

Ultra-high Multiplex PCR Uniformity is Enhanced by Carbon Nanotube-Dendrimer-Encapsulated Gold Nanoparticles

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Table S1. Primer sequences and amplification length for ultra-high multiplex PCR and qPCR.

RS_ID	Forward primers (5'-3')	Reverse primers (5'-3')	Amplification length (bp)
rs13476 262	<u>ACGACGTGTCGAGTTCA</u> <u>GGTGGAGCCTTGTTAAT</u> AAATGACGC	<u>CAGTGAGTCGCCACAGG</u> <u>TCAAGGCAGGGTCCTAC</u> CTGTCC	209
rs37071 98	<u>ACGACGTGTCGAGTTCA</u> <u>GGTGACATTGTATTTTA</u> GTTTCATATATGTTTCAG	<u>CAGTGAGTCGCCACAGG</u> <u>TCATAAGCATACCACAC</u> ATATATTATGCAAA	225
rs41363 70	<u>ACGACGTGTCGAGTTCA</u> <u>GGTAGCATGAGCAAAAC</u> CATAGGTTC	<u>CAGTGAGTCGCCACAGG</u> <u>TCAACAAGGTGGGACTT</u> GGGGAC	216
rs36841 10	<u>ACGACGTGTCGAGTTCA</u> <u>GGTTGAACATAATATAT</u> TTTAATTTGCCATG	<u>CAGTGAGTCGCCACAGG</u> <u>TCAATTGCAGCAGGAGG</u> ACAGC	226
rs36941 00	<u>ACGACGTGTCGAGTTCA</u> <u>GGTGGCTTCACGTTGGT</u> AGCAGG	<u>CAGTGAGTCGCCACAGG</u> <u>TCATGTGAGTGGATGCA</u> GCAACC	218

rs36938 53	<u>ACGACGTGTCGAGTTCA</u> <u>GGTTGTAATTATCAGCT</u> TCCCTTTCTG	<u>CAGTGAGTCGCCACAGG</u> <u>TCATTAAAGGAATGTTA</u> GTTAGACTTTGGC	224
rs36998 42	<u>ACGACGTGTCGAGTTCA</u> <u>GGTCATGTCGACAGTAA</u> TTGGCAAT	<u>CAGTGAGTCGCCACAGG</u> <u>TCACCCTCATTTTGTCT</u> CTTGTGC	229
rs37110 88	<u>ACGACGTGTCGAGTTCA</u> <u>GGTCCACCTGCTAAGCT</u> GCACTG	<u>CAGTGAGTCGCCACAGG</u> <u>TCAGTTGGACCTCAATT</u> CTCCTGTCT	224
rs37048 89	<u>ACGACGTGTCGAGTTCA</u> <u>GGTTTCAATGTCCGGA</u> GAGATGG	<u>CAGTGAGTCGCCACAGG</u> <u>TCACTCTGGCCATGACT</u> GAAGAGC	215
rs36622 46	<u>ACGACGTGTCGAGTTCA</u> <u>GGTTAGGACTGCGGCCA</u> CAATG	<u>CAGTGAGTCGCCACAGG</u> <u>TCACTGAAAGCCTCAGA</u> AGCAGAAG	216
rs36852 76	<u>ACGACGTGTCGAGTTCA</u> <u>GGTCATGTAAATGCTAA</u> CCATGTTGCT	<u>CAGTGAGTCGCCACAGG</u> <u>TCAGAGAGAGAGACTTT</u> CCTAGCTCCAG	220
rs36896 02	<u>ACGACGTGTCGAGTTCA</u> <u>GGTTCAGCCCTGAGAGT</u> GGAACC	<u>CAGTGAGTCGCCACAGG</u> <u>TCACAGCAGCCTGACAG</u> TTGCC	229
rs42269 97	<u>ACGACGTGTCGAGTTCA</u> <u>GGTTTCGAGGAAGCAG</u> TTGGAG	<u>CAGTGAGTCGCCACAGG</u> <u>TCAGTGTCATGGCGAGA</u> AAGTGG	211
rs36677 65	<u>ACGACGTGTCGAGTTCA</u> <u>GGTGAGACAGGGTACT</u> CTCTGTGGC	<u>CAGTGAGTCGCCACAGG</u> <u>TCATACAAATGATCTGG</u> CCAGGATAAC	213
rs36912 95	<u>ACGACGTGTCGAGTTCA</u> <u>GGTCAGCTAACGGAAGA</u> ACCTCAGAG	<u>CAGTGAGTCGCCACAGG</u> <u>TCACTTTAATTCTTCCTC</u> CGGTTTG	217
rs30232 03	<u>ACGACGTGTCGAGTTCA</u> <u>GGTTTTTGCCTTGGTCTC</u> TTGGC	<u>CAGTGAGTCGCCACAGG</u> <u>TCACCAAGTCCTAGGTT</u> AGTCATTTGG	216
rs36721 56	<u>ACGACGTGTCGAGTTCA</u> <u>GGTCCACAGGAGGCTCT</u> GGAGTG	<u>CAGTGAGTCGCCACAGG</u> <u>TCAGCCTCTGGTGTCTA</u> TCTCCCAG	222
rs37134 41	<u>ACGACGTGTCGAGTTCA</u> <u>GGTGCTGGACAGCCCTA</u> ATGACTG	<u>CAGTGAGTCGCCACAGG</u> <u>TCATGCTTGGAACCTATT</u> CCCACCTAC	219
rs13480 567	<u>ACGACGTGTCGAGTTCA</u> <u>GGTTTGACTGCTTTGAC</u> ATAGAAACGTT	<u>CAGTGAGTCGCCACAGG</u> <u>TCAATCTCTACTACATG</u> ATGCCTCAACC	221
rs42287 72	<u>ACGACGTGTCGAGTTCA</u> <u>GGTGCTGAGGCCTTTTG</u>	<u>CAGTGAGTCGCCACAGG</u> <u>TCAGTCCCGACACACTA</u>	220

	CTGAGT	ATAAAGGC	
rs36827 98	<u>ACGACGTGTCGAGTTCA</u> <u>GGTCACCCAAGGAAACC</u> CACGT	<u>CAGTGAGTCGCCACAGG</u> <u>TCACACTAAGCAAAACC</u> GTATCGTAAC	233
rs36954 86	<u>ACGACGTGTCGAGTTCA</u> <u>GGTTCTTGACCTTGACC</u> TAGCTGCTC	<u>CAGTGAGTCGCCACAGG</u> <u>TCATGTTGGTTTGTGAG</u> AGGAAAGG	226
rs37032 17	<u>ACGACGTGTCGAGTTCA</u> <u>GGTATGGATGAGCTGAC</u> AGGCCA	<u>CAGTGAGTCGCCACAGG</u> <u>TCAAAATCGCACCCCTGT</u> CTCATTG	215
rs37263 73	<u>ACGACGTGTCGAGTTCA</u> <u>GGTGCTGCCACCAGGAG</u> CTCTAA	<u>CAGTGAGTCGCCACAGG</u> <u>TCAACTCTTCCTAGTTG</u> AGTGTCTGTGG	219
rs37074 14	<u>ACGACGTGTCGAGTTCA</u> <u>GGTGCAACCTAATGGAC</u> AGATAATGG	<u>CAGTGAGTCGCCACAGG</u> <u>TCATGATAATTAATTAT</u> TAACCAAAATGCC	218
rs42220 40	<u>ACGACGTGTCGAGTTCA</u> <u>GGTTAAATGTCAATTGT</u> CACTTCTGAAGG	<u>CAGTGAGTCGCCACAGG</u> <u>TCAAAAGCACATAACAC</u> CCAAGGAAG	217
rs30898 00	<u>ACGACGTGTCGAGTTCA</u> <u>GGTCAGAAAGGCTTGGA</u> TTGAAGTG	<u>CAGTGAGTCGCCACAGG</u> <u>TCATTACAGGGCACTGA</u> ATAAATCAGAG	228
rs37155 21	<u>ACGACGTGTCGAGTTCA</u> <u>GGTTGGGAATGGGATCT</u> CAGTGG	<u>CAGTGAGTCGCCACAGG</u> <u>TCAGCTGTAGTATGGCA</u> GAGGGAGT	224
rs13481 831	<u>ACGACGTGTCGAGTTCA</u> <u>GGTAGGTTTCATGTACAG</u> GTGCGTG	<u>CAGTGAGTCGCCACAGG</u> <u>TCAGGTGGCATCCTTGT</u> TCCCT	211
rs37103 70	<u>ACGACGTGTCGAGTTCA</u> <u>GGTTGTTTAGCTTGACA</u> GAACTCCTGAG	<u>CAGTGAGTCGCCACAGG</u> <u>TCACAAAGAGAAATTCA</u> GAGCCGC	216
rs37078 42	<u>ACGACGTGTCGAGTTCA</u> <u>GGTACTCTGGCCTTGGT</u> GAGAGAG	<u>CAGTGAGTCGCCACAGG</u> <u>TCAAAGATGAAATAAAT</u> AACTCTAACTTGGC	221
rs36892 86	<u>ACGACGTGTCGAGTTCA</u> <u>GGTTTGTATAAAGTTTA</u> ACACTGCAGAATG	<u>CAGTGAGTCGCCACAGG</u> <u>TCACCTGTAAAGACTCA</u> GTATTAAAATCCAG	233
rs13476 630	<u>ACGACGTGTCGAGTTCA</u> <u>GGTCTGACAGAGGAATG</u> TCCTGGAA	<u>CAGTGAGTCGCCACAGG</u> <u>TCATCCACTCCAGACTT</u> CATGCAC	222
rs41519 26	<u>ACGACGTGTCGAGTTCA</u> <u>GGTTAGGCTTCAAAGAC</u> AAAAATGTCC	<u>CAGTGAGTCGCCACAGG</u> <u>TCAGTTATTTCTGATGCC</u> AACAGCAT	218
rs37110	<u>ACGACGTGTCGAGTTCA</u>	<u>CAGTGAGTCGCCACAGG</u>	226

16	<u>GGTAGGTGTTCA</u> <u>TTTAC</u> TGATGTCTCCTT	<u>TCACCCTCTCCA</u> <u>ATATA</u> CAATGCCC	
rs62454 12	<u>ACGACGTGTCGAGTTCA</u> <u>GGTGTGGA</u> <u>ACTTTT</u> <u>TAG</u> TCTGACTTAAGC	<u>CAGTGAGTCGCCACAGG</u> <u>TCACGGTTGATCTTAAC</u> TTCTAAGGTG	219
rs36671 61	<u>ACGACGTGTCGAGTTCA</u> <u>GGTTTCTGTTCAACACC</u> ACTAAATGCTG	<u>CAGTGAGTCGCCACAGG</u> <u>TCAGGTCTGACAGAAAG</u> TCTGCGTATG	224
rs37067 67	<u>ACGACGTGTCGAGTTCA</u> <u>GGTCAGGCAAACCAAA</u> GCATGG	<u>CAGTGAGTCGCCACAGG</u> <u>TCACAAGTTTCCAATCT</u> GGATGGG	205
rs41930 65	<u>ACGACGTGTCGAGTTCA</u> <u>GGTTCATTACAAAGTAG</u> TACAGATTAGACAAAG	<u>CAGTGAGTCGCCACAGG</u> <u>TCAGGATCAATGGAATA</u> ATGAATTATTCAG	233
rs36689 27	<u>ACGACGTGTCGAGTTCA</u> <u>GGTTAGGAGTACCAAGA</u> GGTAAAGGATG	<u>CAGTGAGTCGCCACAGG</u> <u>TCAGTGATTCACTCATG</u> AGTTATACACGG	215
rs30236 88	<u>ACGACGTGTCGAGTTCA</u> <u>GGTTGT</u> <u>TAGTCTTGCAA</u> TTCATTCCGG	<u>CAGTGAGTCGCCACAGG</u> <u>TCACTGTGGACTGGGCT</u> GGCTT	220
rs37075 64	<u>ACGACGTGTCGAGTTCA</u> <u>GGTGTA</u> <u>AAATTGAGCTG</u> GCAACCTC	<u>CAGTGAGTCGCCACAGG</u> <u>TCAATTTCTGATTTAAA</u> ATCAGAAGCAGG	221
rs30235 17	<u>ACGACGTGTCGAGTTCA</u> <u>GGTGGCCTTCATTGGGC</u> TTTG	<u>CAGTGAGTCGCCACAGG</u> <u>TCACATGAATCAGCAGC</u> AGCTCG	212
rs13477 034	<u>ACGACGTGTCGAGTTCA</u> <u>GGTGAGTGCATGGCTCT</u> TTCCAG	<u>CAGTGAGTCGCCACAGG</u> <u>TCACCAGAATCACCTAG</u> TGATGACAGG	223
rs36646 01	<u>ACGACGTGTCGAGTTCA</u> <u>GGTGAAGAAGAGAGGC</u> CAAAATACTCAG	<u>CAGTGAGTCGCCACAGG</u> <u>TCACTACTATGCCTTCC</u> ATTCCTAACC	226
rs36931 31	<u>ACGACGTGTCGAGTTCA</u> <u>GGTCTCTAAATCAATTT</u> TAAGTCAGTTTGCG	<u>CAGTGAGTCGCCACAGG</u> <u>TCATAGGGCAATATCAA</u> GACACACTGAG	219
rs36740 66	<u>ACGACGTGTCGAGTTCA</u> <u>GGTGCTGCCTTCCTTTGT</u> GTTGG	<u>CAGTGAGTCGCCACAGG</u> <u>TCATATTCTATTTGTATG</u> ATTAGAGACCAAAG	237
rs37042 24	<u>ACGACGTGTCGAGTTCA</u> <u>GGTGTC</u> <u>CAGAATCATGG</u> ATAGTACTTGG	<u>CAGTGAGTCGCCACAGG</u> <u>TCACATAGCATGTATTC</u> TTATTGTTTTAGCTC	222
rs36744 70	<u>ACGACGTGTCGAGTTCA</u> <u>GGTCTGAGTTTATAGAC</u> AATCCTTCCACC	<u>CAGTGAGTCGCCACAGG</u> <u>TCACTGCAATCCCTCAG</u> TCCGA	215

rs37080 40	<u>ACGACGTGTCGAGTTCA</u> <u>GGT</u> AACCAGGCTCTACC TATTAAAGGT	<u>CAGTGAGTCGCCACAGG</u> <u>TCACTACGTAGCAAGAT</u> TCAAATATAAAGC	226
rs42223 82	<u>ACGACGTGTCGAGTTCA</u> <u>GGT</u> ACCAGTGAAGTAAG ATGTCAGGTCA	<u>CAGTGAGTCGCCACAGG</u> <u>TCACTGAGTAAGACCTT</u> TAAGGAGCTTCA	220
rs37013 95	<u>ACGACGTGTCGAGTTCA</u> <u>GGTCTGTGTCTCCATAA</u> GAGAATCAAGG	<u>CAGTGAGTCGCCACAGG</u> <u>TCACATATCAGTTTCTA</u> ATTCCTCATCTCAG	206
rs36885 69	<u>ACGACGTGTCGAGTTCA</u> <u>GGT</u> CACAGATCCTCAGG AAATGGC	<u>CAGTGAGTCGCCACAGG</u> <u>TCATACTCCATTGATTCT</u> GAACACTAGGTG	220
rs36770 05	<u>ACGACGTGTCGAGTTCA</u> <u>GGT</u> ATTTGGTGACTCAT GCTGGGT	<u>CAGTGAGTCGCCACAGG</u> <u>TCACA</u> ACTATCCTGATA TAAAGTAGCACAG	220
rs37241 92	<u>ACGACGTGTCGAGTTCA</u> <u>GGT</u> GGGGTTACAGGTGA ATATCAGC	<u>CAGTGAGTCGCCACAGG</u> <u>TCAGGGG</u> ACTCAGTGTT CTAGGGC	200
rs13476 538	<u>ACGACGTGTCGAGTTCA</u> <u>GGT</u> GGGTGGTGGTGGTG GATA	<u>CAGTGAGTCGCCACAGG</u> <u>TCAATGGATTATCCTTCT</u> GTTCTTTG	221
rs13478 622	<u>ACGACGTGTCGAGTTCA</u> <u>GGT</u> GCCCTTAGTGCTTC AGGGAAG	<u>CAGTGAGTCGCCACAGG</u> <u>TCAAAAGGCAGCTGTAT</u> ATTATACACATACAG	217
rs41775 40	<u>ACGACGTGTCGAGTTCA</u> <u>GGTCTTGTGAGAAGGAG</u> ACAAAAATGG	<u>CAGTGAGTCGCCACAGG</u> <u>TCAACGAGAGGAATCAC</u> AGCTTGTC	215
rs29171 198	<u>ACGACGTGTCGAGTTCA</u> <u>GGT</u> TAAATGGGCAATAC GAAGCAAG	<u>CAGTGAGTCGCCACAGG</u> <u>TCAGTAGCCACTGGAAG</u> TAGCCTGT	231
rs13482 740	<u>ACGACGTGTCGAGTTCA</u> <u>GGT</u> TCCAGACTTCATCTA CCTGCGG	<u>CAGTGAGTCGCCACAGG</u> <u>TCACCACACTTAGCAGC</u> CTGGCT	214
rs27687 437	<u>ACGACGTGTCGAGTTCA</u> <u>GGT</u> GAGACAGCTTTGTA ACTGATGGGA	<u>CAGTGAGTCGCCACAGG</u> <u>TCAAGGGATCTGACTAT</u> TCCAAGAAGC	218
rs82372 29	<u>ACGACGTGTCGAGTTCA</u> <u>GGT</u> GTGTTAGAAACATC CCAACTCCTC	<u>CAGTGAGTCGCCACAGG</u> <u>TCATTTATGGGCATTAG</u> AGCATCTAGG	216
rs29687 299	<u>ACGACGTGTCGAGTTCA</u> <u>GGT</u> AATCTCGTTTCTTAT CTTTCAAACAAG	<u>CAGTGAGTCGCCACAGG</u> <u>TCAAGTGCACAGTTAGT</u> GCCTGCC	208
rs31281 387	<u>ACGACGTGTCGAGTTCA</u> <u>GGT</u> GATATTCTTTGACA	<u>CAGTGAGTCGCCACAGG</u> <u>TCAGGGCTCAAAGGTTC</u>	233

	TAGCTGTGGG	TTCCATC	
rs29581 676	<u>ACGACGTGTCGAGTTCA</u> <u>GGTGCTAGGGTGTCTGG</u> AGAGAGC	<u>CAGTGAGTCGCCACAGG</u> <u>TCAGGACACAGCATGGC</u> TGTAGG	214
rs29518 789	<u>ACGACGTGTCGAGTTCA</u> <u>GGTCTTTGTACAACAGG</u> ACCAAAAAGC	<u>CAGTGAGTCGCCACAGG</u> <u>TCACTTCTAAGACTCCC</u> TTCCCGC	222
rs13480 113	<u>ACGACGTGTCGAGTTCA</u> <u>GGTCAAGTTTGAAGCGC</u> CAAGCT	<u>CAGTGAGTCGCCACAGG</u> <u>TCAATTAGTGCCTTATT</u> AAGCAGATGG	219
rs13483 732	<u>ACGACGTGTCGAGTTCA</u> <u>GGTACAACAGAATGTCC</u> CACAGGC	<u>CAGTGAGTCGCCACAGG</u> <u>TCAGTCCCATGGTTAAG</u> TTTGAGATACTG	208
rs82619 44	<u>ACGACGTGTCGAGTTCA</u> <u>GGTCCAGGGCACTGCGG</u> C	<u>CAGTGAGTCGCCACAGG</u> <u>TCATAGTGTTGGGCTGC</u> GAGGTAC	210
rs13483 736	<u>ACGACGTGTCGAGTTCA</u> <u>GGTATTGATTCTGATAA</u> GTGGACCCTC	<u>CAGTGAGTCGCCACAGG</u> <u>TCAGCAATGATTTATTC</u> TCAAACCATTC	227
rs13480 491	<u>ACGACGTGTCGAGTTCA</u> <u>GGTGCTCAGTCAGTGAG</u> AAGCAGGA	<u>CAGTGAGTCGCCACAGG</u> <u>TCAGGAAGGCCGACTCT</u> TCCC	228
rs29669 790	<u>ACGACGTGTCGAGTTCA</u> <u>GGTAATTGCACATGTCC</u> CAACTCAG	<u>CAGTGAGTCGCCACAGG</u> <u>TCAGCTTCAGCTTCTGG</u> AAAGGAC	221
rs32123 873	<u>ACGACGTGTCGAGTTCA</u> <u>GGTCATCTGAAGGTATA</u> GTTGATGAGGTG	<u>CAGTGAGTCGCCACAGG</u> <u>TCAGCCAGTCTAGTTTG</u> TAGAGCAAGG	231
rs29395 004	<u>ACGACGTGTCGAGTTCA</u> <u>GGTCATACACATGACAG</u> GTGTGCATG	<u>CAGTGAGTCGCCACAGG</u> <u>TCAGTTTCACTAAGACC</u> TTGTAATATCCG	219
rs30307 865	<u>ACGACGTGTCGAGTTCA</u> <u>GGTCTTATGTTACCTGT</u> ATCCTGGCAG	<u>CAGTGAGTCGCCACAGG</u> <u>TCAGGAGGAAGCAAGG</u> AAAGGAA	230
rs13480 972	<u>ACGACGTGTCGAGTTCA</u> <u>GGTAAGATTACAGCATG</u> GAAATTTAGGA	<u>CAGTGAGTCGCCACAGG</u> <u>TCATTTGTACTCTAGTCA</u> ATAGCTGGTCC	209
rs13476 971	<u>ACGACGTGTCGAGTTCA</u> <u>GGTATAAAGGGAGGGA</u> ATAACTGGC	<u>CAGTGAGTCGCCACAGG</u> <u>TCAGAAGTCACTGCCCA</u> CCAGTTC	218
rs13476 543	<u>ACGACGTGTCGAGTTCA</u> <u>GGTAGCTGAGTAATGTT</u> TGCTGTTGG	<u>CAGTGAGTCGCCACAGG</u> <u>TCACTGAAACAAGGTAA</u> TTTCCAGCC	213
rs13480	<u>ACGACGTGTCGAGTTCA</u>	<u>CAGTGAGTCGCCACAGG</u>	204

075	<u>GGTGCCAGGA</u> ACTAGAA TTCCCAG	<u>TCAAAGAGGTCCAGGAG</u> GCAGAC	
rs29660 436	<u>ACGACGTGTCGAGTTCA</u> <u>GGTTGTAGG</u> ACTAGGGT ACTGACAATGC	<u>CAGTGAGTCGCCACAGG</u> <u>TCATGCTCTTTTAAAGTC</u> CCATGGTC	212
rs36995 31	<u>ACGACGTGTCGAGTTCA</u> <u>GGTCAGCCAGCCTAGCC</u> TACTTAGTG	<u>CAGTGAGTCGCCACAGG</u> <u>TCATTTTGTGTGTCTGTG</u> TATTTCTATGTG	216
rs13475 716	<u>ACGACGTGTCGAGTTCA</u> <u>GGTAGTAGCAA</u> AAGCAT TATAAAAGTGCTG	<u>CAGTGAGTCGCCACAGG</u> <u>TCACTTCCTCTCTTGCTC</u> TTCTGTGC	208
rs13484 116	<u>ACGACGTGTCGAGTTCA</u> <u>GGTCCAAATATGACTTA</u> TAGCAAGGATTAA	<u>CAGTGAGTCGCCACAGG</u> <u>TCACTTTATGAGATGCA</u> GGACTTCCTAA	215
rs13482 069	<u>ACGACGTGTCGAGTTCA</u> <u>GGTGCTGGAGAGTACAG</u> TCACAATGC	<u>CAGTGAGTCGCCACAGG</u> <u>TCAACCTCCATCAACTG</u> AGAGTGCTT	208
rs13475 728	<u>ACGACGTGTCGAGTTCA</u> <u>GGTGGAAGAGCACTGAT</u> GAACAATACAG	<u>CAGTGAGTCGCCACAGG</u> <u>TCAATATACAGGCAAAA</u> TACCTGTGCAC	206
rs29528 790	<u>ACGACGTGTCGAGTTCA</u> <u>GGTCCCATCATAGAGAT</u> GGATTCCA	<u>CAGTGAGTCGCCACAGG</u> <u>TCATCTAGCATACAAAT</u> TGTGCTTGCTAT	225
rs13476 973	<u>ACGACGTGTCGAGTTCA</u> <u>GGTGTAATTTCTGATTT</u> GGCTTTGTGAG	<u>CAGTGAGTCGCCACAGG</u> <u>TCACTAAACTATTGGTC</u> ATCAGCCAAG	225
rs29176 743	<u>ACGACGTGTCGAGTTCA</u> <u>GGTGCTGTCTGAAGATA</u> GGCTCCATT	<u>CAGTGAGTCGCCACAGG</u> <u>TCATTTCTGGCTCAGAA</u> CATGGTACTC	224
rs13483 212	<u>ACGACGTGTCGAGTTCA</u> <u>GGTAGACA</u> ACTGAACCT GGTTTACTGG	<u>CAGTGAGTCGCCACAGG</u> <u>TCAA</u> ACTTGCTGTGTAG ATCAGGCTG	218
rs30666 086	<u>ACGACGTGTCGAGTTCA</u> <u>GGTCTGAGTTCTAGGAT</u> TGTAATGTGAGC	<u>CAGTGAGTCGCCACAGG</u> <u>TCATTCCAAAGTTGGGG</u> AGGTCTG	231
rs82545 00	<u>ACGACGTGTCGAGTTCA</u> <u>GGTAAAGGGGAACGAA</u> CCTTAACG	<u>CAGTGAGTCGCCACAGG</u> <u>TCAGGAAGTATCTGATG</u> ACATTGGCC	213
rs29315 008	<u>ACGACGTGTCGAGTTCA</u> <u>GGTGGCATCGAGGGAA</u> ATTCG	<u>CAGTGAGTCGCCACAGG</u> <u>TCACCCAATTTCTCTCT</u> CAGGAC	211
rs82713 67	<u>ACGACGTGTCGAGTTCA</u> <u>GGTGCATGAATCCAGTT</u> AGAATGACC	<u>CAGTGAGTCGCCACAGG</u> <u>TCACAAAATTAACATT</u> TATTTATTCTAGGTTG	227

rs63737 56	<u>ACGACGTGTCGAGTTCA</u> <u>GGTAATTGAGAGAAATA</u> ACTGGGCTTAA	<u>CAGTGAGTCGCCACAGG</u> <u>TCATACACCGTCCACCT</u> CCTTTGA	223
rs30521 859	<u>ACGACGTGTCGAGTTCA</u> <u>GGTAGATAAGGAAAAT</u> AAATCAGATGGTTT	<u>CAGTGAGTCGCCACAGG</u> <u>TCAGCATAGGCTTACTG</u> ACACACCTC	222
rs82496 44	<u>ACGACGTGTCGAGTTCA</u> <u>GGTATTCCACTGGCCTT</u> ACAGCTAC	<u>CAGTGAGTCGCCACAGG</u> <u>TCACACTGGCTTCCTTC</u> AACAGCTG	212
rs41772 03	<u>ACGACGTGTCGAGTTCA</u> <u>GGTGTAATTTGAATTTA</u> AAATGGTAAGTAATG	<u>CAGTGAGTCGCCACAGG</u> <u>TCACTGTTCTAGTTTCCT</u> TAGACACTCCAG	239
rs13484 115	<u>ACGACGTGTCGAGTTCA</u> <u>GGTTTAACAGCAATGTT</u> AGAATATATGATACAG	<u>CAGTGAGTCGCCACAGG</u> <u>TCAACTGTCTCAAACCT</u> ACTGTCACTGC	224
rs13477 094	<u>ACGACGTGTCGAGTTCA</u> <u>GGTAGGAAGGTGTCAGG</u> TTCCCG	<u>CAGTGAGTCGCCACAGG</u> <u>TCACCTATAAGCAGAAG</u> CTTTTATAACTGC	241
rs32390 670	<u>ACGACGTGTCGAGTTCA</u> <u>GGTTAGGGATGTAAGAG</u> CTGGAAGATG	<u>CAGTGAGTCGCCACAGG</u> <u>TCATCTATTATAGCCCA</u> GACCCTCAAC	218
rs42239 79	<u>ACGACGTGTCGAGTTCA</u> <u>GGTAGTATAGGTCAGTC</u> CCTTTACCTCTCT	<u>CAGTGAGTCGCCACAGG</u> <u>TCAGGACTCAAGACTCA</u> GTCTAAATGCAG	211
rs13479 279	<u>ACGACGTGTCGAGTTCA</u> <u>GGTTCTCTTATGGGCTC</u> CTATCCC	<u>CAGTGAGTCGCCACAGG</u> <u>TCACAGGACCACCATCC</u> CAACC	221
rs41673 17	<u>ACGACGTGTCGAGTTCA</u> <u>GGTTCTATAATGTGGGG</u> AAACGCTG	<u>CAGTGAGTCGCCACAGG</u> <u>TCAAGTATAGGGAGAGC</u> ATAGCCTGC	217
rs36649 86	<u>ACGACGTGTCGAGTTCA</u> <u>GGTCATCCACTTAACAC</u> CATTAGATCC	<u>CAGTGAGTCGCCACAGG</u> <u>TCATTATGTAAATGGAT</u> TTAAAACAGGC	216
rs36756 32	<u>ACGACGTGTCGAGTTCA</u> <u>GGTGTGTGTGTGTACAC</u> ACAAGAGTGTATG	<u>CAGTGAGTCGCCACAGG</u> <u>TCAGGTACTGCGAGCAG</u> GGCAT	208
rs13481 932	<u>ACGACGTGTCGAGTTCA</u> <u>GGTGTTTTGTCCAGGTTT</u> TACACATAAG	<u>CAGTGAGTCGCCACAGG</u> <u>TCAAACAATGCTACAAA</u> AATATTTAGCATC	214
rs36659 05	<u>ACGACGTGTCGAGTTCA</u> <u>GGTAGGCACACGCCCTC</u> TCG	<u>CAGTGAGTCGCCACAGG</u> <u>TCAGGGCAGCGTTTGTA</u> AAGTCC	208
rs42173 72	<u>ACGACGTGTCGAGTTCA</u> <u>GGTATGCAAACCAAACA</u>	<u>CAGTGAGTCGCCACAGG</u> <u>TCAGAGTTTCCAACCTGC</u>	219

	GGCACA	TGCTTCTG	
rs36968 34	<u>ACGACGTGTCGAGTTCA</u> <u>GGTCATGCCACAGAGCT</u> TTTCTTG	<u>CAGTGAGTCGCCACAGG</u> <u>TCAACTCTTTCCTTCCTC</u> TTTTTCCC	221
rs30236 59	<u>ACGACGTGTCGAGTTCA</u> <u>GGTTGAATAGTAGTAAC</u> ATTAGGACAAAGTAAG	<u>CAGTGAGTCGCCACAGG</u> <u>TCATATAGGAAGACAAA</u> TGAAATAGACCC	212
rs37045 03	<u>ACGACGTGTCGAGTTCA</u> <u>GGTGGAGAAAACCATTGA</u> CAAAGATGG	<u>CAGTGAGTCGCCACAGG</u> <u>TCACTATCAGGAACAAG</u> CCAAAGCTT	209
rs13477 946	<u>ACGACGTGTCGAGTTCA</u> <u>GGTGTCAAAGCCTGCGA</u> TGGAAG	<u>CAGTGAGTCGCCACAGG</u> <u>TCATGGGTTGCACTTCT</u> GTGGC	206
rs37230 83	<u>ACGACGTGTCGAGTTCA</u> <u>GGTCCACATAAACTGGG</u> TTACATGCA	<u>CAGTGAGTCGCCACAGG</u> <u>TCAGGGCCCGACTTGGG</u> AC	210
rs13478 801	<u>ACGACGTGTCGAGTTCA</u> <u>GGTAAAGGAACCTACGC</u> ACTGTGAG	<u>CAGTGAGTCGCCACAGG</u> <u>TCAGAGACAGTCAGTCA</u> TTCTGTTTAATACC	221
rs36842 85	<u>ACGACGTGTCGAGTTCA</u> <u>GGTTTTGGAAGTTTGCA</u> GTAGAATACAG	<u>CAGTGAGTCGCCACAGG</u> <u>TCACTTGTGACATCTCA</u> CACCCAGG	211
rs13480 017	<u>ACGACGTGTCGAGTTCA</u> <u>GGTTAACCAAGAGAGCA</u> GCCCCCT	<u>CAGTGAGTCGCCACAGG</u> <u>TCATGCTTTCGGATGAA</u> ATGCC	228
rs37093 87	<u>ACGACGTGTCGAGTTCA</u> <u>GGTGGGGAGCTAAGCTT</u> TTATAGTGAAG	<u>CAGTGAGTCGCCACAGG</u> <u>TCACAGGGGGTACCAGT</u> TTGCA	221
rs36746 46	<u>ACGACGTGTCGAGTTCA</u> <u>GGTAGGGACAGGAAAC</u> ATTCAAGG	<u>CAGTGAGTCGCCACAGG</u> <u>TCACAATTTCAGAACAG</u> AAAATTACTTGG	229
rs36800 33	<u>ACGACGTGTCGAGTTCA</u> <u>GGTATTCATACTGTCAG</u> AAACTGTTGCTAAG	<u>CAGTGAGTCGCCACAGG</u> <u>TCACAATAAGGAGTTTC</u> TAAGTAAACCCAC	219
rs42325 94	<u>ACGACGTGTCGAGTTCA</u> <u>GGTCTCTGGCCAGCAAT</u> ACCAGC	<u>CAGTGAGTCGCCACAGG</u> <u>TCAGCCAAGGTCCTCCT</u> CCTTTC	208

The underlined parts represent universal sequences.

Table S2. Universal index PCR primer sequences.

Smple_ID	I5 primers (5'-3')	I7 primers (5'-3')
5X	AATGATACGGCGACCACCGA	CAAGCAGAAGACGGCATACG

	GATCTACACTCTTTCCCTACA CGACGCTCTTCCGATCTATCA CGACGACGTGTCGAGTTCAGG	AGATAGAGAGGTGACTGGAG TTCAGACGTGTGCTCTTCCGA TCTCAGTGAGTCGCCACAGGT CA
7X	AATGATACGGCGACCACCGA GATCTACACTCTTTCCCTACA CGACGCTCTTCCGATCTCGAT GTACGACGTGTCGAGTTCAGG	CAAGCAGAAGACGGCATAACG AGATAGAGAGGTGACTGGAG TTCAGACGTGTGCTCTTCCGA TCTCAGTGAGTCGCCACAGGT CA
10X	AATGATACGGCGACCACCGA GATCTACACTCTTTCCCTACA CGACGCTCTTCCGATCTTTAG GCACGACGTGTCGAGTTCAGG	CAAGCAGAAGACGGCATAACG AGATAGAGAGGTGACTGGAG TTCAGACGTGTGCTCTTCCGA TCTCAGTGAGTCGCCACAGGT CA
13X	AATGATACGGCGACCACCGA GATCTACACTCTTTCCCTACA CGACGCTCTTCCGATCTTGAC CAACGACGTGTCGAGTTCAGG	CAAGCAGAAGACGGCATAACG AGATAGAGAGGTGACTGGAG TTCAGACGTGTGCTCTTCCGA TCTCAGTGAGTCGCCACAGGT CA
16X	AATGATACGGCGACCACCGA GATCTACACTCTTTCCCTACA CGACGCTCTTCCGATCTACAG TGACGACGTGTCGAGTTCAGG	CAAGCAGAAGACGGCATAACG AGATAGAGAGGTGACTGGAG TTCAGACGTGTGCTCTTCCGA TCTCAGTGAGTCGCCACAGGT CA
Hi-Plex PC R	AATGATACGGCGACCACCGA GATCTACACTCTTTCCCTACA CGACGCTCTTCCGATCTCGGT TAACGACGTGTCGAGTTCAGG	CAAGCAGAAGACGGCATAACG AGATTATAGTGACTGGAGT TCAGACGTGTGCTCTTCCGAT CTCAGTGAGTCGCCACAGGTC A
adapter	AATGATACGGCGACCACCGA G	CAAGCAGAAGACGGCATAACG AG

The underlined parts represent universal sequences. The gray parts represent index sequences.

Table S3. Primer sequences for multiplex methylation-specific PCR (multiplex MSP) and qPCR.

ID	Forward primers (5'-3')	Reverse primers (5'-3')
cg1181 0135	GGTTGAGTATCGGTGGGTAGGG AT	TCCTCGTAATAAAACCAATACAA AATCGA
cg1212 9480	TGGGTTTAATTTGGGTGGATAGG T	ACAATTTATACCACCAATCCCA AA
cg0947 3613	GGATGTTTTTTTTTTGGAGTTGTT TGTTTGTG	AACCCAAAACCAAACAAACAAA AACAT
cg0793	TTAGGTTTCGCGGTTGGGTTTTG	ACCTCAAACCCCCATAACCTACC

4434	A	T
cg0431 7927	TGGTTGTATTGAGATTTTTATTTT TATTGTAATGG	ACAAAAATAATAATCTATCTCAT TAAATCCACA
cg1611 2157	GGAAAGAAATTTTTGGTAGAAG TTAGGT	CCTCCCTTATATCCTAAACATAA AAACGA
cg0274 5494	AGGTTGAAGGCGTAGGGGTTAG AT	TCCCCAAAACACCCAACACATTC C
cg1870 5301	TTGTTTGAGGTTTTAAAAGGTCG A	ACAACAAAATAAAACTCCGTCT CAA
cg0983 0162	GAGGGAAGGAGGGTAGGTAGAG GA	ACCCTAAACTACAAATTTTCATCT ATAACA
cg0221 9949	GGAGAGGGAGGGAGAGGAGGA C	TCCTAACCTTCCCATCCTCCAAC C
cg2081 1857	TGTTAGTATGATGGGGAGGGCG AC	AACAAAACTTAATAAATCCTA AACACGT
cg1352 3654	TGTAGTTTGGGTTTATTTTGTTA AAGTT	ACTCAAATATAAATACAATATCC CAAAACATTT
cg0827 1804	ACGTTGGGTCGAATGAGGATAG AG	ACCTAAACGACAAAATAAAACT CTATCT
cg0815 5759	TGCGTTAATATTTTGAATTTAA TATTGTGT	ACTTCGAATTTTATCAATTCCT ATCATCA
cg0359 5348	AGTGTATGTAGGAAGTACGGTC GGT	CCCAAAACACCCTTAAACCCTCG A
cg1223 9580	ACGTGAATTTTAGTTAATTAAGA GTTGATTG	CCACCCTAACCTTTCTCTCTTAC CG
cg1629 5030	TTTTTATTTGGTAATGTTATAGG TTTGTTATTG	ACATCTATCCAAACTCATTACTT ATAATTCA
cg2642 9140	TGTTAATAAGGATTATGTAGGTG TTTGTT	TTTTCCCATAAATTTCAATTCCTT TCAA
cg1488 4160	AGTTATTGCGGTTTTAGAAGGTA AATGGT	CGAAAATACCCTTTCATAAAAAC TCCCTCG
cg2260 1108	TGAGAAGGGTTTCGTGCGTATA GT	AAAATATCCACTTCTCTATCCTT CCT
cg0393 8978	TTTTTGTTTGTAGGTGAGGTTTTA GTTACGG	ATACCAAATAATCTCAAAAATC AAAACTTTTCA
cg0946 7607	TTTGGTTTAAATGTGGTTAAAAT AAAGGA	ACAAAATCTAACCAATACTTTAC ACGT
cg1993 0620	TTTTTGTAAGTGTATTAAAGGGT ATTGT	ACACCATACTAAATCCTAAAATA TTATTCATACC
cg0402 9027	GTAGAGAGAGGGTTGGCGATGG AT	ACCGTAACTTCGACAATAACCTC CG
cg0371 9092	GGATAGTTTTTGTAGTGGTCGGC G	AATACCCTACTACGCGACCCTAC G
cg0781	AGGATGAATTGCGGATTTAGAG	ACTTTTAAATCTCAATACGCAAC

3377	GGA	TCCA
cg0513 9728	TTGAGTTGATTTGAGTTGGTACG T	ACAACACGTACCCTACCATACGC T
cg0237 6178	TTTTCGCGTCGGTAAGAAGATCG G	ACGACGAACTAATAATTCAACG CACCT
cg0476 0448	AGAGAGTTGGAATAGGAGGGAG TT	CCCAACAACACAAAACCCGTAA CG
cg0815 4348	TTCGTAGTTATGTGTCGAAGGGC G	ACCCGAACTTTATATAACCCTCG CG
cg0364 0110	GGTGATGAGTATGGTTAGAAAG TAAGAGGT	TCATCAATATCAATTCCAAACTC ATACA
cg1521 2455	TTTGGTCGTTTTGGTTGGAGGAG G	TCATTACAACCTTTATACACACT TCTCA
cg0729 9736	TGGGTCGGTTGTTTTATAGTTTG T	AAAAACCCAACCTCCAACCACAC GA
cg2232 5292	TCGGGGTTTTTAGAGGTTAGCGA T	CCCCCAAACATCAAAACGATTA CCA
cg2089 4457	TGCGTCGTAGGAAGGGTAATAC GT	ACGAAAATCGCAAAACTAAACT ACCT
cg2524 3455	TGTTTTTATTTTTATATATATGGG GTATTATCGT	AACGTTATCTTTCCTACAACCTT ATTCT
cg0851 3547	AGGTTTGGAAGAAAGAATGGAG TT	ACACCTAATTCTATATAATCATA TCATAATCACA
cg1142 7463	TCGTTAGTTGTTAGCGAAGGGTG T	AACCCCCAAAAACCTACGACTC CT
cg0107 5459	TGGTTTATTTGAAATTTTAAGGT TAGAGTGT	ACACTCCTAAAACAATCTCTAAA CTAACA
cg0427 1617	GGGTTATAGGACGATTATGAGT AATTTGAA	ACCTTTCTCCCCCAAATACTATC CT

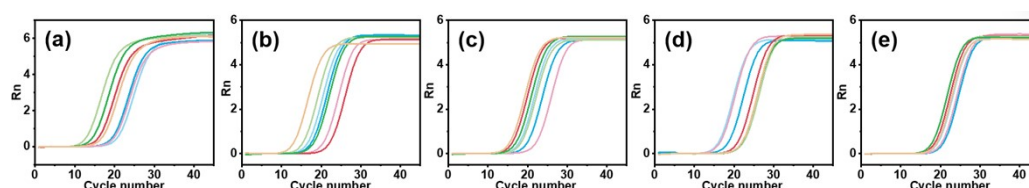


Figure S1. Impact of different nanomaterials on qPCR amplification curves. (a) Control group without nanomaterials; (b) CNT-COOH; (c) AuNPs; (d) G3-Au; (e) CNT-G3-Au.

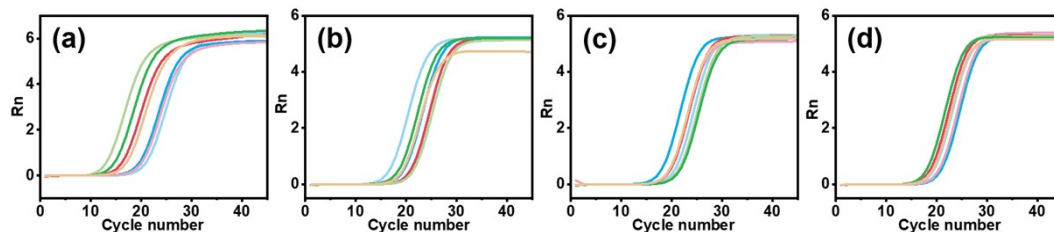


Figure S2. qPCR amplification curves for CNT-G3-Au nanocomposites with different AuNPs:G3 molar ratios: (a) without nanomaterial, (b) 5:1, (c) 15:1, (d) 10:1.

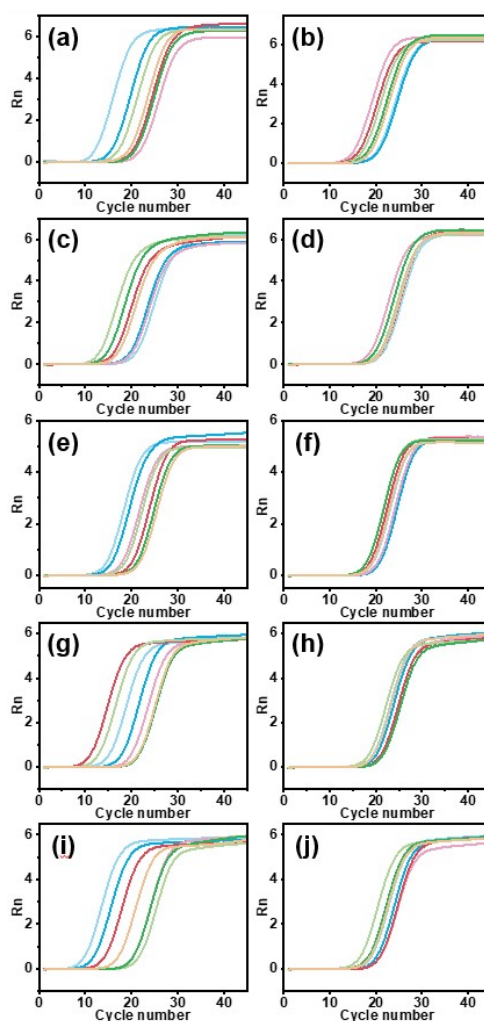


Figure S3. Effect of CNT-G3-Au on multiplex MSP amplification under different thermal cycling rates and reaction volumes. Amplification curves for seven representative amplicons are shown. (a, b) High-rate cycling (4 °C/s); (c, d) standard-rate cycling (3 °C/s); (e, f) low-rate cycling (2 °C/s); (g, h) standard-rate cycling (3 °C/s) with a 50 µL reaction volume; and (i, j) standard-rate cycling (3 °C/s) with a 100 µL volume. Panels (a, c, e, g, i) show reactions without CNT-G3-Au added, while panels (b, d, f, h, j) show reactions with CNT-G3-Au.

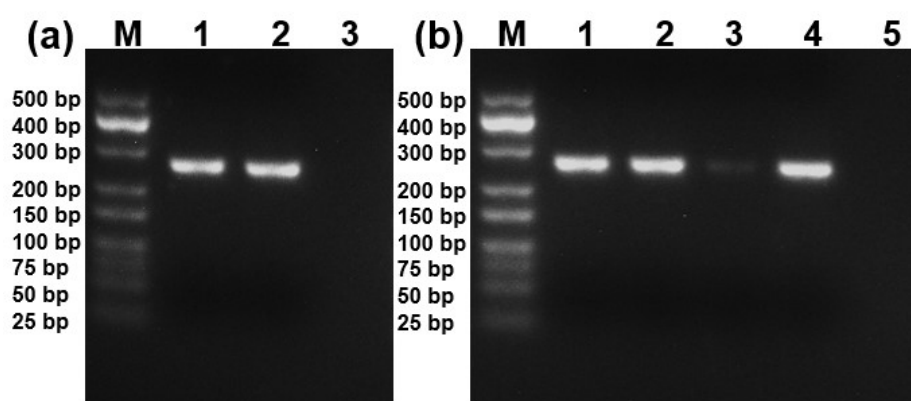


Figure S4. Agarose gel electrophoresis of PCR products. Lane M: DNA marker; last lane: negative control. (a) Lane 1: Final product of ultra-high multiplex PCR; Lane 2: Product obtained with the addition of an interfering template (human genomic DNA). (b) Lane 1: multiplex MSP product; Lane 2: Product with 0.3 nM CNT-G3-Au; Lane 3: Product with inhibitor (0.173 mM NaCl); Lane 4: Product with both inhibitor and CNT-G3-Au.

Table S4. Representative strategies for improving PCR amplification uniformity.

Method/Reference	Reported performance	Main drawbacks	Advantages of our approach
Bead-linked transposomes¹	Better amplification in GC-rich regions, but weak performance with short DNA fragments (<250 bp).	Limited by fragment length.	Works well even with 120 very short fragments (<250 bp).
Three-round multiplex PCR²	Achieved 90.5% coverage in a 37-plex SNP system.	Small scale, incomplete coverage, complicated workflow and time-consuming.	Delivers 97.8% coverage in much larger systems (120-plex in ultra-high multiplex PCR; 40-plex for multiplex MSP), with simpler steps and faster turnaround.
Molecular Inversion Probes³	Reasonable coverage in non-model species (about 80% of probes show uniform performance).	Coverage still uneven; affected by ligation bias and probe design; sensitive to	Provides both high coverage (97.8%) and greater uniformity, with lower cost and simpler handling.

		genomic context.	
CNT-G3-Au (This work)	In 120-plex PCR: qPCR $\Delta C_t < 4$; sequencing uniformity up to 85.1%, coverage up to 97.8%.	Large multiplexing may still introduce some bias.	Combines electrostatic DNA enrichment with improved heat transfer, leading to higher uniformity, sequencing depth, and reproducibility.

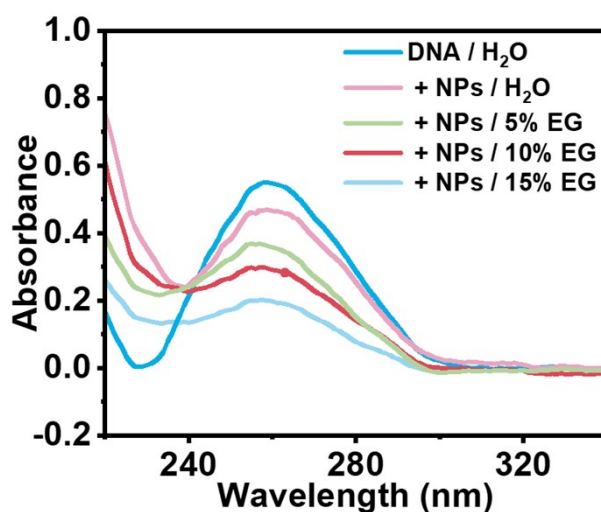


Figure S5. UV–Vis spectra of DNA supernatants for DNA in water without nanomaterials, and for DNA mixed with CNT-G3-Au in ethylene glycol–water solutions containing 0%, 5%, 10% and 15% ethylene glycol (v/v).

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