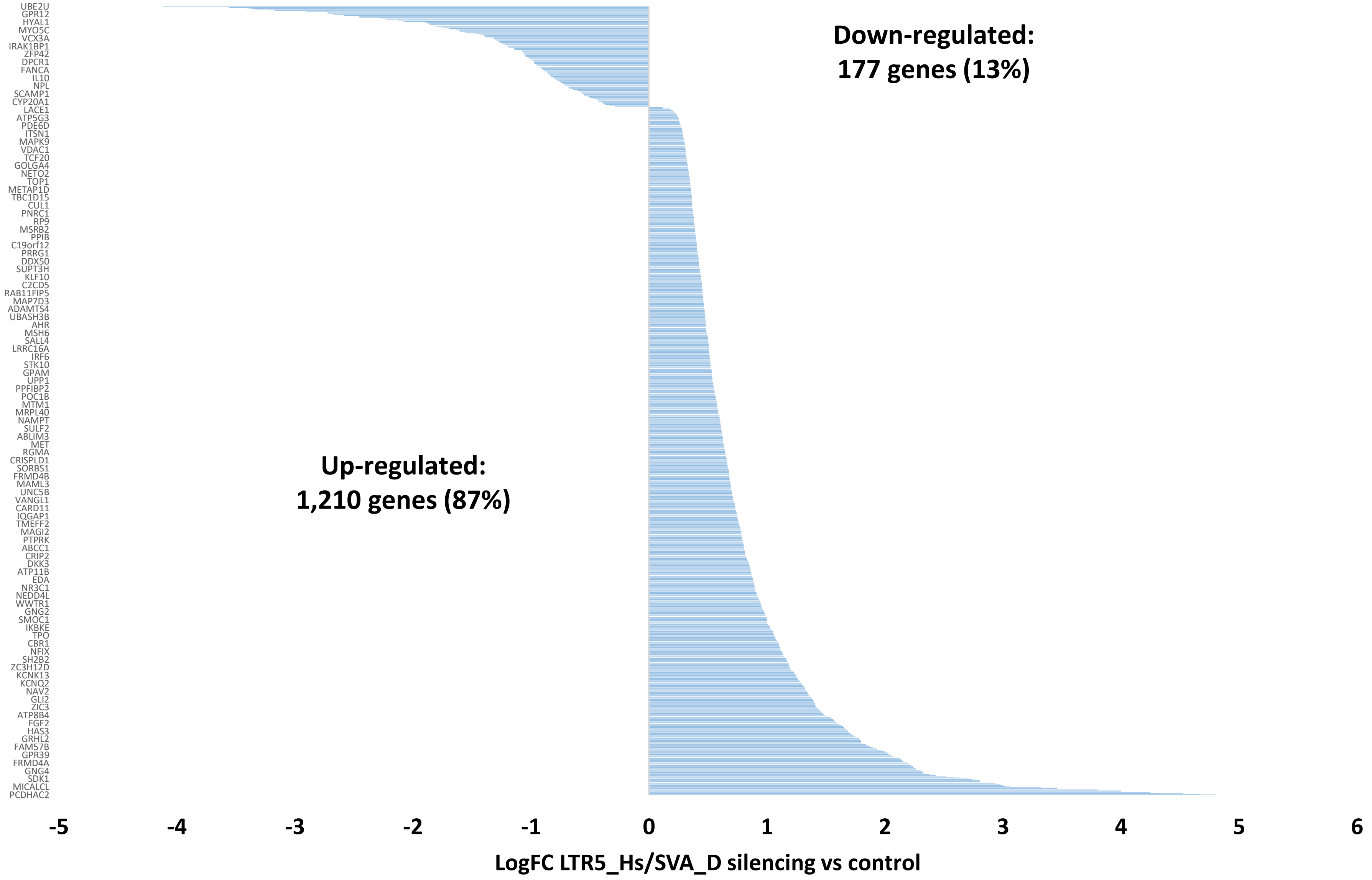
Supplemental Figure S9. Structurally, functionally, and evolutionary distinct classes of HSRS share the relatively restricted elite set of common genetic targets.

Association with networks of human-specific regulatory sequences (HSGRS) and stem cell-associated retroviral sequences (SCARS) of 8,405 genes associated with 35,074 fixed human-specific single nucleotide changes located in differentially-accessible chromatin regions during human neurogenesis in cerebral organoids

Classification category	Number of genes	Perent
Unique genes	8405	100.00
In network of human-specific genomic regulatory sequences (HSGRS)	7406	88.11
LTR5_Hs/SVA_D enhancers-regulated genes	1387	16.50
HERVH lncRNA-regulated genes	3191	37.97
LTR7Y/B enhancers-regulated genes	3306	39.33
In network of stem cell-associated retroviral sequences (SCARS)	5389	64.12
Both HSRGS & SCARS-regulated genes	4805	57.17
All HSGRS & SCARS-regulated genes	7990	95.06

Effect of CRISPR-guided epigentic silencing of LRT5_Hs/SVA_D enhancers on expression of 1,387 genes associated with human-specific SNC in DA chromatin regions



Down-regulated:
177 genes (13%)

Up-regulated:
1,210 genes (87%)

Effects of stem cell-associated retroviral sequences (SCARS) on expression of 5,389 genes associated with human-specific neuro-regulatory SNC located in DA chromatin regions during brain development in cerebral organoids

Classification category	Number of genes	Down-regulated	Percent	Up-regulated	Percent
LTR5_Hs/SVA_D enhancers-regulated genes	1387	1210	87.24	177	12.76
HERVH lncRNA-regulated genes	3191	1733	54.31	1458	45.69
LTR7Y/B enhancers-regulated genes	3306	2494	75.44	812	24.56