Supporting Information

A restriction enzyme-powered autonomous DNA walking machine: Application for highly sensitive electrochemiluminescent assay of DNA

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Comparison of the walking machines with different stators

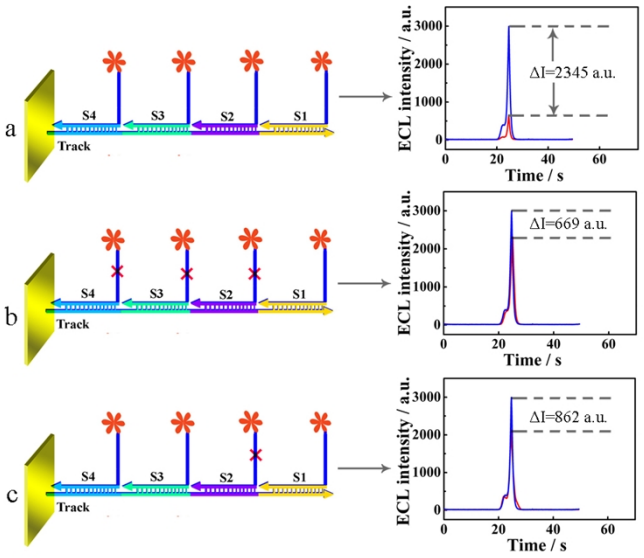

Fig. S1 Typical ECL-time profiles of the walking machine with different stators to the DNA walker (1 nM): (a) stators without any base mismatches; (b) base mismatches were introduced to S2, S3 and S4; (c) base mismatches were introduced to S2 only. The nucleic acid nanostructure track-modified AuEs were incubated with the DNA walker and Nt.A1wI (5 U) for 1 h. The base mismatched sequences were listed as follows: S2,

5’-COOH-$(CH_2)_6$-TTTT TGG TTC AGT GCT TAT TCG ATT TCC AAT GCT CAA GAT CGA-3’; S3, 5’-COOH-$(CH_2)_6$-TTTT TGG TTC AGT GCT TAT TCG ATT TTC CAT GCG TTA GAT ACT-3’; S4, 5’-COOH-$(CH_2)_6$-TTTT TGG TTC AGT GCT TAT TCG ATT TGC TAT GCC ACA GAT GGT-3’. Other conditions, as in Fig. 2B.

To investigate the effect of the base mismatches of the stators to the ECL signal suppressions in the presence of the walker DNA, we have performed experiments by introducing base mismatches (indicated as red crosses in Fig. S1) to the DNA stators. The base mismatches are located at the recognition site of Nt.AlwI to prevent the cleavage by Nt.AlwI when the DNA walkers hybridize with the mismatched binding arms. As shown in Fig. S1, the introduction of base mismatches to S2, S3 and S4 leads to much less ECL signal suppression compared with the one without any base mismatches (b vs. a in Fig. S1) due to the fact that the introduction of the base mismatches prevents the removal of the $Ru(bpy)_2$phen labels on the binding arms of S2, S3 and S4. When the base mismatch is introduced to S2 only, small increase in ECL signal suppression is observed (c vs. b in Fig. S1) because of the possible removal of $Ru(bpy)_2$phen labels on the binding arms of S3 and S4 upon binding to the DNA walkers. Such increase in ECL signal suppression is insignificant when compared with the situation without any base mismatches (c vs. a in Fig. S1), indicating the preferable hybridizations between the DNA walkers and the binding arms of S1.