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SUPPLEMENTARY INFORMATION

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Detection and identification of genetic material via single-molecule conductance

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Supplementary Information

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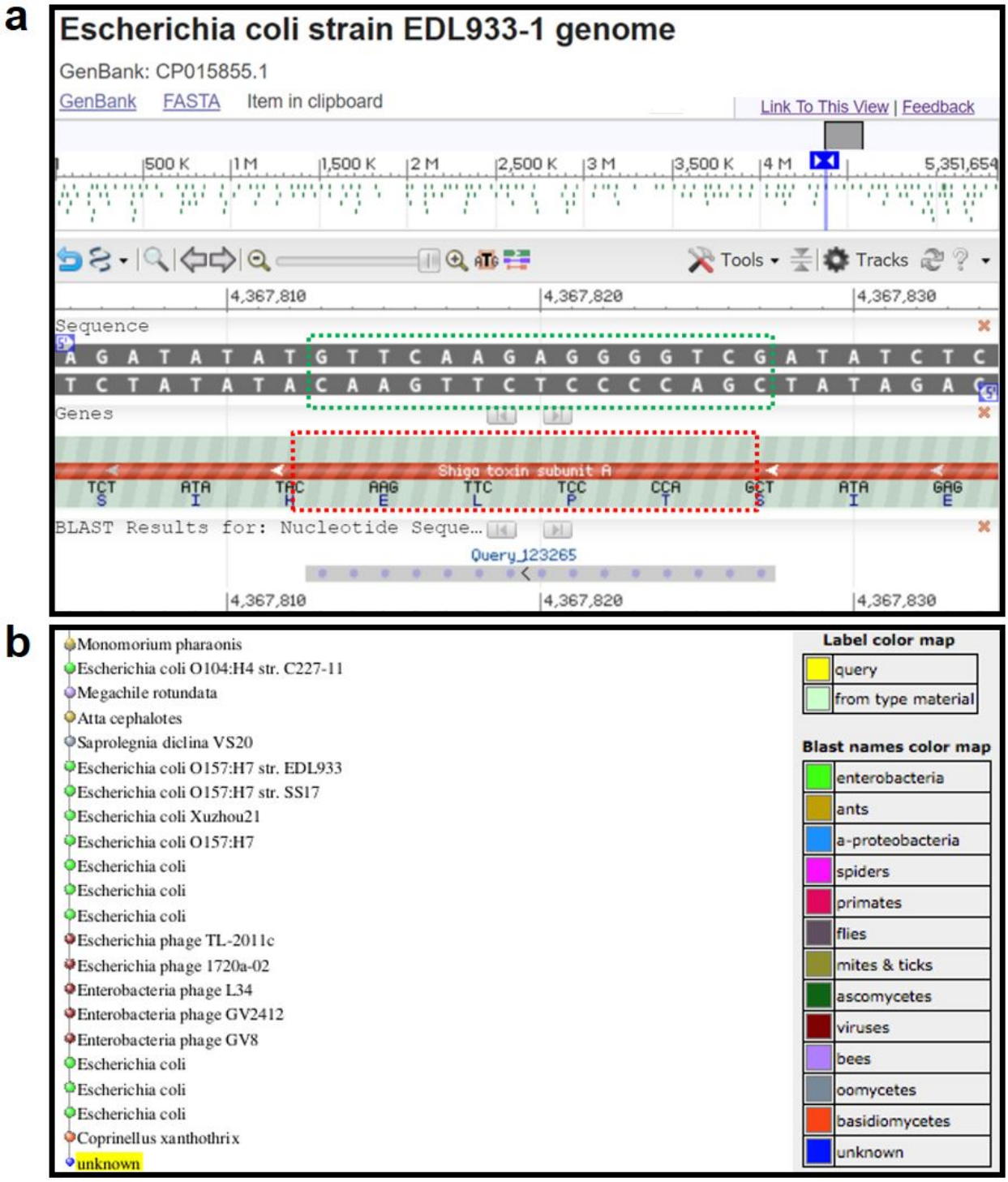
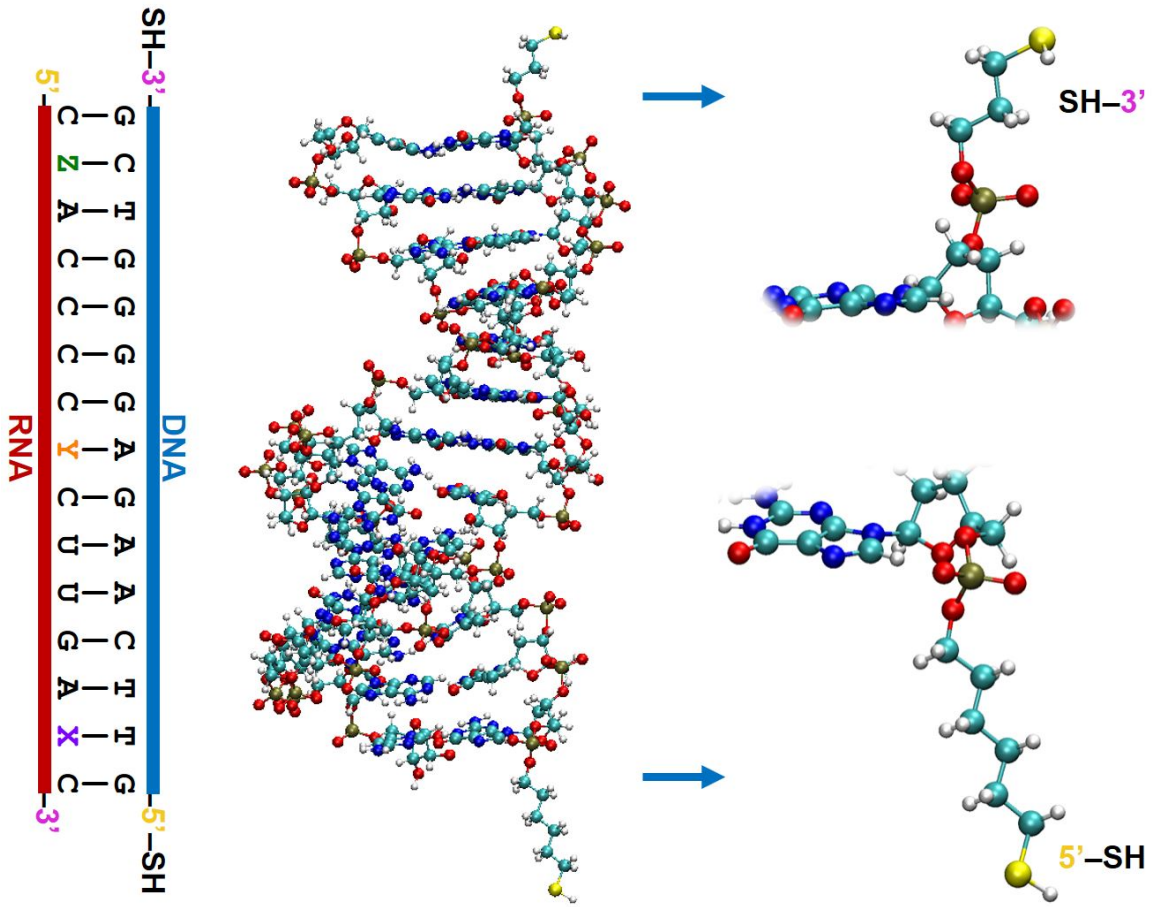
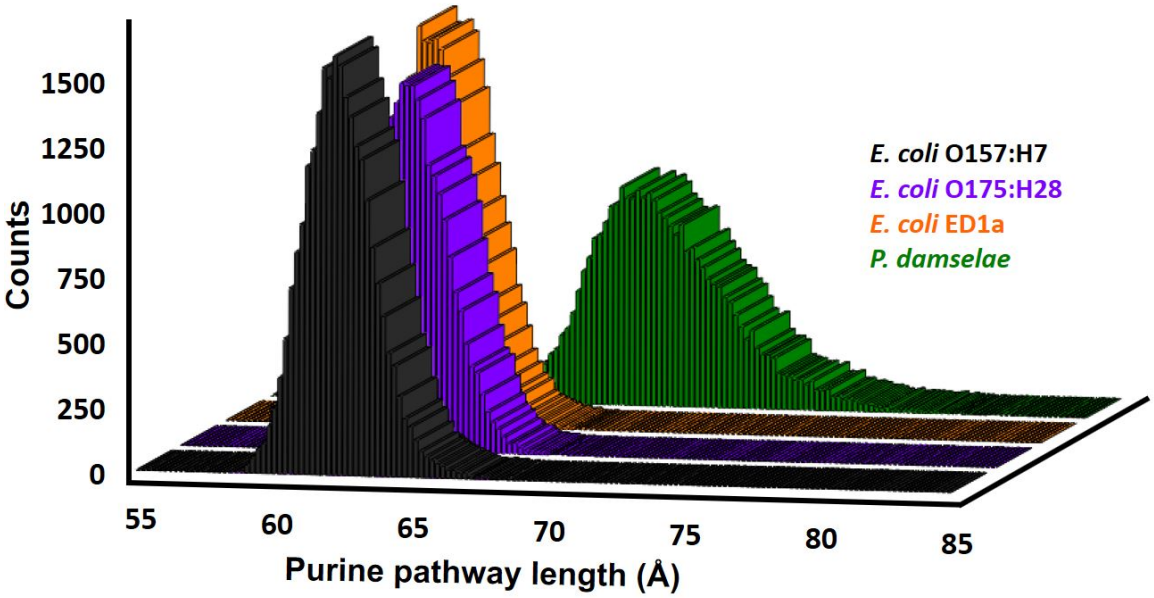


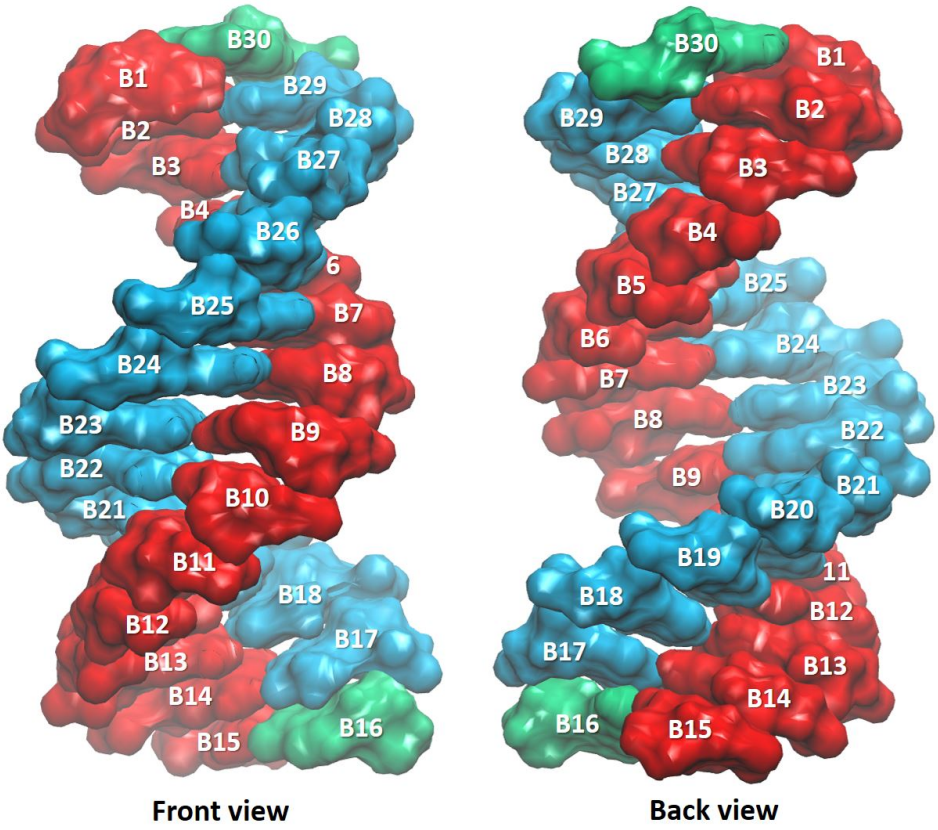
Supplementary Fig. 1 | Verification of perfectly matched RNA sequence. a, 5'-CGACCCCUCUUGAAC-3' in *E. coli* O157:H7 demonstrating that the sequence probed is expressed in the Shiga Toxin subunit A. **b**, Blast tree view (taxonomic name) of the matching cases, using BLASTn 2.6.1+[29].



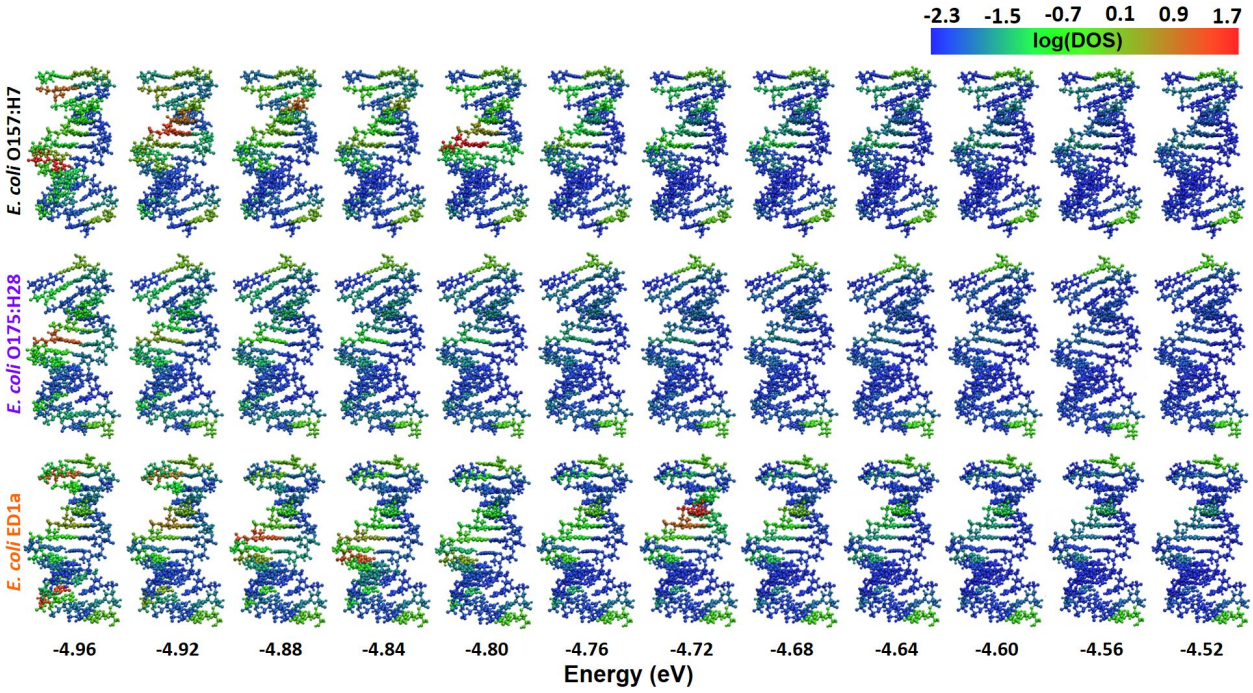
Supplementary Fig. 2 | Connectivity of the linkers to the terminal nucleotides. The structures of the thiol linkers connected to the terminal nucleotides of DNA.



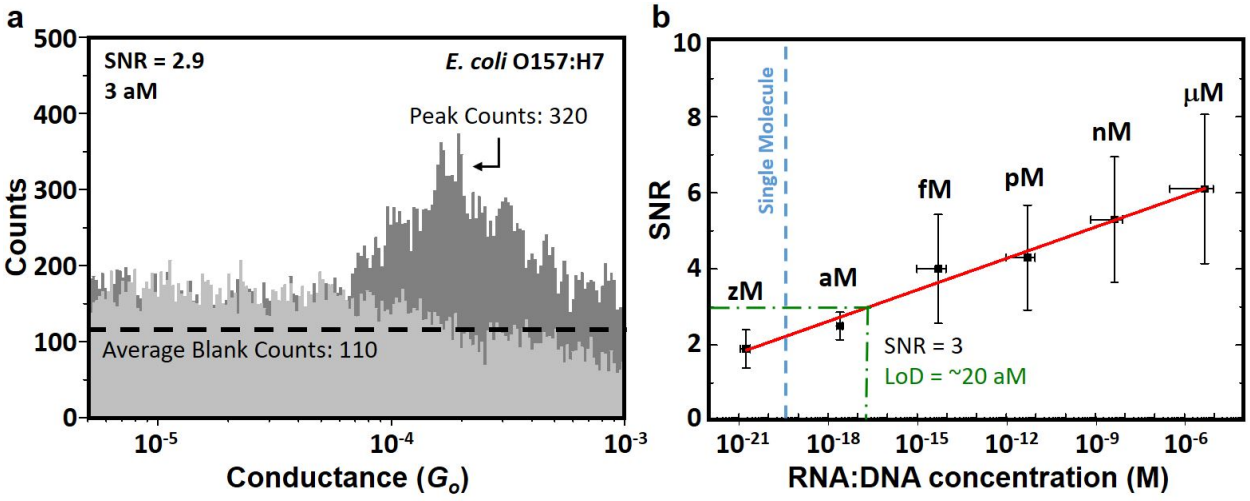
Supplementary Fig. 3 | Purine pathway length histograms. Histograms for all four RNA:DNA hybrids.



Supplementary Fig. 4 | The blocking scheme for the transport calculations. The green blocks B16 and B30 are the left and right contacts respectively. The Büttiker probes are attached to red and blue nucleotides (backbone + base).



Supplementary Fig. 5 | Projected density of states (DoS). DoS mapped on the corresponding RNA:DNA hybrids at different Energy Levels. DoS is calculated per base thus each base is coloured according to its DoS value. A close inspection indicates that the purines dominate the DoS at each energy level within this range, indicating that charge transport proceeds through the purine pathway.



Supplementary Fig. 6 | Limit of Detection (LoD). a, Example of SNR calculation for a 3 aM concentration sample. **b,** Average SNR for each concentration with a linear fit to obtain the concentration for a SNR = 3 (~20 aM).

Supplementary Table 1 | Melting temperature measurements. Melting temperatures (T_m) obtained from calculation using the IDT DNA OligoAnalyzer 3.1 software package[47] and the CD experiments in each case. For the calculation a Na^+ concentration of 100 mM, an RNA:DNA concentration of 2 μM, and RNA as the target molecule type was used.

	RNA sequence	T_m in 100 mM phosphate buffer IDT calculation	CD measurement
***E. coli* O157:H7** Perfectly matched	CGACCCCUCUUGAAC	57.5 ºC	55.0 ºC
***E. coli* O175:H28** Mismatch X=G	CGACCCCUCUUGA**G**C	52.9 ºC	54.2 ºC
***E. coli* ED1a** Mismatch Y=C	CGACCCC**C**CUUGAAC	49.6 ºC	48.3 ºC
P. damselae Mismatch Z=A	C**A**ACCCCUCUUGAAC	45.7 ºC	44.9 ºC