

Additional File S1: List of physicochemical properties related to DPCP and TPCP.

Physicochemical properties for DPCP

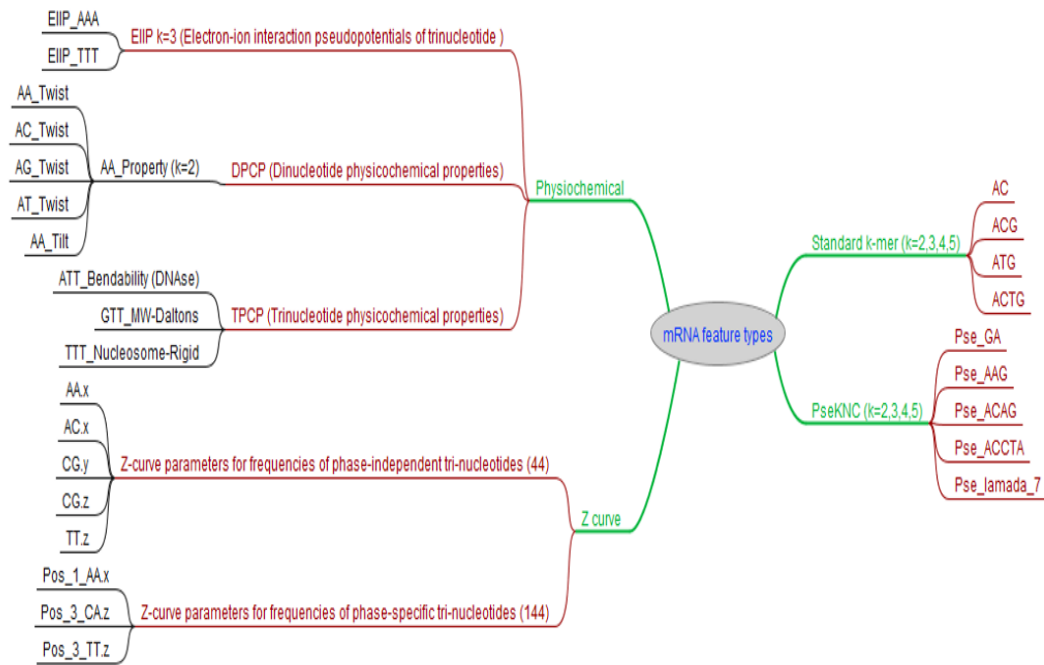
Base stacking	Protein induced deformability	B-DNA twist	Propeller twist	Duplex stability:(freeenergy)
Duplex tability(disruptenergy)	Protein DNA twist	Stabilising energy of Z-DNA	Aida_BA_transition	Breslauer_dS
Electron_interaction	Hartman_trans_free_energy	Lisser_BZ_transition	Polar_interaction	SantaLucia_dG
Sarai_flexibility	Stability	Stacking_energy	Sugimoto_dS	Watson-Crick_interaction
Twist	Shift	Slide	Rise	Twist stiffness
Tilt stiffness	Shift_rise	Twist_shift	Enthalpy1	Twist_twist
Shift2	Tilt3	Tilt1	Slide (DNA-protein complex)1	Tilt_shift
Twist_tilt	Roll_rise	Stacking energy	Stacking energy1	Propeller Twist
Roll11	Rise (DNA-protein complex)	Roll2	Roll3	Roll1
Slide_slide	Enthalpy	Shift_shift	Flexibility_slide	Minor Groove Distance
Rise (DNA-protein complex)1	Roll (DNA-protein complex)1	Entropy	Cytosine content	Major Groove Distance
Twist (DNA-protein complex)	Purine (AG) content	Tilt_slide	Major Groove Width	Major Groove Depth
Free energy6	Free energy7	Free energy4	Free energy3	Free energy1
Twist_roll	Flexibility_shift	Shift (DNA-protein complex) 1	Thymine content	Tip
Keto (GT) content	Roll stiffness	Entropy1	Roll_slide	Slide (DNA-protein complex)
Twist2	Twist5	Twist4	Tilt (DNA-protein complex)1	Twist_slide
Minor Groove Depth	Persistence Length	Rise3	Shift stiffness	Slide3
Slide2	Slide1	Rise1	Rise stiffness	Mobility to bend towards
Dinucleotide GC Content	A-philarity	Wedge	DNA denaturation	Bending stiffness
Free energy5	Breslauer_dG	Breslauer_dH	Shift (DNA-	Helix-Coil_transition
Ivanov_BA_transition	Slide_rise	SantaLucia_dH	SantaLucia_dS	Minor Groove Width

Sugimoto_dG	Sugimoto_dH	Twist1	Tilt	Roll
Twist7	Clash Strength	Roll_roll	Roll (DNA-protein)	Adenine content
Direction	Probability contacting	Roll_shift	Shift_slide	Shift1
Tilt4	Tilt2	Free energy8	Twist (DNA-	Tilt_rise
Free energy2	Stacking energy2	Stacking energy3	Rise_rise	Tilt_tilt
Roll4	Tilt_roll	Minor Groove Size	GC content	Inclination
Slide stiffness	Melting Temperature1	Twist3	Tilt (DNA-protein)	Guanine content
Twist6	Major Groove Size	Twist_rise	Rise2	Melting Temperature
Free energy	Mobility to bend towards	Bend		

Physicochemical properties for TPCP

Dnase I	Bendability (DNase)	Bendability	Trinucleotide GC
Nucleosome positioning	Consensus_roll	Consensus-Rigid	Dnase I-Rigid
MW-Daltons	MW-kg	Nucleosome	Nucleosome-

Additional File S2: Name of the features and their mapping.



Additional File S3: Selected top features and their importance based on SHAP analysis for locations

Cytoplasm	
col_name	feature_importance_vals
Pse_CCT	206.673056
Pse_AAAAA	116.444305
Pos_2_AT.x	74.121072
Pse_GTATG	48.02352
Pse_GACG	46.29276
Pse_CCGG	43.248298
Pse_TTCA	42.917792
GTG_Bendability (DNase)	41.368288
AACGA	39.938774
CGT_Consensus_roll	38.964102
Pse_GGGGC	35.182722
CATTT	28.860437
Pse_GAT	27.656036
AGGGT	26.523641
GCTCT	24.929051
Pse_TCTAC	23.68738
Pse_CAGT	23.544006
Pse_GT	21.557911
AGCCG	18.609311
TCTG	18.351851

Nucleus	
col_name	feature_importance_vals
Pse_CCT	187.077578
CATAG	103.88836
AA.z	92.803388
EIIP_GGG	87.853341
CA.z	6.833876
Pse_TCCC	50.697388
Pse_GGCC	41.466302
Pos_2_AG.z	33.834258
Pse_TCA	30.258604
AGCAG	29.527333
GACAG	29.239678
CGAAT	26.264532
Pse_CCCCT	25.990881
CC.y	25.816443
TATCA	21.579559
Pos_3_GC.y	20.970483
TCCC	20.635664
GTTA	19.271744
Pse_AATAA	19.06901
Pse_CCC	17.802511

ER	
col_name	feature_importance_vals
GG.z	62.424883
Pse_CGA	46.826436
TAG_MW-kg	25.152063
Pse_AGT	18.673658
Pse_CGAAA	14.414912
Pse_TCG	13.482978
CAGA	11.115082
Pse_AGTTT	10.804254
AGC_Consensus-Rigid	10.618663
AA.y	10.461962
Pse_AGTGT	9.715807
Pse_CTGGG	9.417216
AAT	9.14116
TGTTA	7.662036
GGGAG	7.484691
TACAG	6.898512
ACAAA	6.744645
Pse_TGTGA	6.548677
Pse_GTTA	6.360968
AAGAT	5.77078

EXR	
col_name	feature_importance_vals
Pse_GTCT	28.846373
Pse_CCTAC	24.563183
TCCA	17.138336
GCACC	13.030264
Pse_TCCTA	12.843472
AGGGG	10.559118
Pse_GGCC	8.395368
Pse_GGG	7.892994
Pse_GACTT	7.254099
GT_Protein DNAtwist	5.718517
Pse_CGAA	5.530338
TCGTC	5.309657
Pse_TATGC	5.038264
Pos_2_CA.x	5.01998
Pse_GGGA	4.821176
CAT_Nucleosome	4.737092
GGG_Trinucleotide GC Content	4.697096
Pse_CCGT	4.304871
CCTCT	3.969292
GTGA	3.670255

Mitochondria		
col_name	feature_importance_vals	
CA.z	29.34091	
Pos_1_TA.x	14.02338	
Pos_2_AC.x	12.214785	
Pos_3_AT.x	7.009193	
Pos_2_CC.x	5.582243	
CTA_Bendability (consensus)	3.881014	
AGGGG	3.022339	
CA.y	2.27599	
CCAAT	1.780037	
ATCGT	1.251607	
Pse_TCAAA	1.048577	
GCTTG	1.016545	
Pos_3_GG.x	0.564205	
GG_Minor Groove Distance	0	
TT_Minor Groove Distance	0	
TG_Minor Groove Distance	0	
CT_Flexibility_slide	0	
CG_Flexibility_slide	0	
CC_Flexibility_slide	0	
CA_Flexibility_slide	0	

Pseudopodium		
col_name	feature_importance_vals	
PseKNC_Iamada_6	13.805925	
PseKNC_CAGAG	6.363826	
GCGCA	5.822396	
Pos_2_AAy	3.624833	
PseKNC_GGTAT	3.404801	
PseKNC_CGTGG	3.32124	
PseKNC_AAAAA	3.260308	
TAAC	2.892381	
Pos_3_CCz	2.695837	
PseKNC_AGAAC	2.267244	
CGTA	2.091755	
PseKNC_TTCCT	2.000825	
PseKNC_TCAG	1.996316	
CCACG	1.164365	
GATA	1.142898	
ATTAG	1.062658	
AATCA	1.05816	
GGCGT	0.970909	
PseKNC_TTGAC	0.851616	
Pos_2_CGy	0.744699	

Exosome		
col_name	feature_importance_vals	
GCGA	22.479522	
CTx	21.370833	
PseKNC_CTGAC	15.862419	
PseKNC_ACTGT	15.024765	
PseKNC_ACACA	10.369668	
GTy	9.329866	
CGAGC	9.075361	
PseKNC_GGCAA	7.670002	
GACAC	6.441558	
PseKNC_CATGC	5.773664	
PseKNC_TATGC	5.754335	
GTC_DnaseI Rigid	5.700318	
PseKNC_TCCT	5.456513	
CCGGA	5.241851	
PseKNC_TATCA	5.085149	
PseKNC_TACGT	5.008218	
Pos_3_TGz	4.584346	
CTCT	4.530319	
GCC_DnaseI	4.192017	
PseKNC_CCTTT	3.86548	

Ribosome		
col_name	feature_importance_vals	
CGz	73.71227	
AAAAA	43.770771	
AC_MinorGrooveDistance	35.896707	
GG_Rise2	22.665376	
PseKNC_ACGAC	18.77651	
AC_Freeenergy8	15.881936	
GGGC	14.824248	
TGTG	14.383809	
PseKNC_ATAG	12.964419	
Pos_2_TTz	12.424472	
AC_Twist_roll	12.124697	
GACTA	9.875691	
PseKNC_GGGAG	9.349708	
CA_Shift1	9.248852	
TTGC	8.904275	
GG_StabilisingenergyofZDNA	8.615998	
PseKNC_GTAC	8.251039	
PseKNC_GCGCC	7.655031	
TCACT	7.579636	
PseKNC_AAAAA	7.407486	

Cytosol		
col_name	feature_importance_vals	
PseKNC_AAAAA	85.929442	
TG_Roll	42.531932	
CCTCC	29.843055	
TGGT	27.115962	
GT_Roll1	19.03369	
PseKNC_CGAA	18.454454	
CGAA	15.675292	
TCy	13.237076	
PseKNC_GCCCC	13.16231	
PseKNC_TTTCT	12.597915	
GGTGT	11.697577	
AGCTA	11.124263	
TCT_Nucleosomepositioning	10.832596	
PseKNC_CCTCT	10.282507	
GACGA	9.901289	
GGAAT	9.487927	
TCCC	9.417518	
PseKNC_GCATA	8.450371	
ATx	8.099528	
GGCTG	8.022591	

Posterior		
col_name	feature_importance_vals	
CGA_Nucleosomepositioning	25.866967	
PseKNC_CCGGG	4.499514	
PseKNC_CTTTT	1.629831	
Pos_1_ATz	1.279826	
CTCGT	1.208085	
AC_MinorGrooveSize	0.961555	