fuel + gate(Quencher):output input(Fluorescence) ↔ gate(Quencher):input(Fluorescence) + output + gate(Quencher):fuel (3).

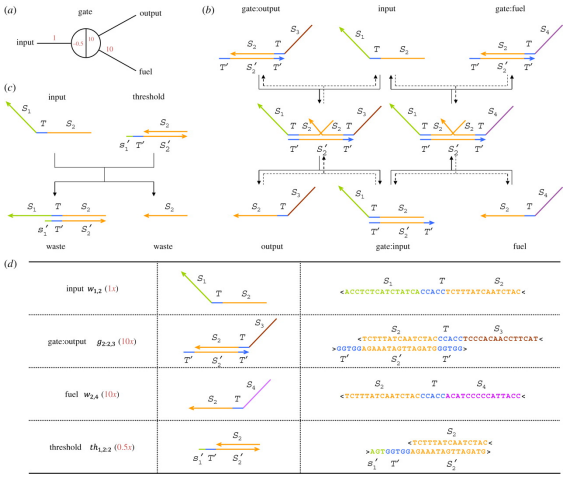

Fig. 2. Seesaw gate reaction [4]: (a) Abstract gate diagram. Red numbers indicate initial concentrations. (b) The DNA gate motif and reaction mechanism. S1, S2, S3 and S4 are the recognition domains; T is the toehold domain; T0 is the Watson–Crick complement of T, etc. Arrowheads mark the 30 ends of strands. Signal strands are named by their domains from 30 to 50, All reactions are reversible and unbiased; solid lines indicate the dominant flows for the initial concentrations shown in (a), while the reverse reactions are dotted. (c)

5. Result

From biochemical experiments, we observed that when we added non-mutated input and mutated input, the system selected higher concentration one (Fig.3). And we also confirmed the behaviors in the time series of the concentration of normal input and mutated input sequences showed oscillations (Fig.3). And when the concentration decreased, the concentration of another input increased, hence we conjecture that the system selects higher concentration one because the selected input sequences were switched among non-mutated and mutated input sequences. These results illustrate that the system made of DNA reaction networks is able to select input sequences in higher concentration so it will be able to adapt to the environmental change. Therefore, from biological and philosophical points of views, this system realizes molecular Artificial Intelligence (Fig.3).

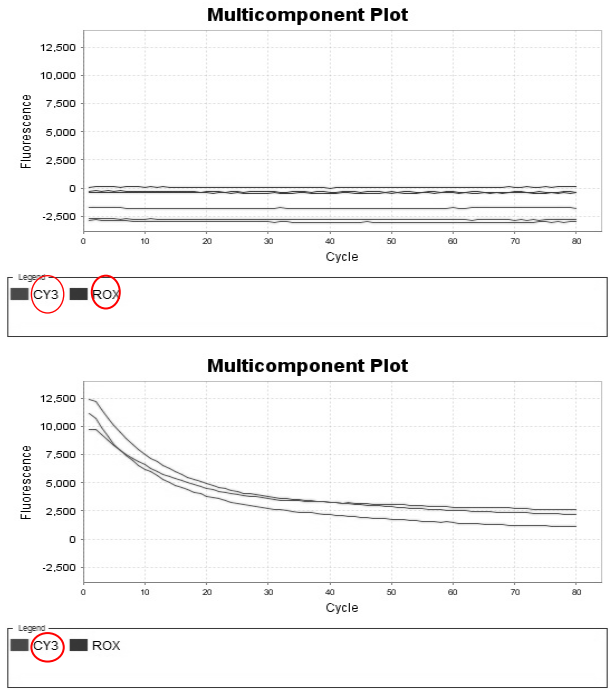

Fig. 3. Time series of concentration of Input sequences obtained by the real time PCR: (Upper) No input sequence, (Lower) Input sequences without toehold, the concentration of input sequences decreased through binding to gate:output sequences. CY3 and ROX are fluorescent dyes to label DNA sequences.

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