF	**XGBoost**	**SVM**	**LASSO**	**NN**	**Intersection**
HOXB3	HOXB3	HOXB3	HOXB6	TRH	SOCS2
SPNS3	SPNS3	HOXB6	IQCJ-SCHIP1	SNRPN	MRC1
SNRPN	HOXB6	IQCJ.SCHIP1	SPNS3	NKX2-3	CIBAR1P1
HOXB2	IQCJ-SCHIP1	MMP2	MMP2	IGFBP2	ENPP2
HOXB6	PBX3	HOXA5	TRH	IQCJ-SCHIP1	MIR155
NKX2-3	TRH	C3orf80	IGFBP2	C3orf80	LGALS3BP
LAPTM4B	SNRPN	IGFBP2	HOXB3	LAPTM4B	TRGC2
					SPINK2
					CTSG
					PDE4B
					ADGRG1
					CPA3
					HOXA9

Summary Conclusion:

This study successfully identified robust biomarkers for FLT3-ITD AML using five machine learning models applied to RNA-seq data. Key genes including SOCS2, MIR155, HOXA9 and CIBAR1P1 were consistently linked to AML pathogenesis and prognosis. A LASSO Cox-derived multigene model showed superior survival prediction, supporting the use of ML-based transcriptomic profiling in AML diagnosis and personalized care.