



Figure S9. Violin plots representing the impact of TE-mediated gene silencing in all six samples. Genes are classified into two scenarios: localized outside (Isolated) and inside (Cluster) a TE cluster. Each term reports two sets of genes: enclosed by TEs at 1kb upstream and/or downstream (+TE) and not enclosed by a TE as control condition (Ctl). For each scenario are reported methylation (A and B), mRNA transcription (C and D) and sRNAs production (E and F).