MiRNA profile in canine oral melanoma

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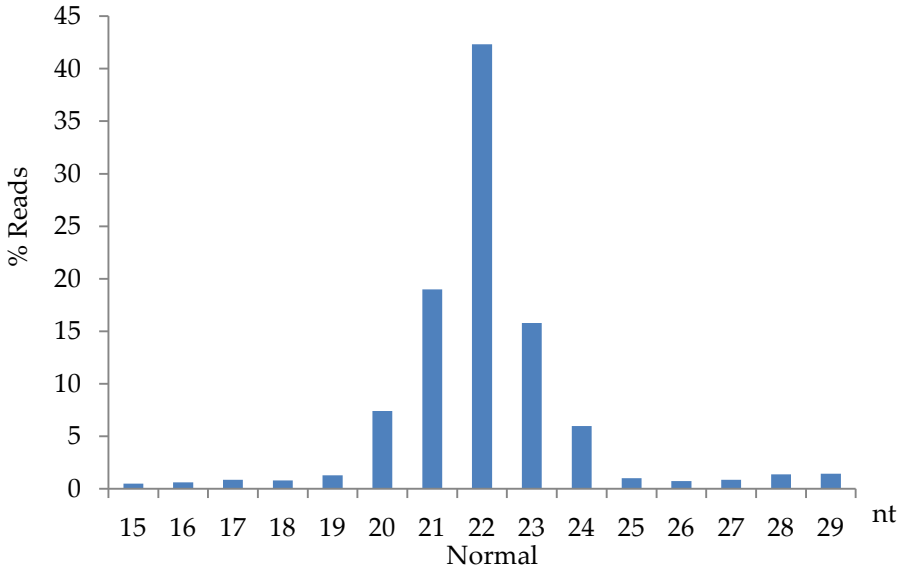
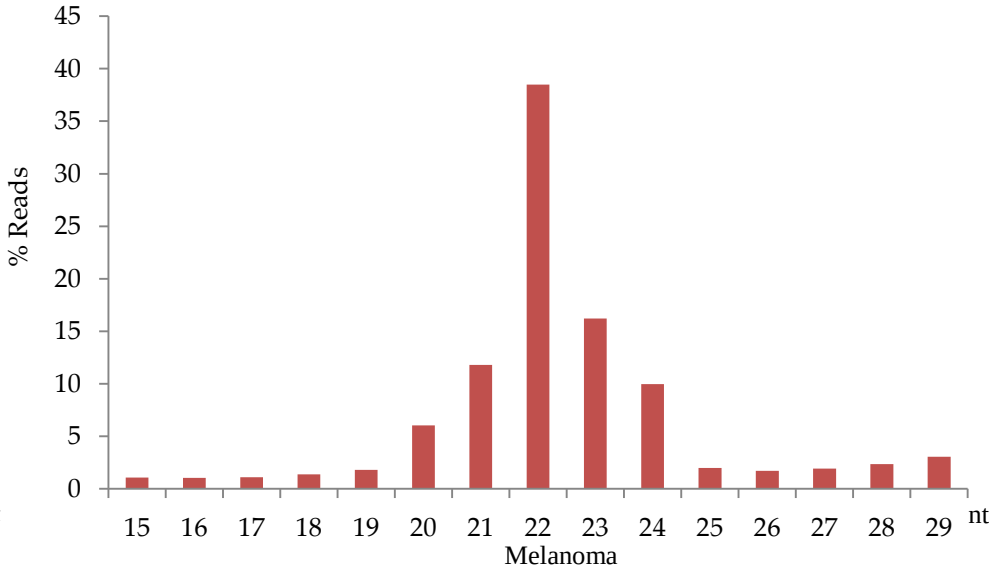
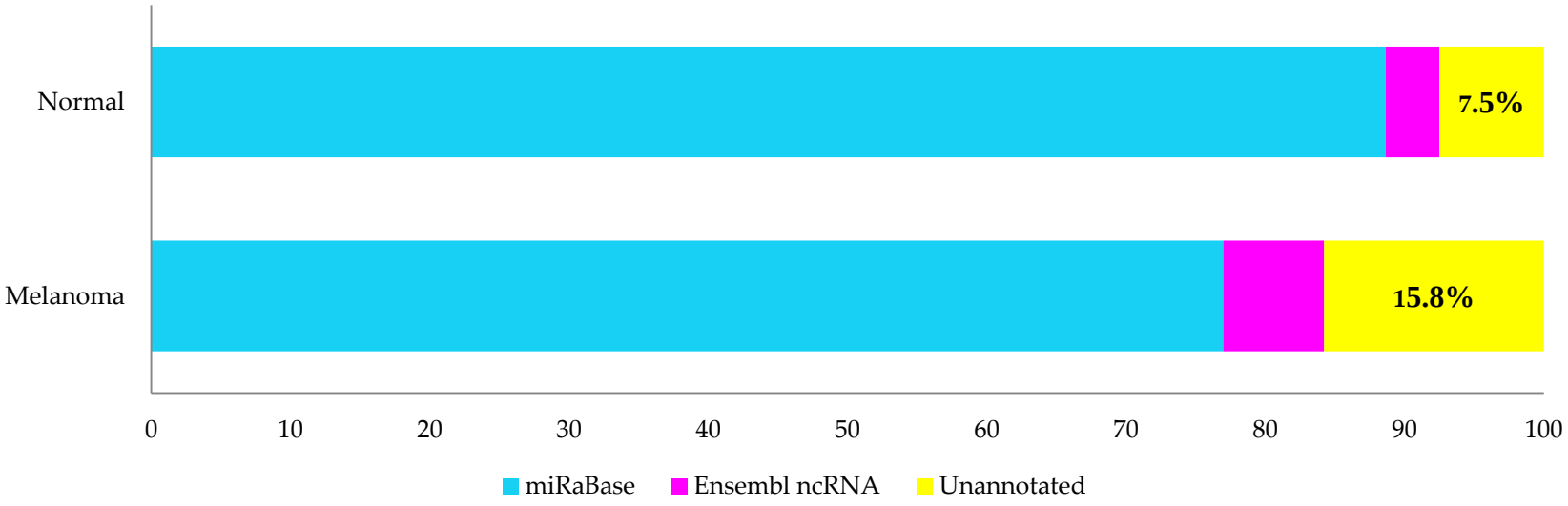
(a)





(b)


Normal
Melanoma
7.5%
15.8%
0
10
20
30
40
50
60
70
80
90
100
miRaBase
Ensembl ncRNA
Unannotated

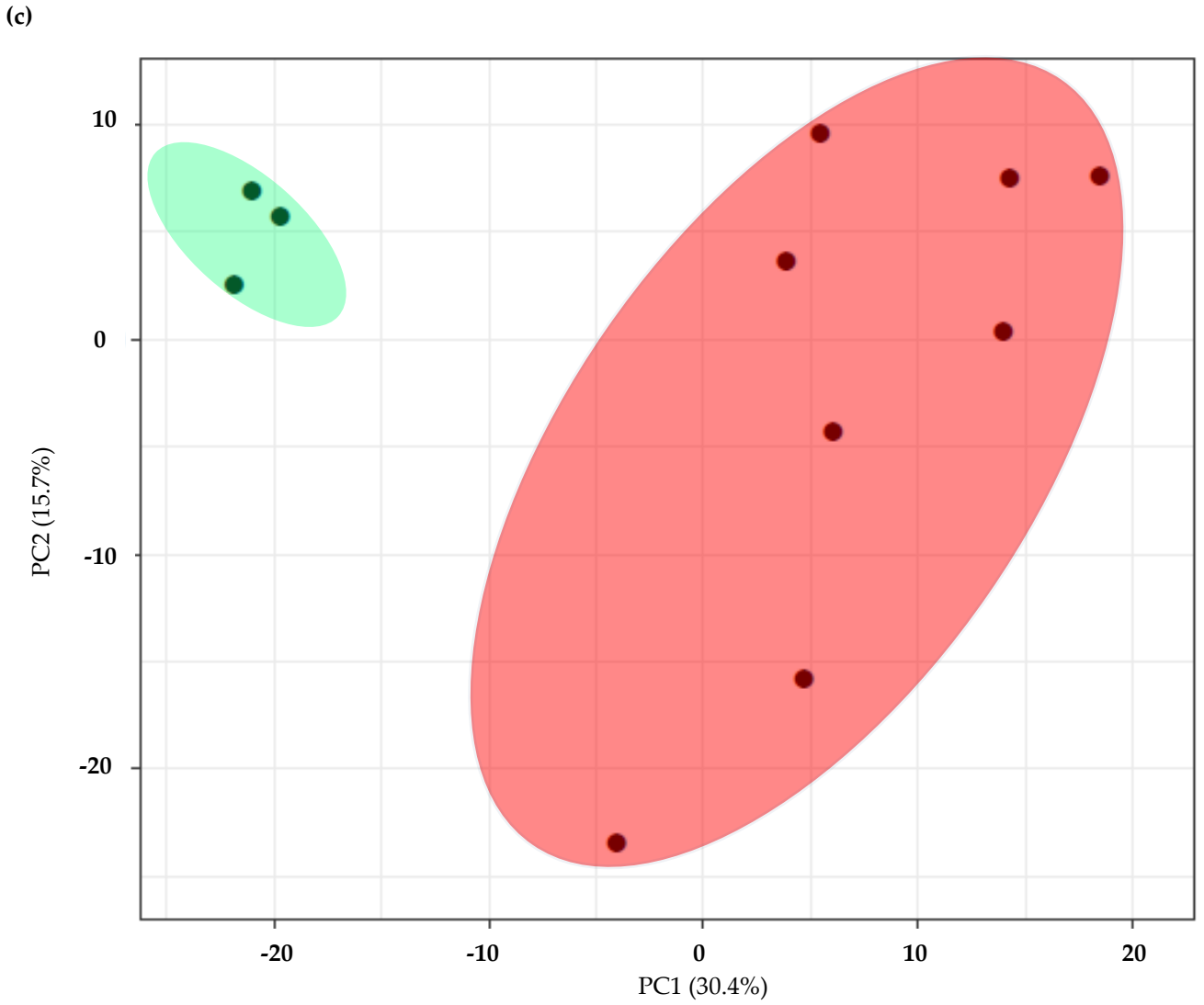
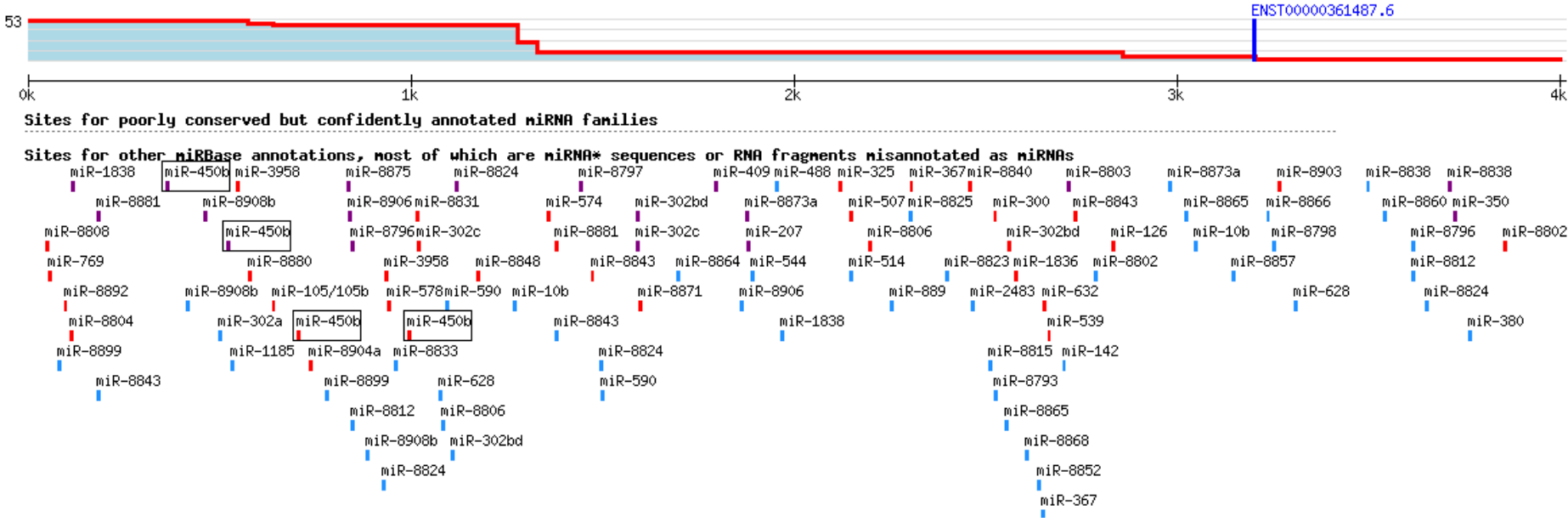


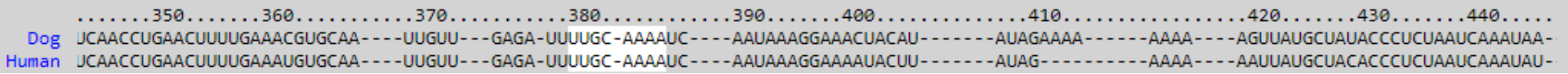
Figure S1. Profile of small RNA reads in canine oral melanoma: **(a)** Length distribution of clean reads in the normal and melanoma libraries; **(b)** Percentages of the clean reads annotated by the miRbase and Ensembl non-coding RNA databases; **(c)** Principal component analysis (PCA) of normal (green) and melanoma (pink) samples. The miRNAs read counts were normalized and transformed before PCA.

(a)

Dog PAX9 ENST00000361487.6 3′ UTR length: 4013

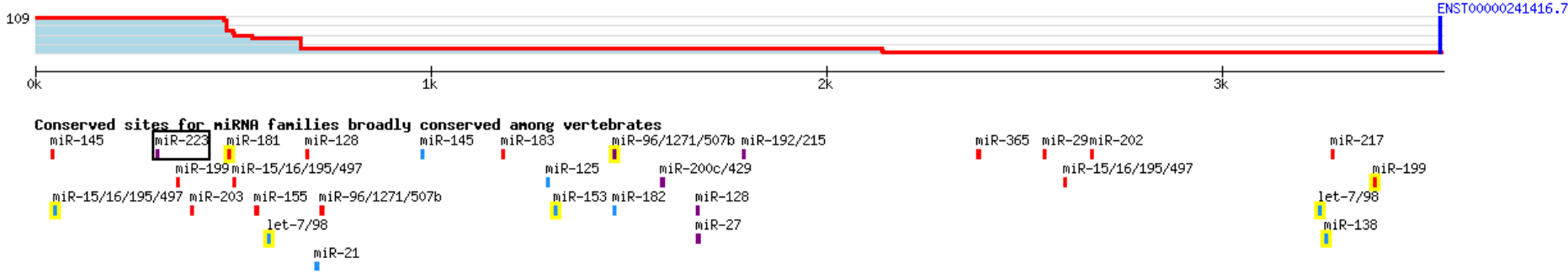


	Predicted consequential pairing of target region (top) and miRNA (bottom)	Site type	Context++ score	Context++ score percentile	Weighted context++ score	Conserved branch length	P_{CT}
Position 380-387 of PAX9 3' UTR cfa-miR-450b	5' ...GCAAUUGUUGAGAUUUUGCAAAA... 3' UAAGUCCUUGUAUAACGUUUU	8mer	-0.22	96	-0.22	0.153	N/A
Position 544-551 of PAX9 3' UTR cfa-miR-450b	5' ...AGAUGACCUAUUUUGUUGCAAAA... 3' UAAGUCCUUGUAUAACGUUUU	8mer	-0.19	94	-0.19	0	N/A
Position 735-741 of PAX9 3' UTR cfa-miR-450b	5' ...UUUUUUUCUUUCUUUUUGCAAAG... 3' UAAGUCCUUGUAUAACGUUUU	7mer-m8	-0.03	50	-0.03	0.233	N/A
Position 1033-1039 of PAX9 3' UTR cfa-miR-450b	5' ...UUAAUGUGAAACGCUUUGCAAAG... 3' UAAGUCCUUGUAU-AACGUUUU	7mer-m8	-0.08	78	-0.07	0.153	N/A



(b)

Dog ACVR2A ENST00000241416.7 3′ UTR length: 3560



	Predicted consequential pairing of target region (top) and miRNA (bottom)	Site type	Context++ score	Context++ score percentile	Weighted context++ score	Conserved branch length	P_{CT}
Position 305-312 of ACVR2A 3' UTR cfa-miR-223	5' ...AAUCAAGUGUUUGAA-AACUGACA... 3' CCCCAUAAACUGUUUGACUGU	8mer	-0.46	98	-0.46	3.283	0.29

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      260.....270.....280.....290.....300.....310.....320.....330.....340.....350.....360.....
Dog   ICUCCAAAU--C---AAGGAUC-UUUUGGACCU--GGCU-AAUCAAGUGU-UUG--AAAACUGACAUCAGAUUUC-----UAAAUGUCUGUCGG---AA---GACACUAAUUCC-UUAAAUGAACUACUGCUA---
Human ICUCCAAAU--C---AAGGAUC-UUUUGGACCU--GGCU-AAUGGAGUGU-UUG--AAAACUGACAUCAGAUUUC-----UUAAUGUCUGUCAG---AA---GACACUAAUUCC-UUAAAUGAACUACUGCU----
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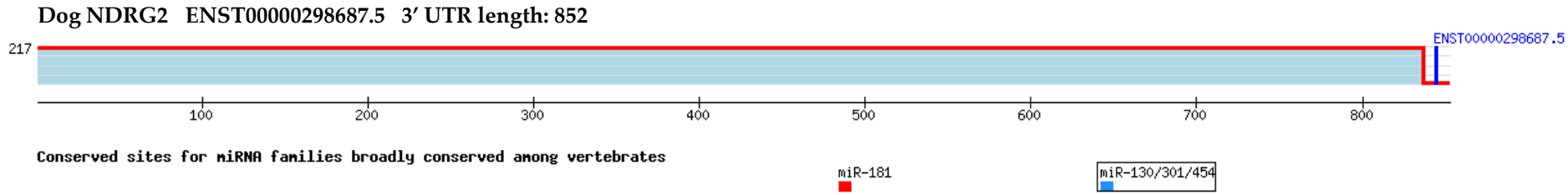
(c)



	Predicted consequential pairing of target region (top) and miRNA (bottom)	Site type	Context++ score	Context++ score percentile	Weighted context++ score	Conserved branch length	P_{CT}
Position 642-648 of NDRG2 3' UTR cfa-miR-130a	5' ...CCUGGGGCCAUUGGCUGCACUAA... 3' UACGGGAAAAUUGUAACGUGAC	7mer-A1	-0.16	80	-0.16	3.672	0.58
Position 642-648 of NDRG2 3' UTR cfa-miR-301b	5' ...CCUGGGGCCAUUGGCUGCACUAA... 3' CGAAACUGUUAUAGUAACGUGAC	7mer-A1	-0.16	80	-0.16	3.672	0.58
Position 642-648 of NDRG2 3' UTR cfa-miR-301a	5' ...CCUGGGGCCAUUGGCUGCACUAA... 3' CGAAACUGUUAUGAUAACGUGAC	7mer-A1	-0.16	80	-0.16	3.672	0.58

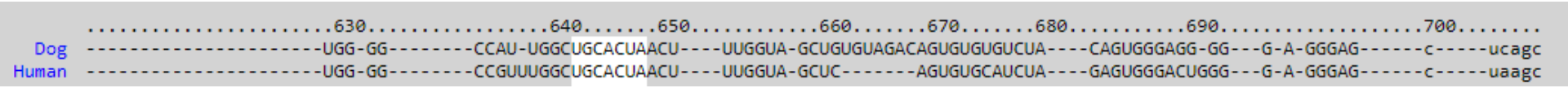


Figure S2. Predicted conserved target binding site of miR-450b-PAX9, miR-223-ACVR2A and miR-301a-NDRG2 from TargetScan: **(a-c)**. Predicted binding sites of respective miRNA-mRNA are conserved between human and dog.