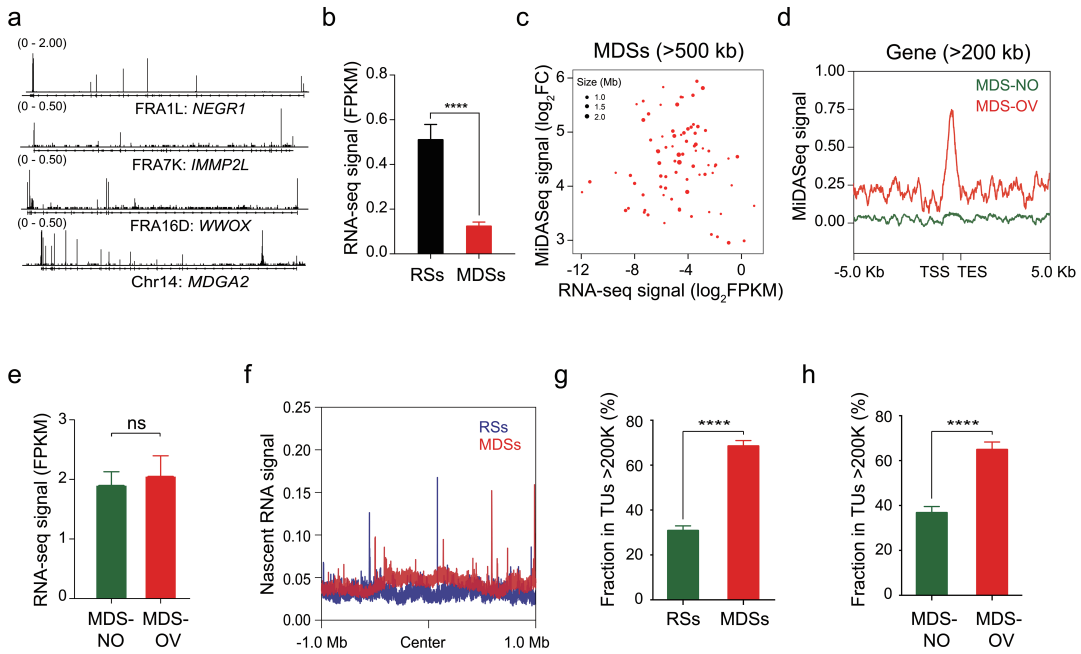
Supplementary information, Fig. S7



Supplementary information, Fig. S7

a Representative view of RNA-seq signal at three known CFSs and a MDS. **b** Quantitative comparison of RNA-seq signal between RSs and MDSs. Data are shown as mean ± S.E.M, ****, P < 0.0001 determined using Wilcoxon rank-sum test. **c** Scatter plot showing the MiDASeq signal and RNA-seq signal in MDSs spanning over 500 kb. **d** Aggregation plots of MiDASeq signal distribution across the gene bodies of large genes (>200 kb as the cutoff). **e** Quantitative analysis of RNA-seq signal in MDS-NO and MDS-OV genes. Data are shown as mean ± S.E.M. P value was determined by Wilcoxon rank-sum test. **f** Aggregation plots of nascent RNA signal distribution across the RSs and MDSs in a 2 Mb window. **g** Fraction of RSs and MDSs in TUs >200 kb. ****, P < 0.0001 determined using Wilcoxon rank-sum test. **h** Fraction of MDS-NO and MDS-OV genes > 500K in TUs >200 kb. ****, P < 0.0001 determined using Wilcoxon rank-sum test.