

Table S3. **Enriched biological process from GREAT analysis of accessible chromatin sites.** Genomic coordinates of accessible chromatin sites were used as input for Genomic Regions Enrichment of Annotations Tool (GREAT) analysis (see Materials and Methods).

Chromatin sites		Total enriched GO terms*	GO biological process	-log ₁₀ (p-value)
Variable	TE (934)	9	negative regulation of cellular carbohydrate metabolic process	5.29
			regulation of gluconeogenesis	4.86
			negative regulation of carbohydrate metabolic process	4.73
			negative regulation of insulin secretion involved in cellular response to glucose stimulus	4.64
			regulation of lipid storage	4.48
			regulation of glucose metabolic process	4.46
			negative regulation of gluconeogenesis	4.43
			negative regulation of lipid storage	4.37
			negative regulation of peptide hormone secretion	4.14
	Younger LINEs (164)	2	negative regulation of gluconeogenesis	7.98
			negative regulation of cellular carbohydrate metabolic process	7.93
	No repeats (1056)	2	filopodium assembly	4.98
			antigen processing and presentation of peptide antigen via MHC class I	4.29
	Other repeats (549)	0		
Common	TE (822)	5	cellular response to peptide hormone stimulus	4.94
			oxaloacetate metabolic process	4.13
			regulation of triglyceride metabolic process	4.01
			response to peptide hormone stimulus	3.99
			triglyceride metabolic process	3.97
	No repeats (1428)	7	cellular response to hydrogen peroxide	7.00
			cellular response to oxidative stress	6.08
			cellular response to reactive oxygen species	5.55
			intestinal absorption	5.38
			response to hydrogen peroxide	4.57
			unsaturated fatty acid biosynthetic process	3.98
			regulation of glycolysis	3.83
	Other repeats (289)	0		