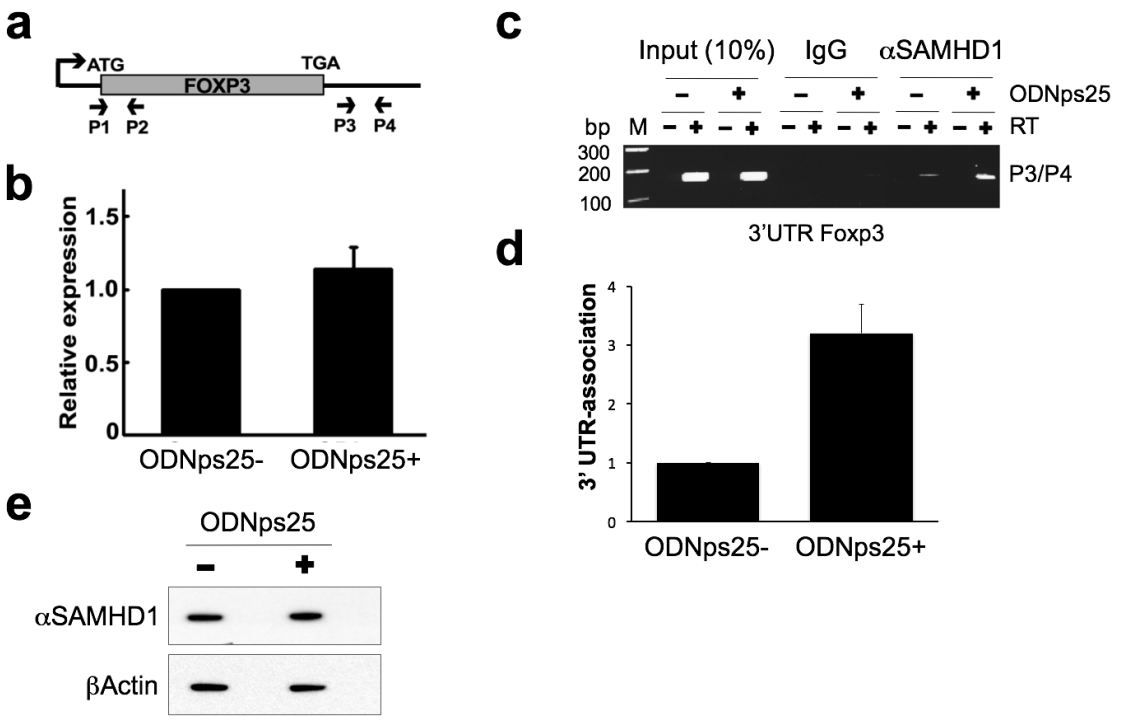
Supplemental Data

Supplemental Figure 1



Supplemental Figure 1. (A) Locations of primer sets (P1/P2 and P3/P4) for RIP-qPCR within Foxp3 transcript. Sequences of primer sets were informed in Methods. (B) Expression of total Foxp3 mRNA in ODNps25-treated or control Tregs. polyclonal Tregs expanded *in vitro* were cultured with rIL-2 (200 IU/ml) in the presence or absence of ODNps25 (2 μM) for 36 hrs. P1 and P2 in (A) were used for the primer set of qRT-PCR. Data was normalized with external HPRT control. (C) RIP-qPCR for the detection of interaction between SAMHD1 and 3'UTR of Foxp3 in the presence or absence of ODNps25. RIP analysis was performed from the whole extract of Tregs in (B), followed by qPCR with P3 and P4 primers specific to 3'UTR of Foxp3. (D) Relative quantification of RIP-qPCR results, was measured by SYBR green-qPCR. (E) Protein quantification of SAMHD1 in ODNps25-treated or control Tregs. Total proteins (5 μg/lane) were extracted from control or ODNps25-treated Tregs at post 36 hr-incubation.