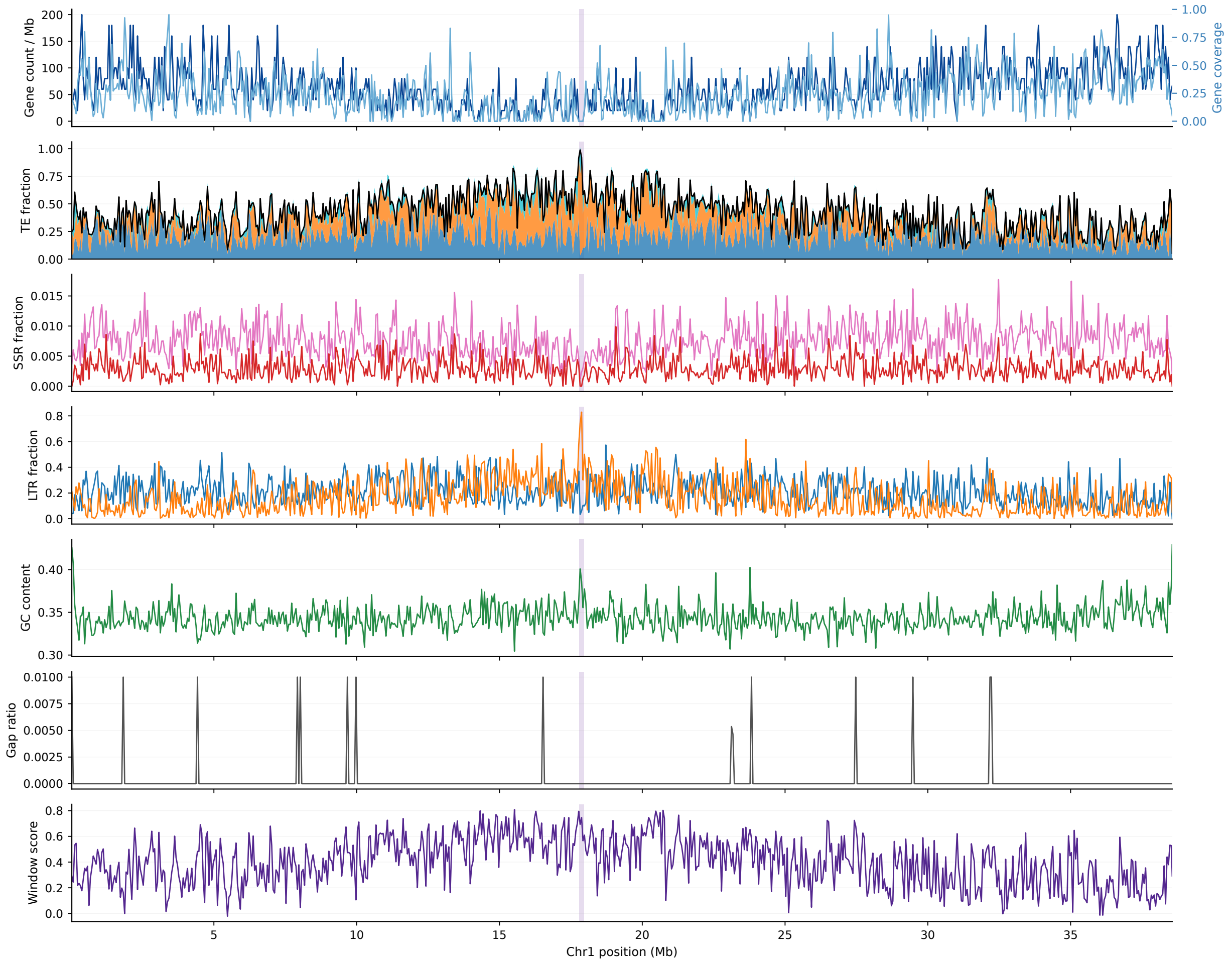
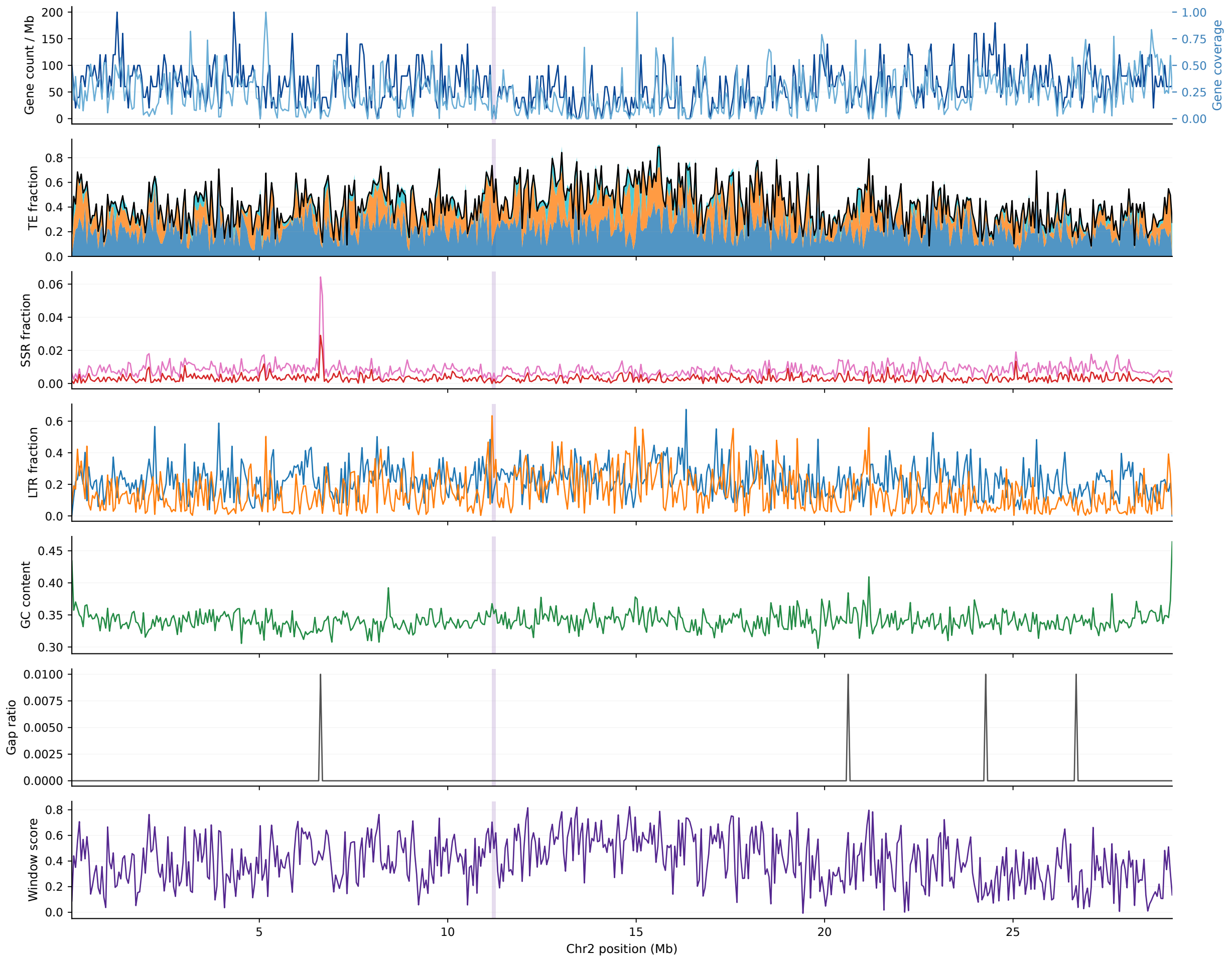


Chr1: TE, microsatellite, and selected putative centromere-like region in 50-kb windows



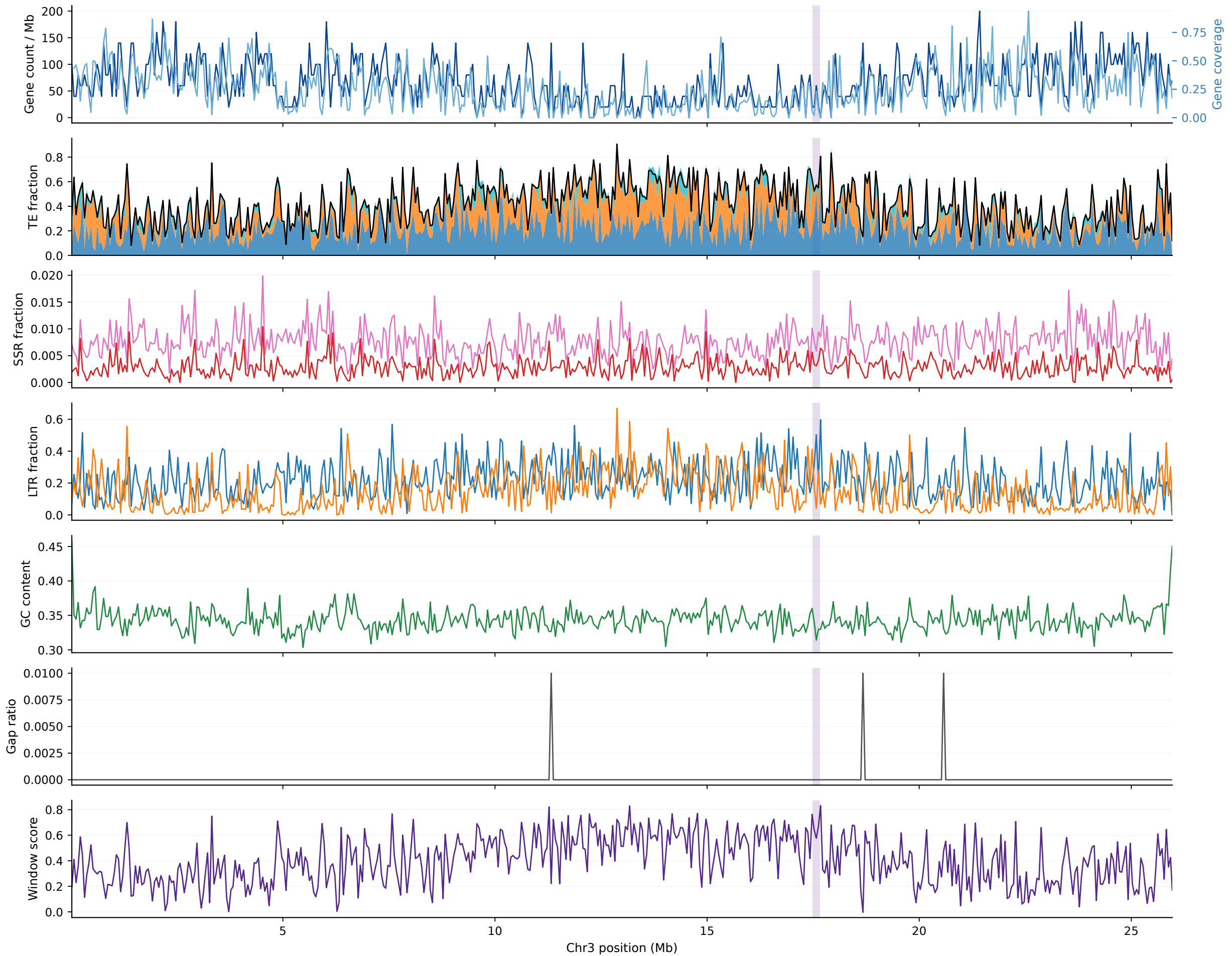
Gene count / Mb	LTR_Gypsy	SSR_total	LTR-Gypsy	Window score
Gene coverage	LTR_other	SSR_without_mono	GC content	selected putative centromere-like region
LTR_Copia	Total TE outline	LTR-Copia	Gap ratio	

Chr2: TE, microsatellite, and selected putative centromere-like region in 50-kb windows



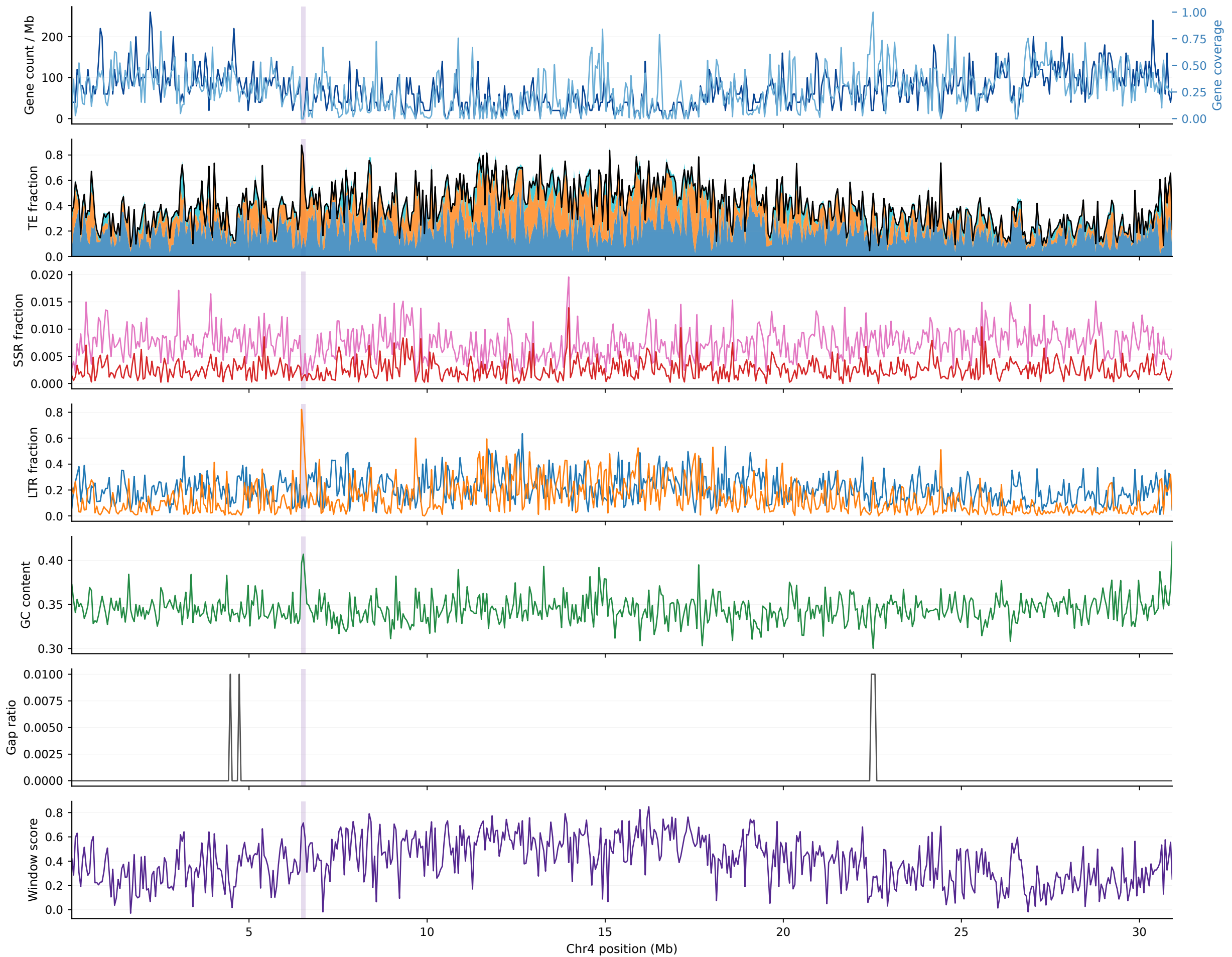
Gene count / Mb	LTR_Gypsy	SSR_total	LTR-Gypsy	Window score
Gene coverage	LTR_other	SSR_without_mono	GC content	selected putative centromere-like region
LTR_Copia	Total TE outline	LTR-Copia	Gap ratio	

Chr3: TE, microsatellite, and selected putative centromere-like region in 50-kb windows



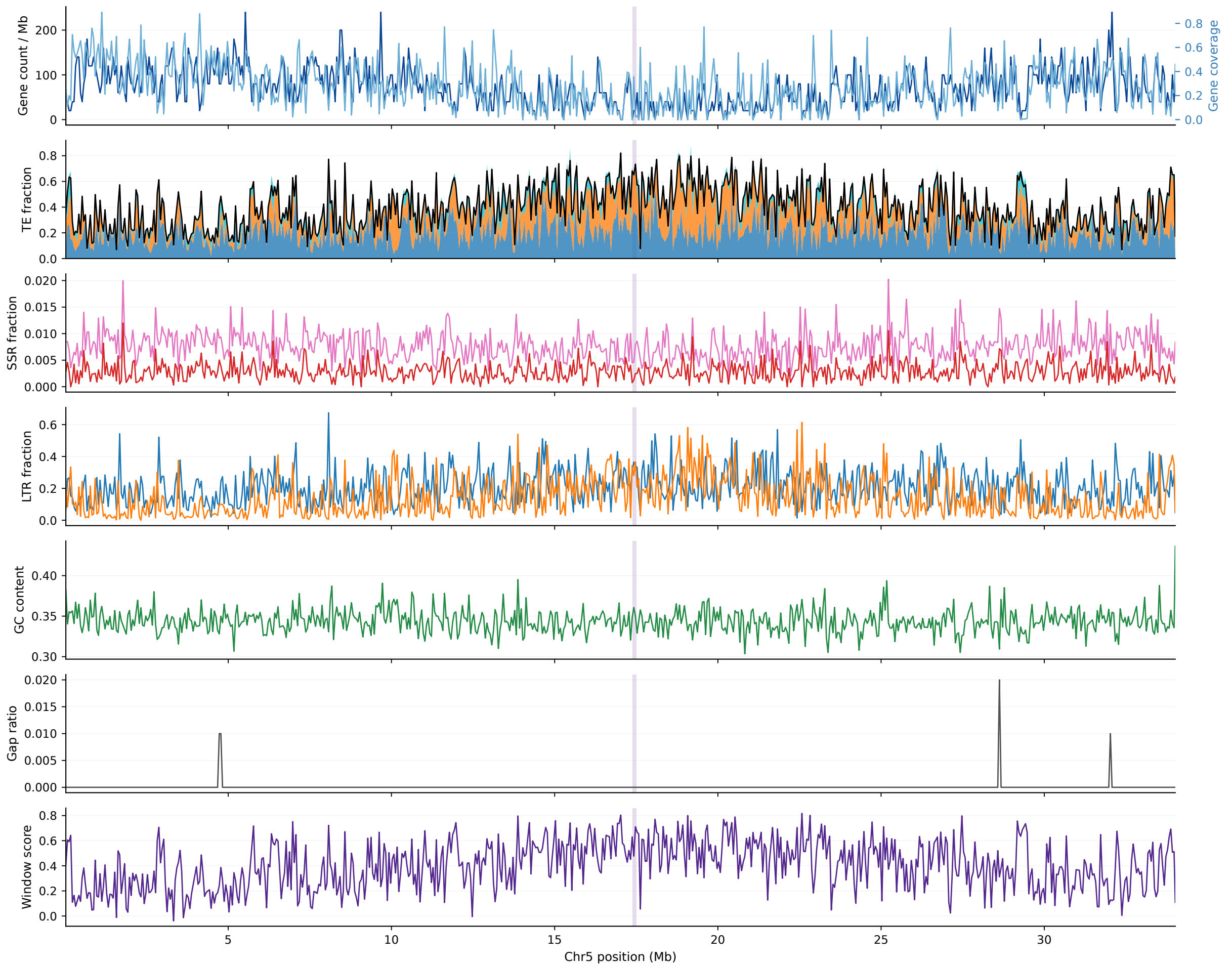
— Gene count / Mb — LTR_Gypsy — SSR_total — LTR-Gypsy — Window score
— Gene coverage — LTR_other — SSR_without_mono — GC content █ selected putative centromere-like region
█ LTR-Copia — Total TE outline — LTR-Copia — Gap ratio

Chr4: TE, microsatellite, and selected putative centromere-like region in 50-kb windows



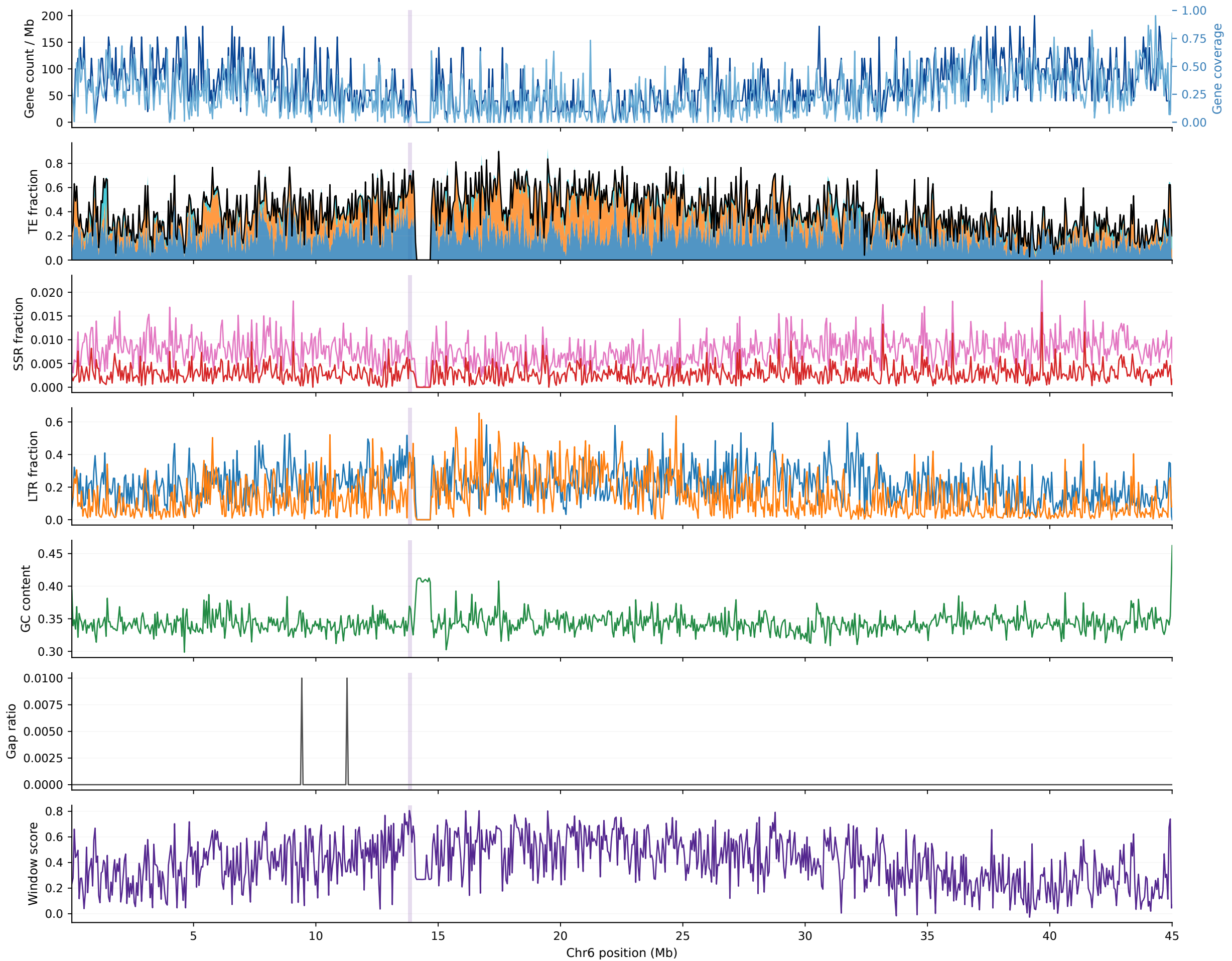
— Gene count / Mb — LTR_Gypsy — SSR_total — LTR-Gypsy — Window score
— Gene coverage — LTR_other — SSR_without_mono — GC content — selected putative centromere-like region
— LTR_Copia — Total TE outline — LTR-Copia — Gap ratio

Chr5: TE, microsatellite, and selected putative centromere-like region in 50-kb windows



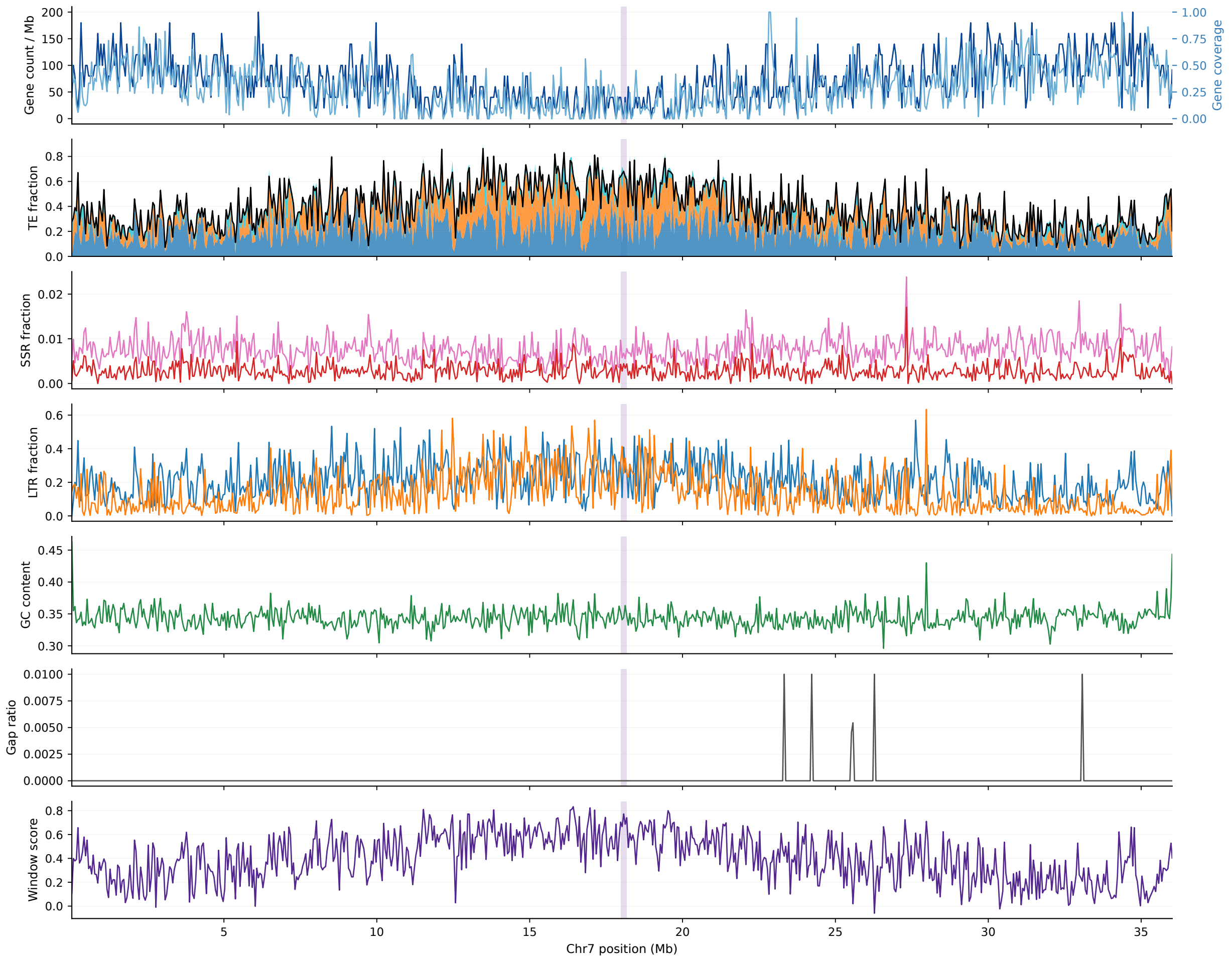
— Gene count / Mb — LTR_Gypsy — SSR_total — LTR-Gypsy — Window score
— Gene coverage — LTR_other — SSR_without_mono — GC content — selected putative centromere-like region
— LTR_Copia — Total TE outline — LTR-Copia — Gap ratio

Chr6: TE, microsatellite, and selected putative centromere-like region in 50-kb windows

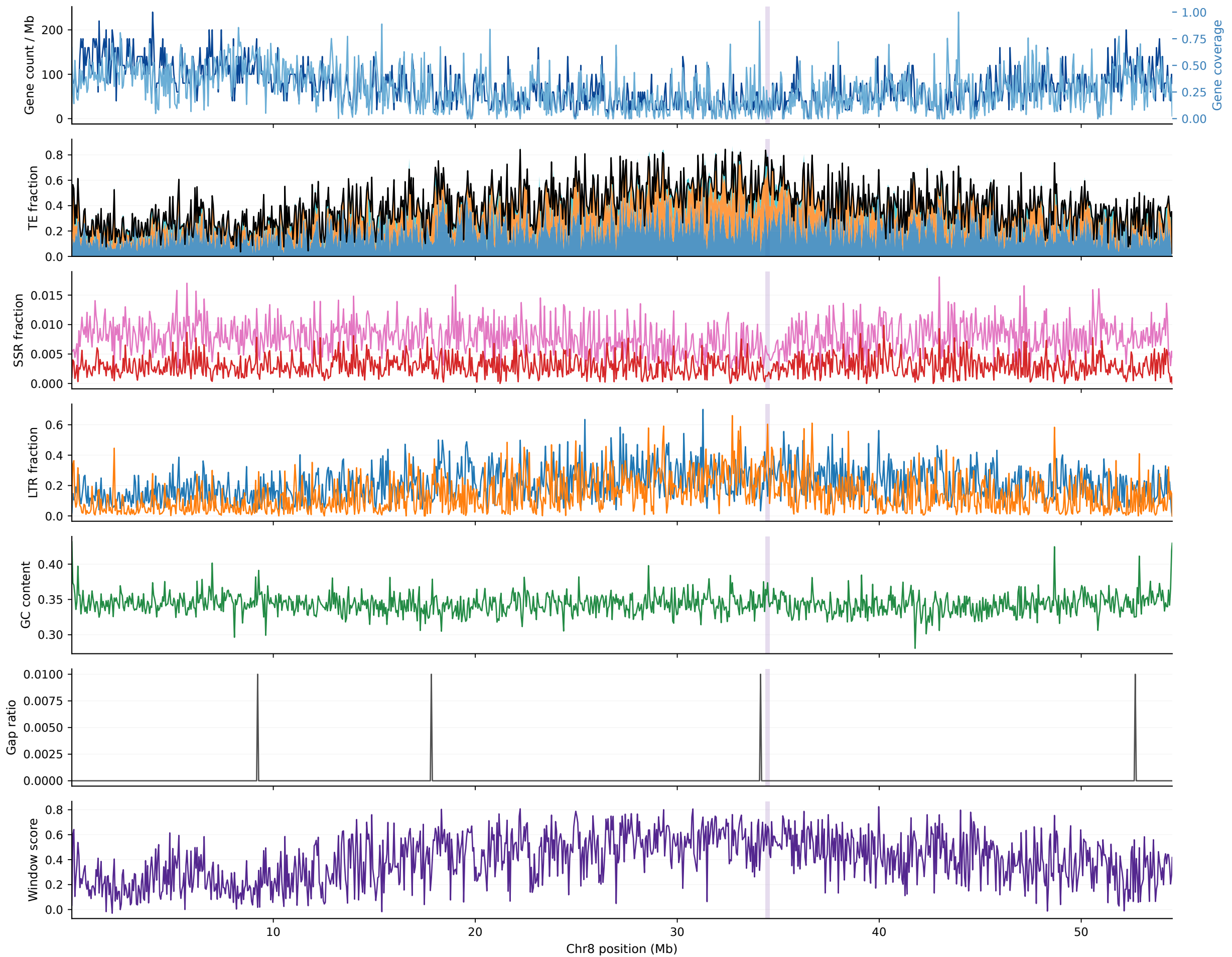


— Gene count / Mb — LTR_Gypsy — SSR_total — LTR-Gypsy — Window score
— Gene coverage — LTR_other — SSR_without_mono — GC content — selected putative centromere-like region
— LTR_Copia — Total TE outline — LTR-Copia — Gap ratio

Chr7: TE, microsatellite, and selected putative centromere-like region in 50-kb windows

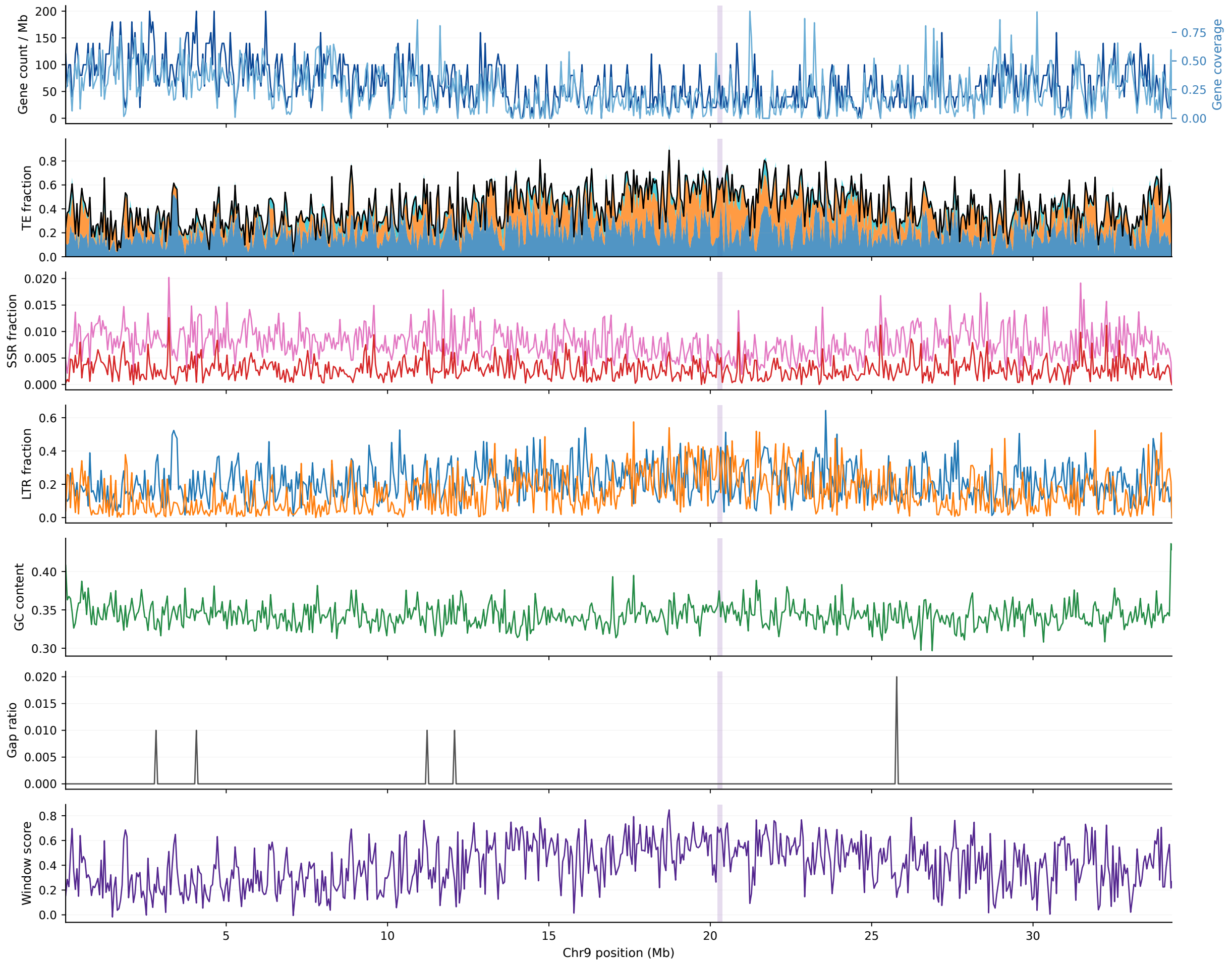


Chr8: TE, microsatellite, and selected putative centromere-like region in 50-kb windows



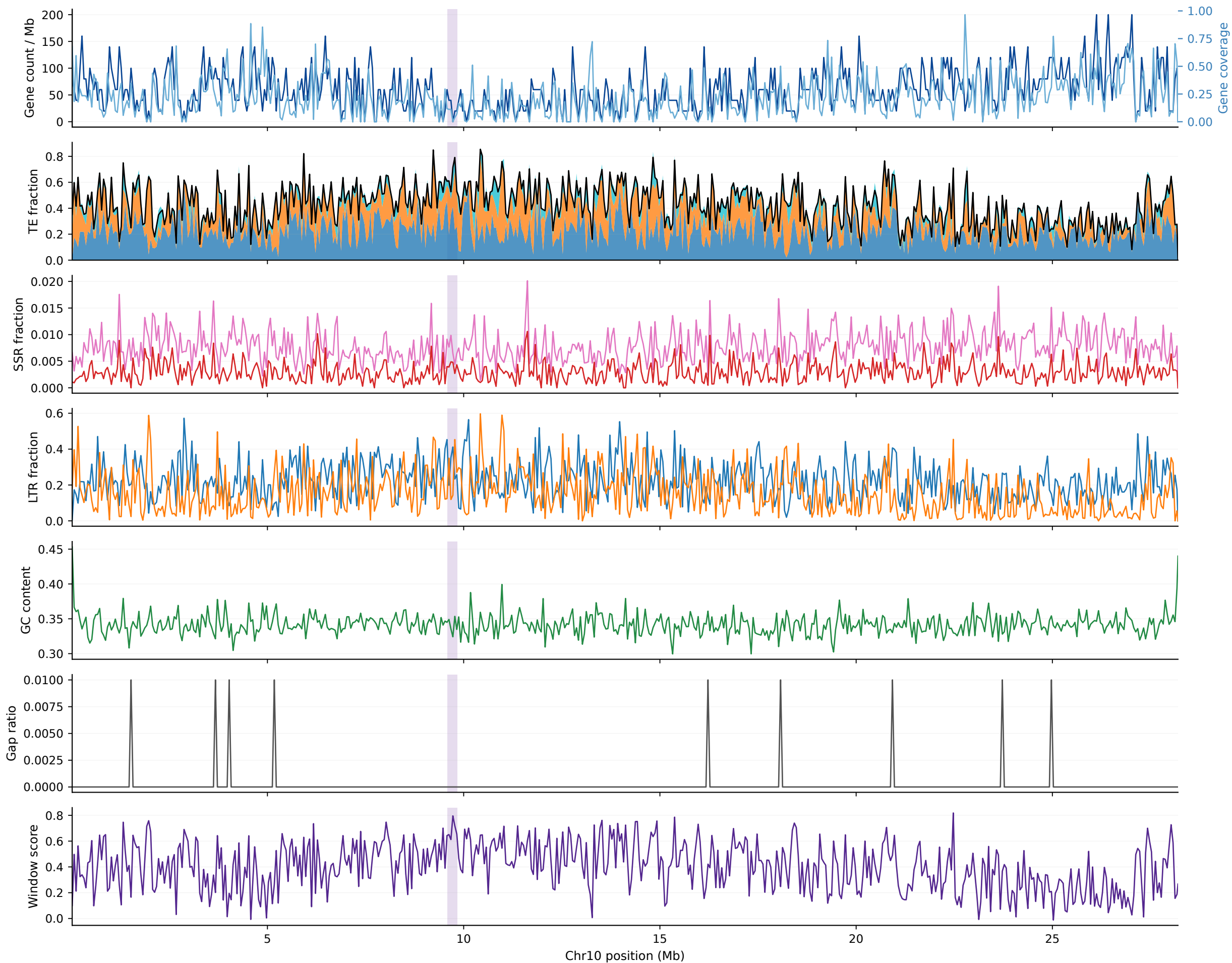
— Gene count / Mb — LTR_Gypsy — SSR_total — LTR-Gypsy — Window score
— Gene coverage — LTR_other — SSR_without_mono — GC content — selected putative centromere-like region
— LTR_Copia — Total TE outline — LTR-Copia — Gap ratio

Chr9: TE, microsatellite, and selected putative centromere-like region in 50-kb windows



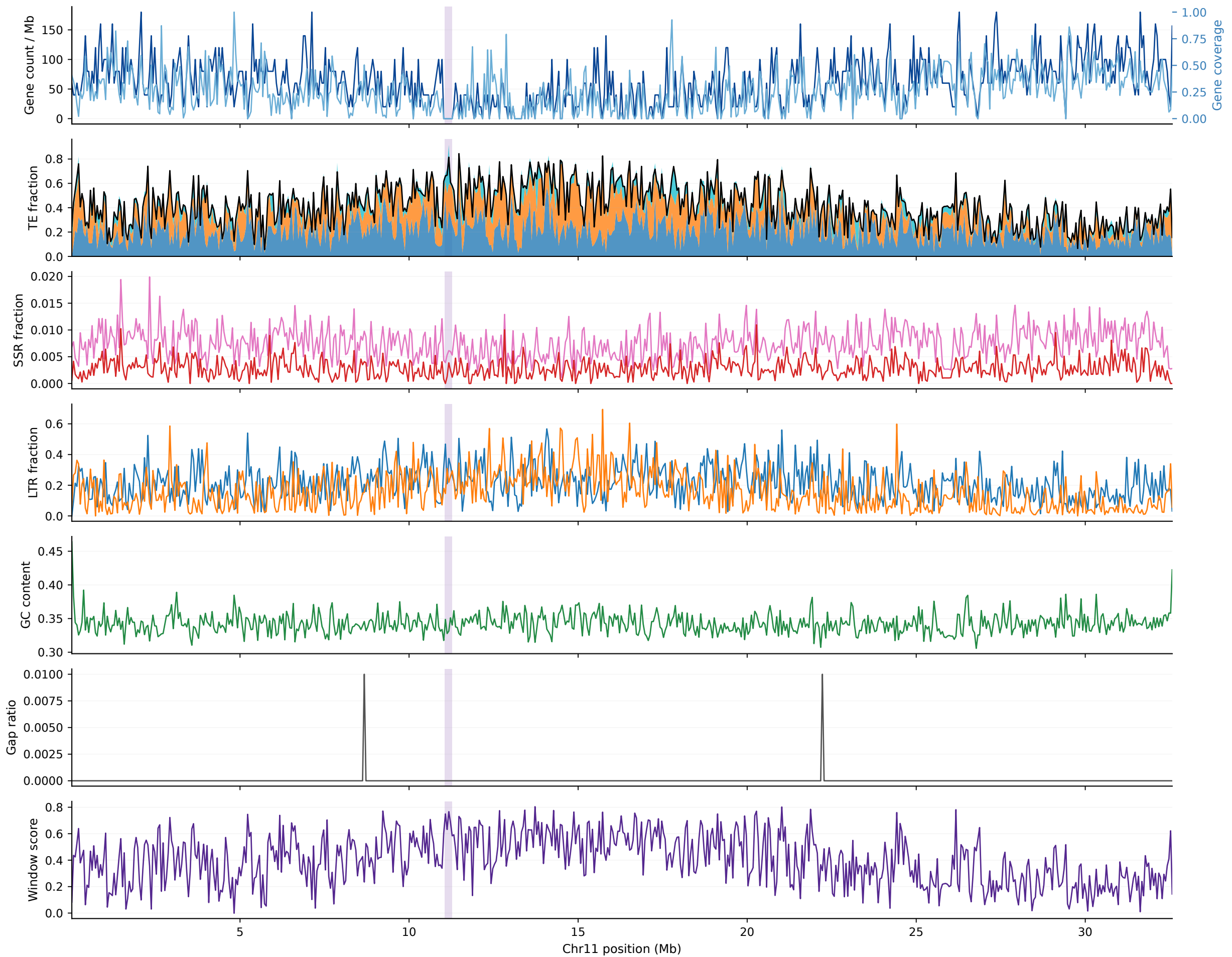
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— Gene coverage — LTR_other — SSR_without_mono — GC content — selected putative centromere-like region
— LTR_Copia — Total TE outline — LTR-Copia — Gap ratio

Chr10: TE, microsatellite, and selected putative centromere-like region in 50-kb windows



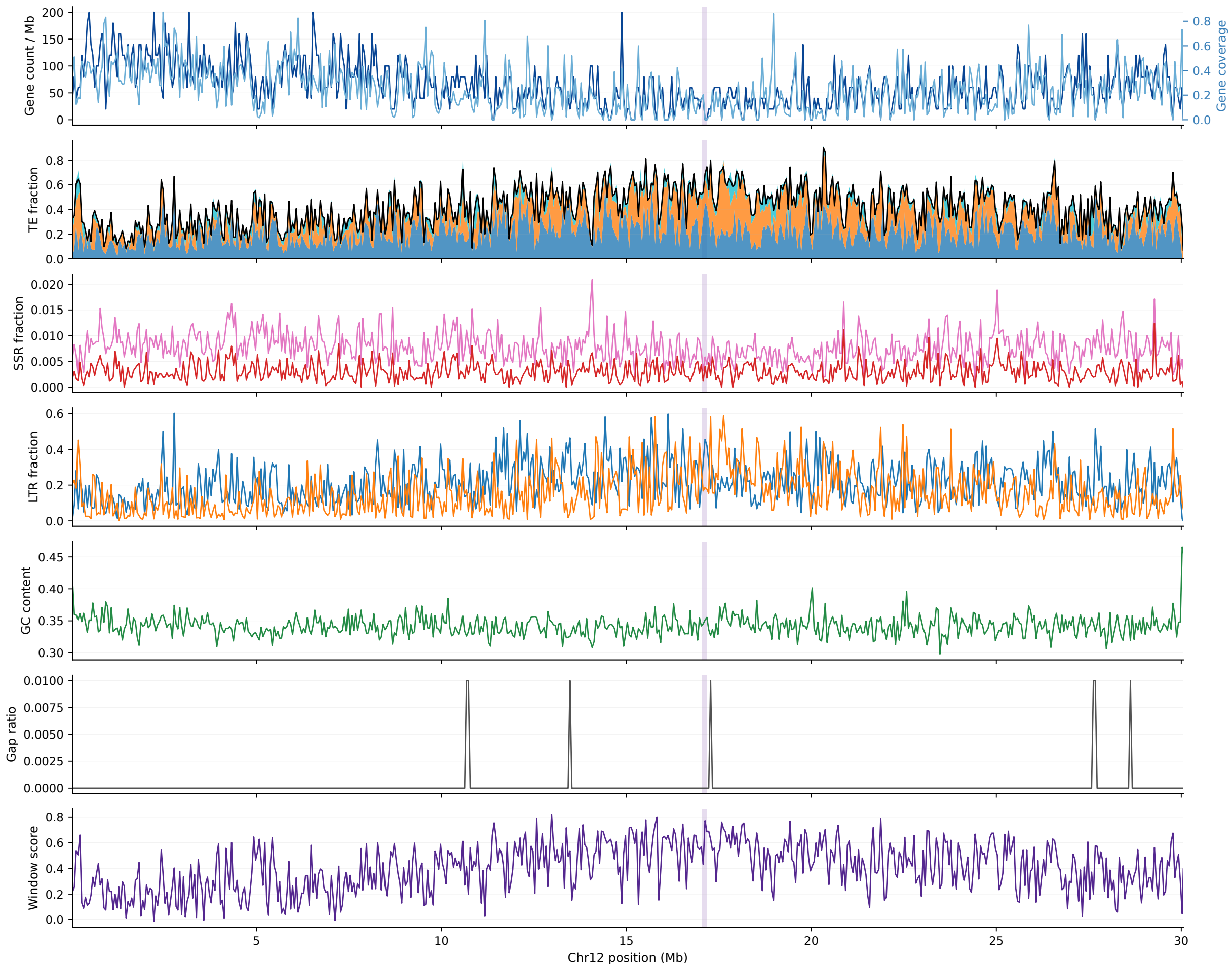
— Gene count / Mb — LTR_Gypsy — SSR_total — LTR-Gypsy — Window score
— Gene coverage — LTR_other — SSR_without_mono — GC content selected putative centromere-like region
— LTR_Copia — Total TE outline — LTR-Copia — Gap ratio

Chr11: TE, microsatellite, and selected putative centromere-like region in 50-kb windows



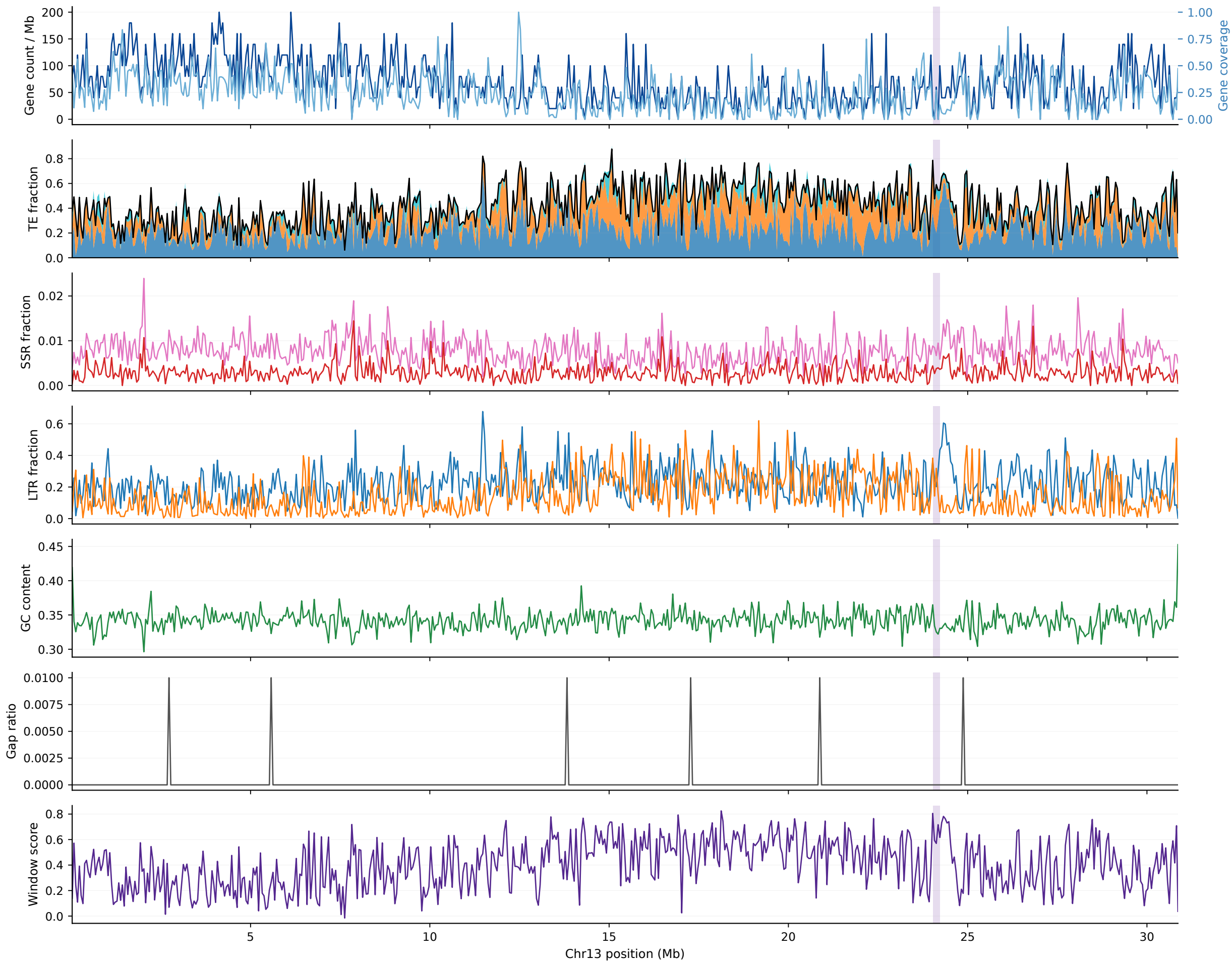
— Gene count / Mb	— LTR_Gypsy	— SSR_total	— LTR-Gypsy	— Window score
— Gene coverage	— LTR_other	— SSR_without_mono	— GC content	— selected putative centromere-like region
— LTR_Copia	— Total TE outline	— LTR-Copia	— Gap ratio	

Chr12: TE, microsatellite, and selected putative centromere-like region in 50-kb windows



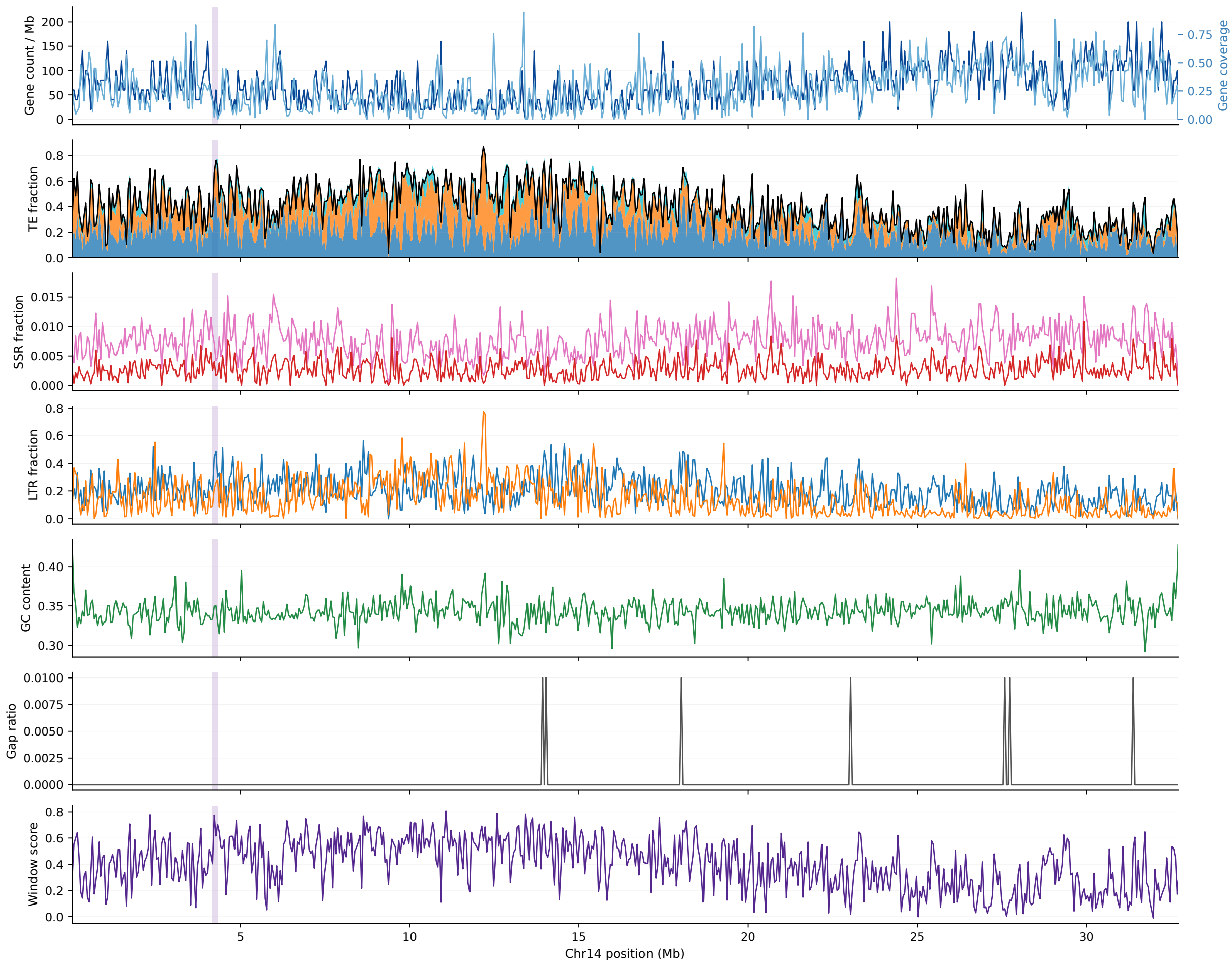
— Gene count / Mb — LTR_Gypsy — SSR_total — LTR-Gypsy — Window score
— Gene coverage — LTR_other — SSR_without_mono — GC content selected putative centromere-like region
— LTR_Copia — Total TE outline — LTR-Copia — Gap ratio

Chr13: TE, microsatellite, and selected putative centromere-like region in 50-kb windows



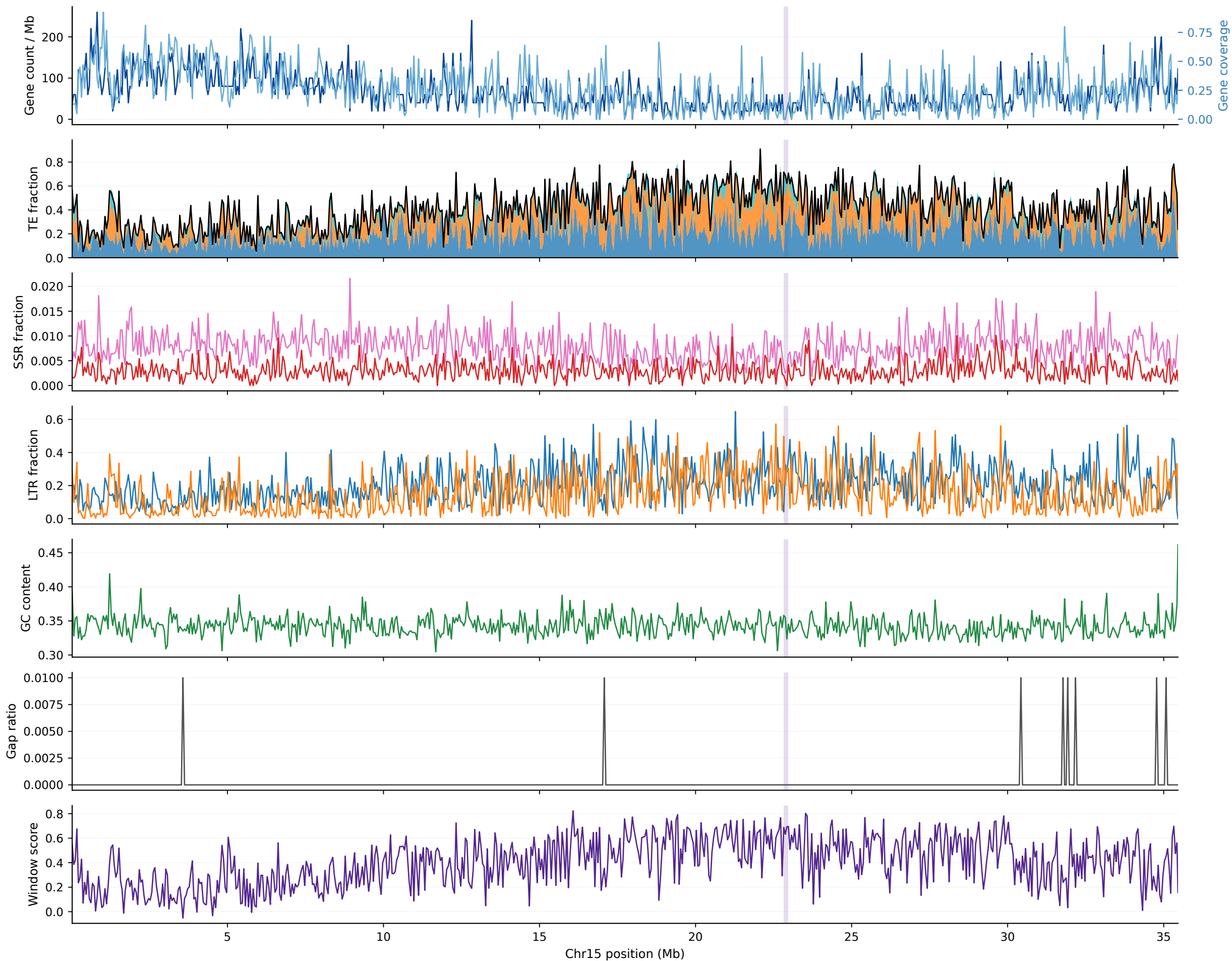
— Gene count / Mb — LTR_Gypsy — SSR_total — LTR-Gypsy — Window score
— Gene coverage — LTR_other — SSR_without_mono — GC content █ selected putative centromere-like region
█ LTR_Copia — Total TE outline — LTR-Copia — Gap ratio

Chr14: TE, microsatellite, and selected putative centromere-like region in 50-kb windows



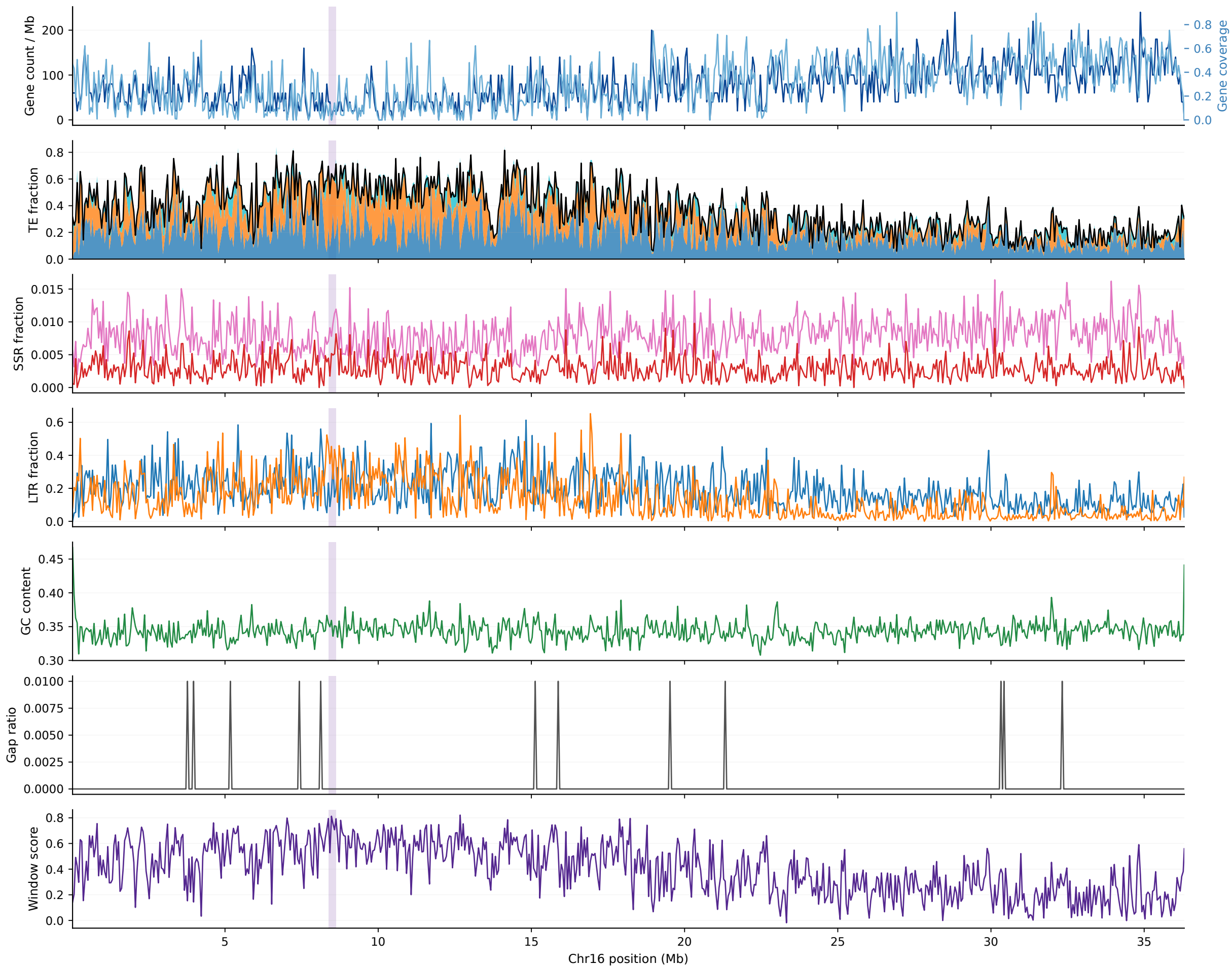
— Gene count / Mb — LTR_Gypsy — SSR_total — LTR-Gypsy — Window score
— Gene coverage — LTR_other — SSR_without_mono — GC content selected putative centromere-like region
— LTR_Copia — Total TE outline — LTR-Copia — Gap ratio

Chr15: TE, microsatellite, and selected putative centromere-like region in 50-kb windows



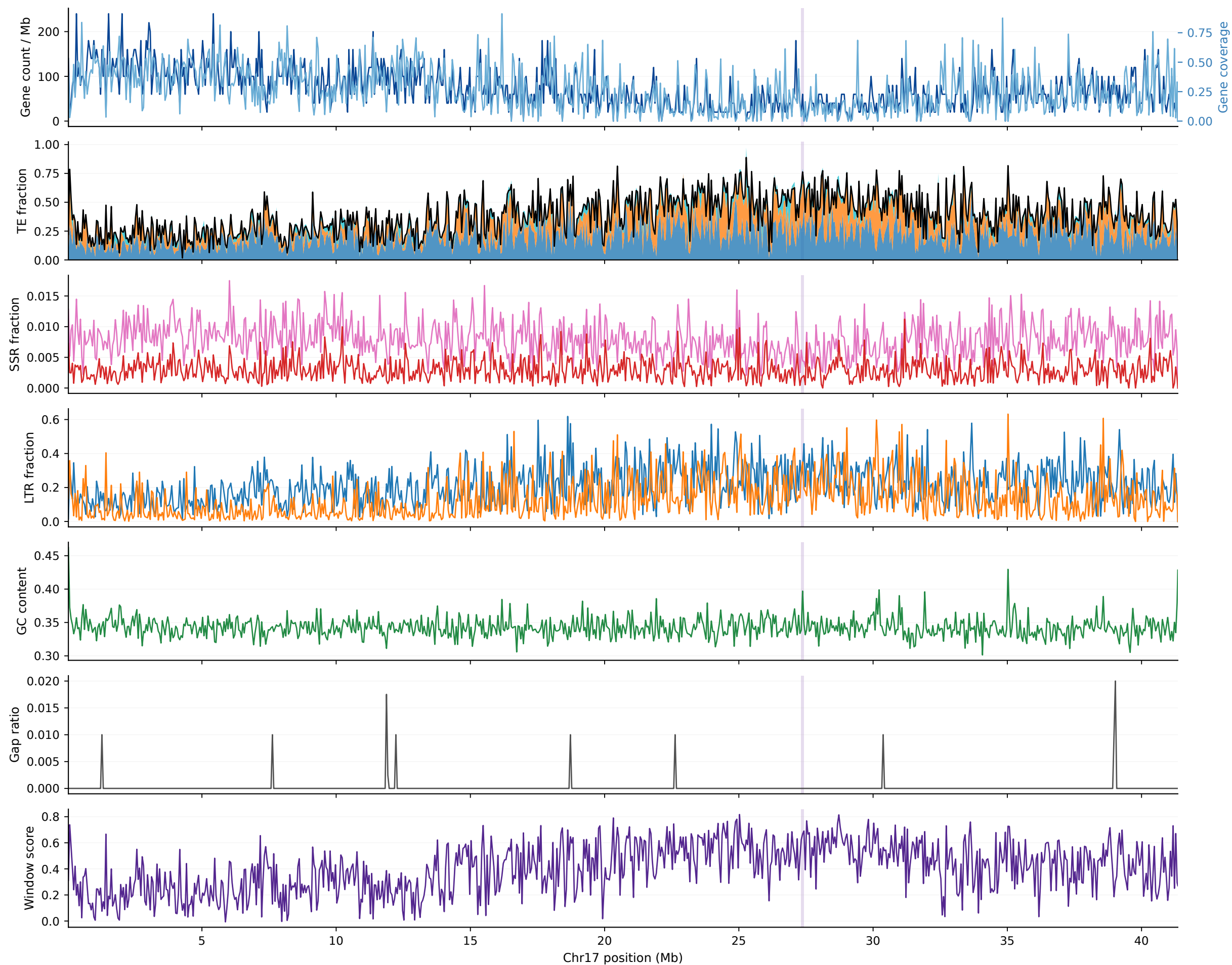
— Gene count / Mb — LTR_Gypsy — SSR_total — LTR-Gypsy — Window score
— Gene coverage — LTR_other — SSR_without_mono — GC content — selected putative centromere-like region
— LTR_Copia — Total TE outline — LTR-Copia — Gap ratio

Chr16: TE, microsatellite, and selected putative centromere-like region in 50-kb windows



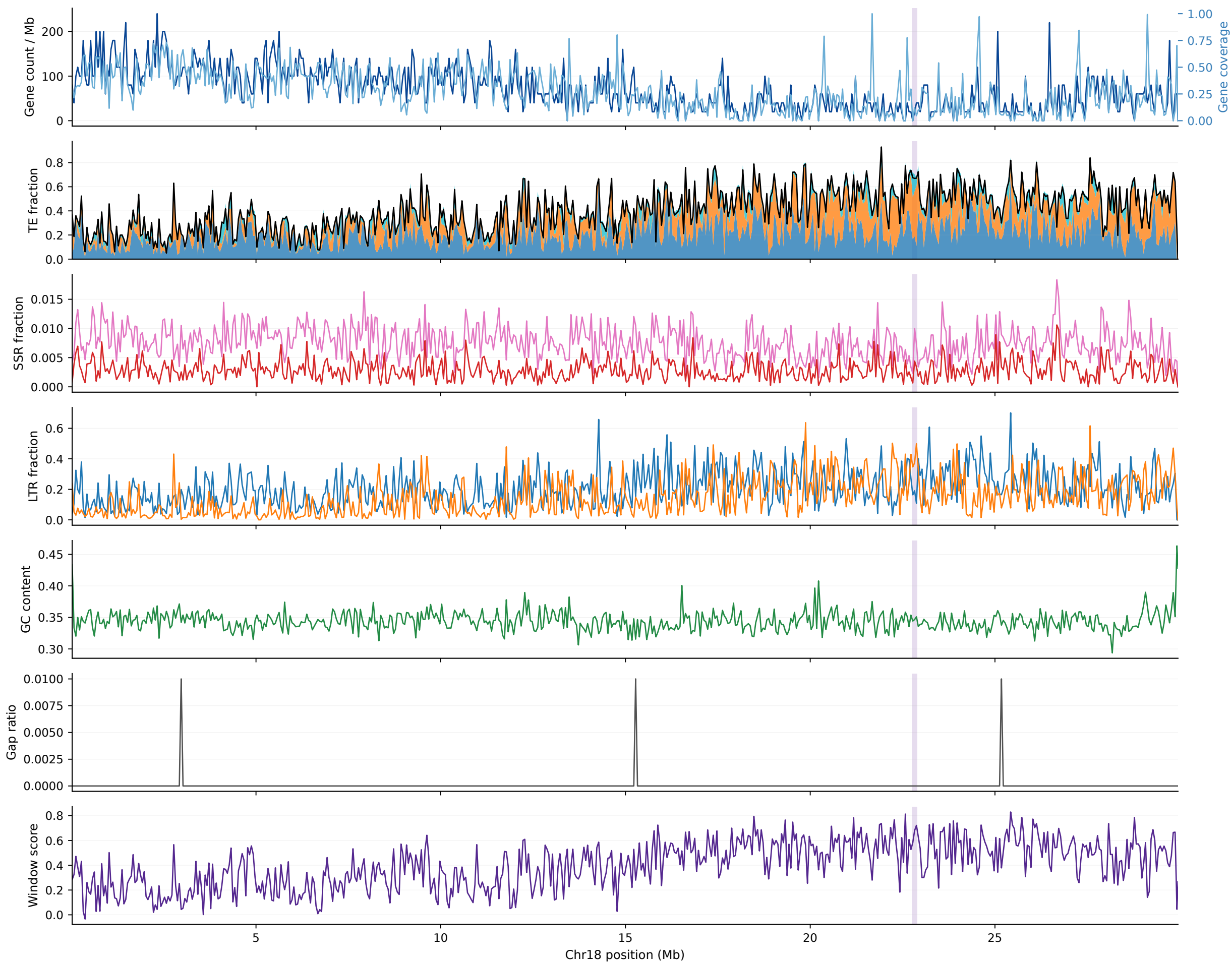
— Gene count / Mb — LTR_Gypsy — SSR_total — LTR-Gypsy — Window score
— Gene coverage — LTR_other — SSR_without_mono — GC content selected putative centromere-like region
— LTR_Copia — Total TE outline — LTR-Copia — Gap ratio

Chr17: TE, microsatellite, and selected putative centromere-like region in 50-kb windows



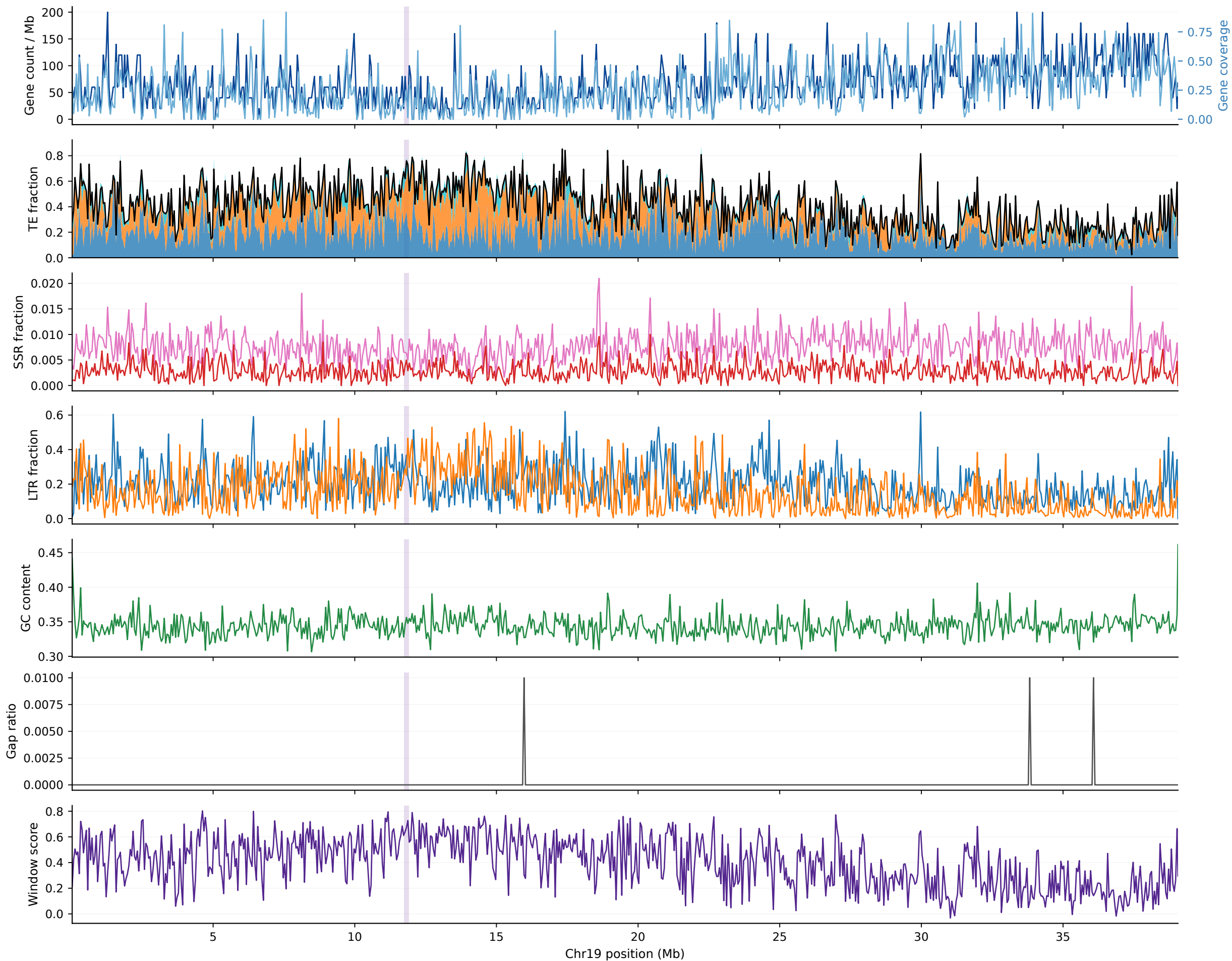
Gene count / Mb	LTR_Gypsy	SSR_total	LTR-Gypsy	Window score
Gene coverage	LTR_other	SSR_without_mono	GC content	selected putative centromere-like region
LTR_Copia	Total TE outline	LTR-Copia	Gap ratio	

Chr18: TE, microsatellite, and selected putative centromere-like region in 50-kb windows



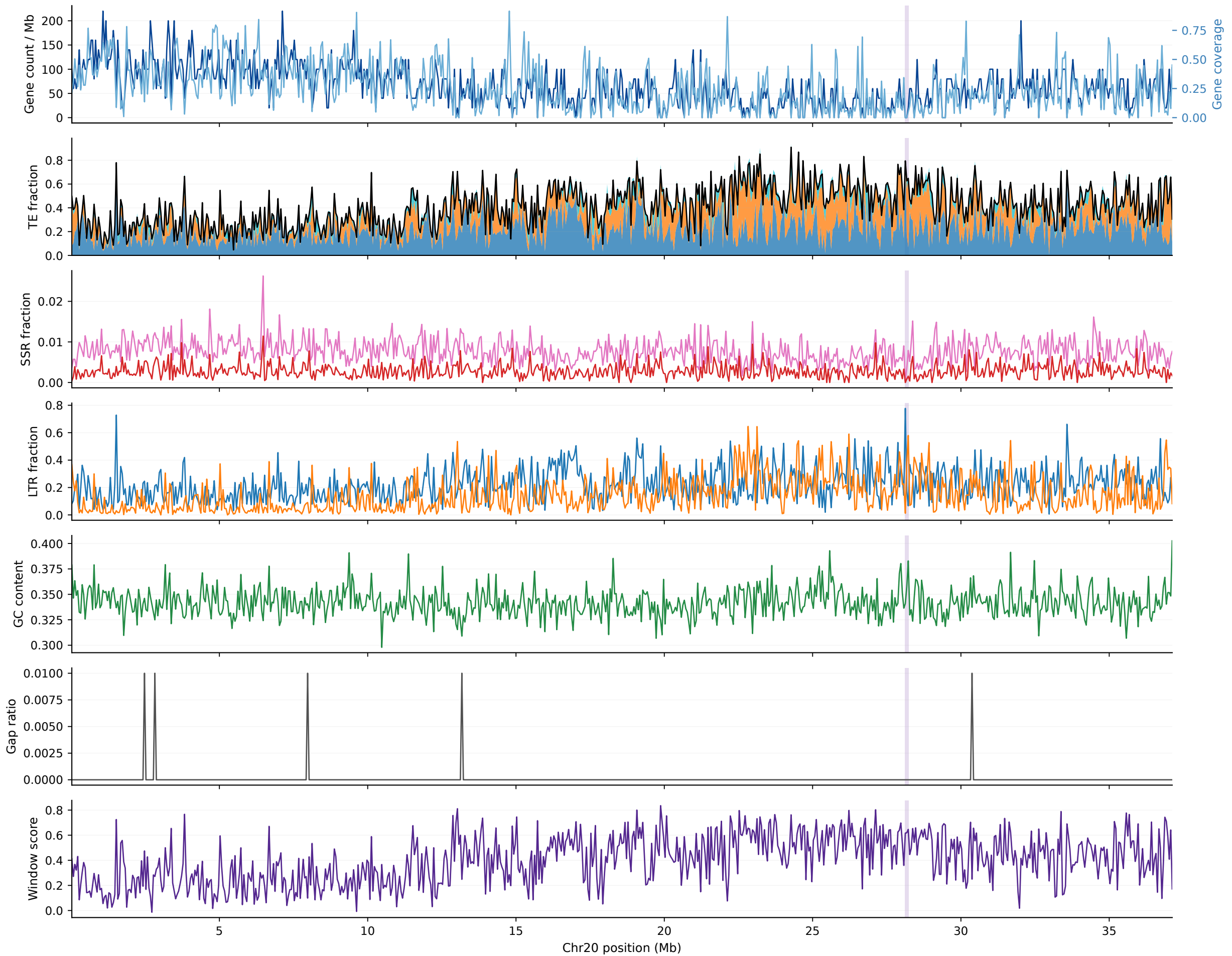
— Gene count / Mb	— LTR_Gypsy	— SSR_total	— LTR-Gypsy	— Window score
— Gene coverage	— LTR_other	— SSR_without_mono	— GC content	— selected putative centromere-like region
— LTR_Copia	— Total TE outline	— LTR-Copia	— Gap ratio	

Chr19: TE, microsatellite, and selected putative centromere-like region in 50-kb windows



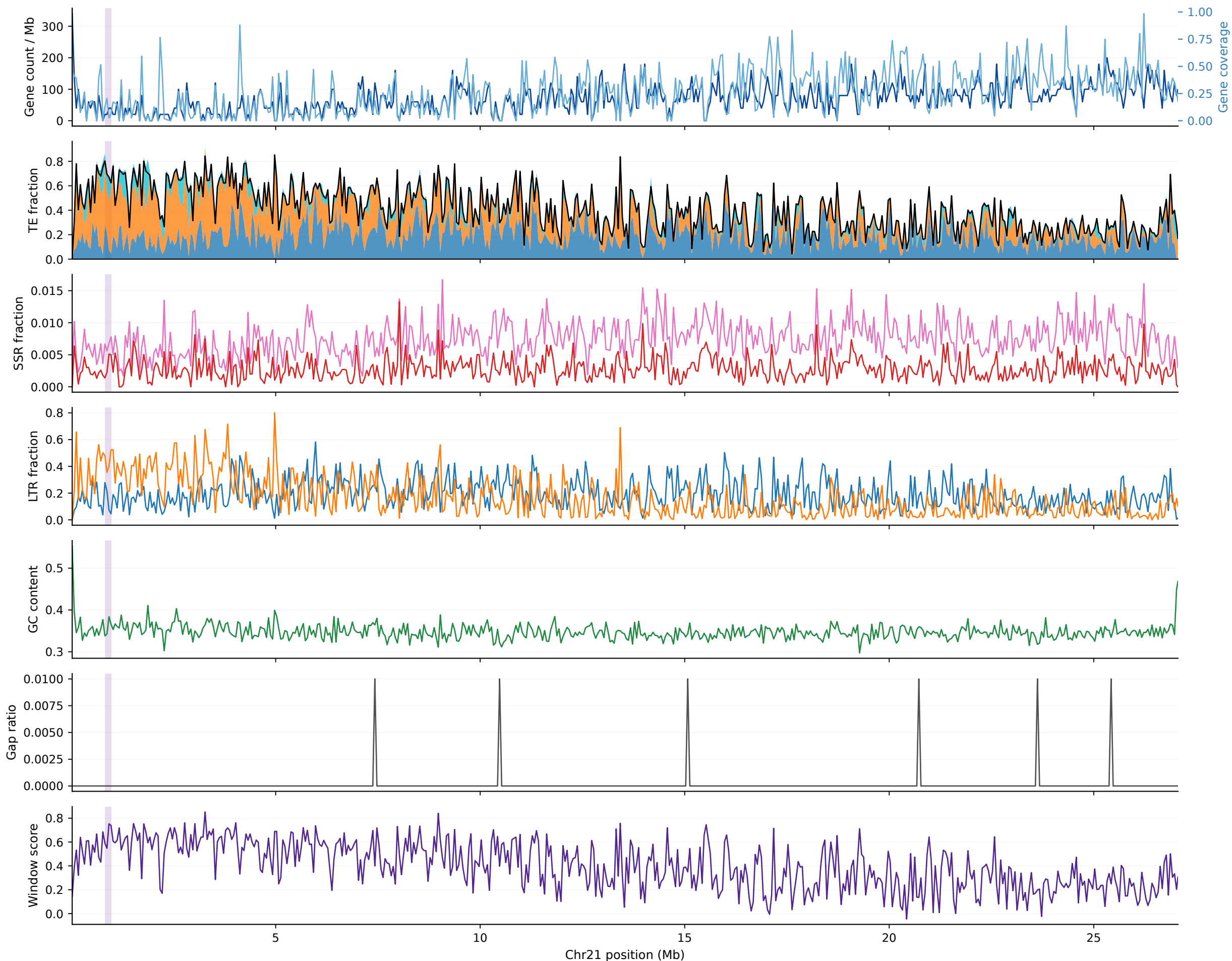
Gene count / Mb	LTR_Gypsy	SSR_total	LTR-Gypsy	Window score
Gene coverage	LTR_other	SSR_without_mono	GC content	selected putative centromere-like region
LTR_Copia	Total TE outline	LTR-Copia	Gap ratio	

Chr20: TE, microsatellite, and selected putative centromere-like region in 50-kb windows



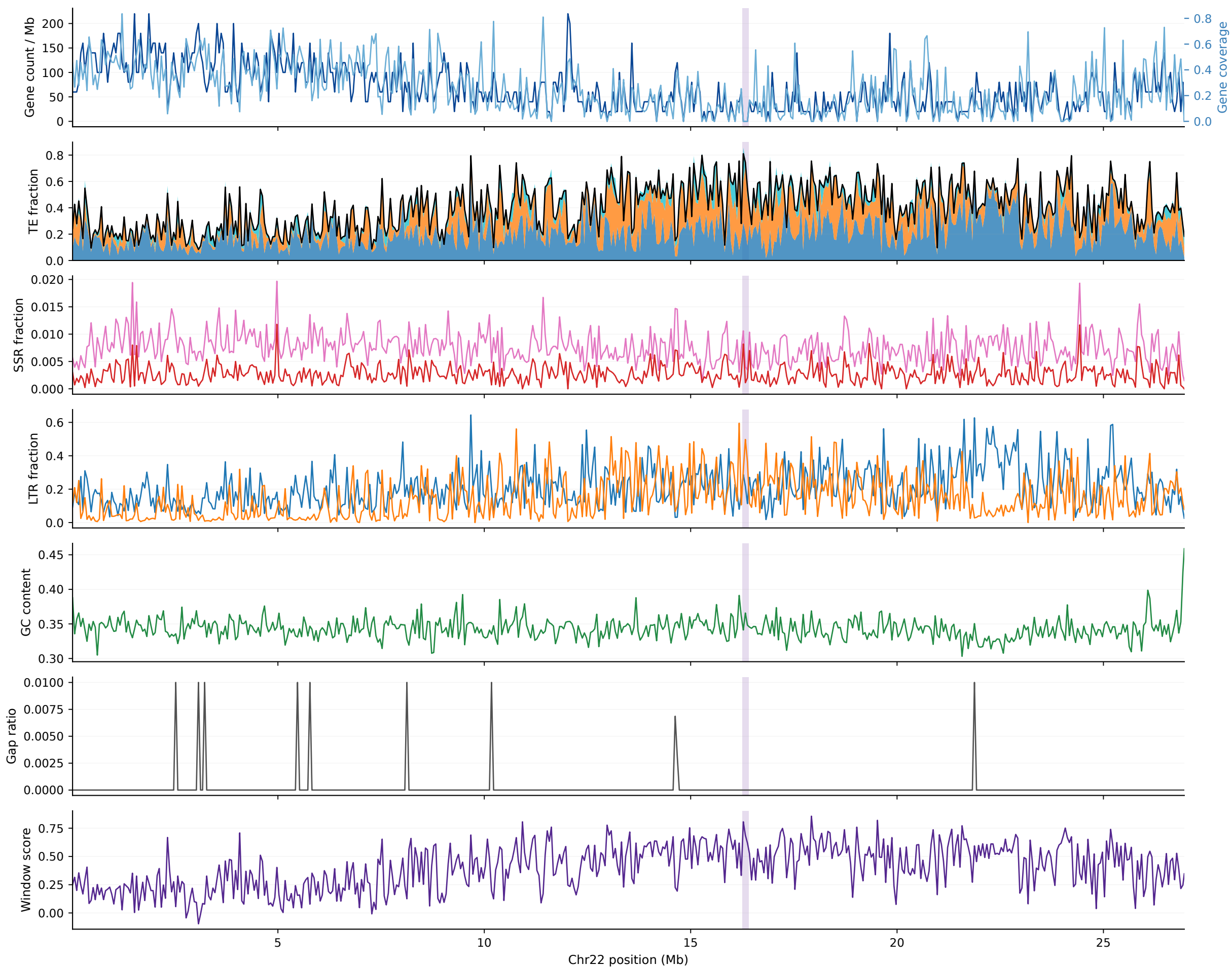
— Gene count / Mb — LTR_Gypsy — SSR_total — LTR-Gypsy — Window score
— Gene coverage — LTR_other — SSR_without_mono — GC content — selected putative centromere-like region
— LTR_Copia — Total TE outline — LTR-Copia — Gap ratio

Chr21: TE, microsatellite, and selected putative centromere-like region in 50-kb windows



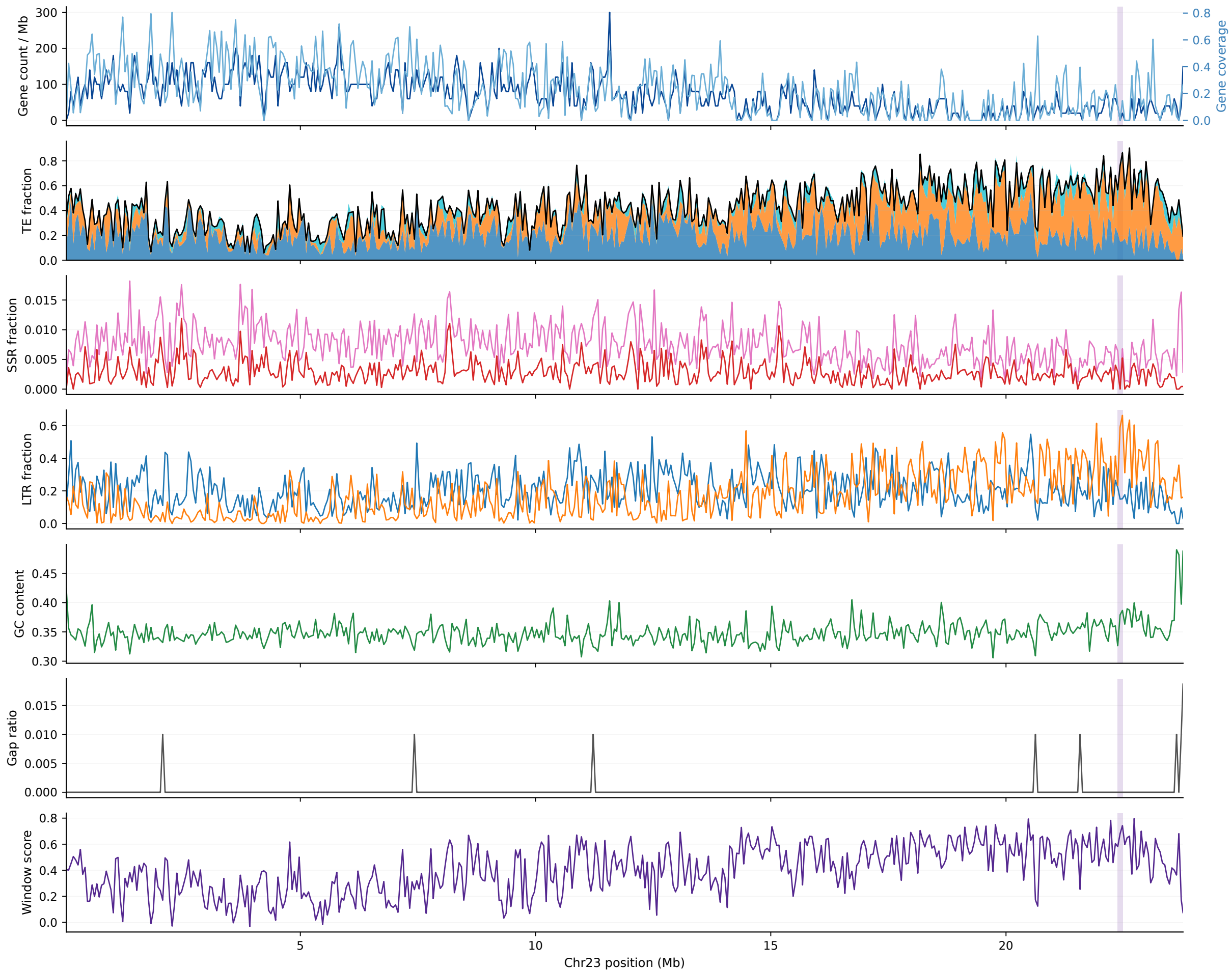
— Gene count / Mb — LTR_Gypsy — SSR_total — LTR-Gypsy — Window score
— Gene coverage — LTR_other — SSR_without_mono — GC content selected putative centromere-like region
— LTR_Copia — Total TE outline — LTR-Copia — Gap ratio

Chr22: TE, microsatellite, and selected putative centromere-like region in 50-kb windows



— Gene count / Mb — LTR_Gypsy — SSR_total — LTR-Gypsy — Window score
— Gene coverage — LTR_other — SSR_without_mono — GC content █ selected putative centromere-like region
█ LTR_Copia — Total TE outline — LTR-Copia — Gap ratio

Chr23: TE, microsatellite, and selected putative centromere-like region in 50-kb windows



— Gene count / Mb — LTR_Gypsy — SSR_total — LTR-Gypsy — Window score
— Gene coverage — LTR_other — SSR_without_mono — GC content █ selected putative centromere-like region
— LTR_Copia — Total TE outline — LTR-Copia — Gap ratio