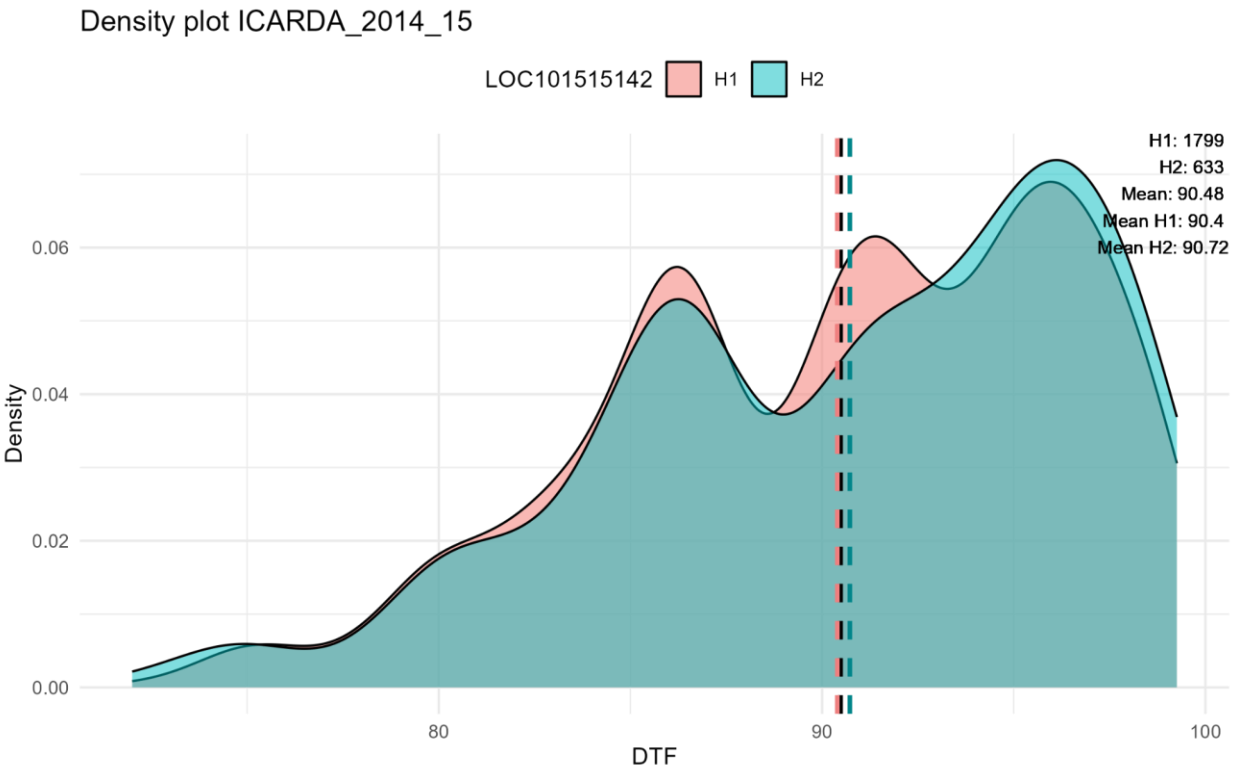


Additional file 10. Table S1 DTF (mean $\pm$ SD) for chickpea accessions at 6 locations acquired from the public repository CicerSeq (Varshney et al. 2021).

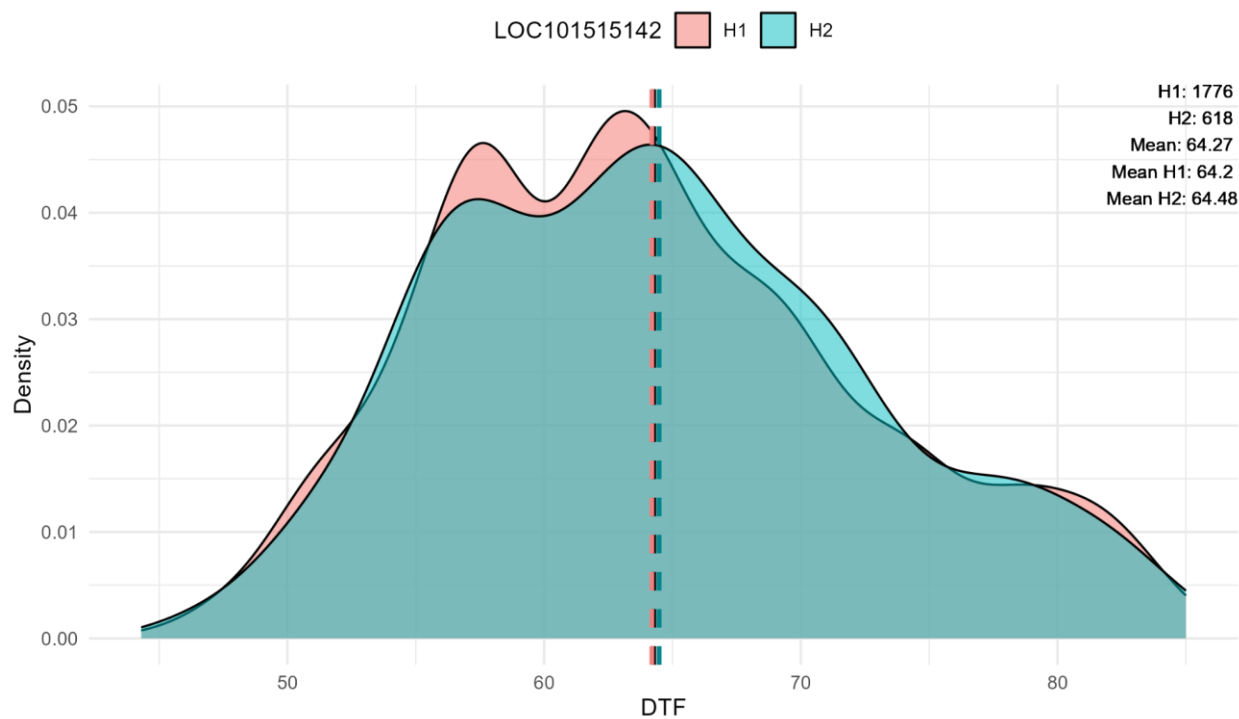
Haplotype			N	ICARDA 14/15	ICARDA 15/16	ICRISAT 14/15	ICRISAT 15/16	IIPR 15/16	JAU 14/16	JAU 15/16	RAKCA 14/15	RAKCA 15/16	RARI 14/15	RARI 15/16
LOC 101515142 <i>MED16</i> -like	Hap1	2219	90.4 ± 5.90	64.2 ± 8.43	56.8 ± 7.87	66.5 ± 16.0	71.3 ± 6.67	63.6 ± 8.30	66.0 ± 8.96	79.0 ± 4.71	70.8 ± 5.97	85.1 ± 8.63	82.5 ± 6.37	
			90.7 ± 6.13	64.5 ± 8.36	57.5 ± 8.50	67.0 ± 17.4	71.3 ± 6.86	64.0 ± 8.54	66.1 ± 9.38	79.5 ± 4.60	71.2 ± 5.41	88.2 ± 9.34	82.4 ± 6.17	
	Hap2		749											
	t-test			ns	ns	ns	ns	ns	ns	ns	*	ns	***	ns
LOC 101499101 B-box zinc finger protein 24	T	2609	90.4 ± 5.94	64.1 ± 8.24	56.8 ± 7.79	66.0 ± 16.0	71.2 ± 6.69	63.5 ± 8.32	65.8 ± 9.03	79.1 ± 4.63	70.8 ± 5.77	85.8 ± 8.89	82.5 ± 6.23	
			91.3 ± 5.94	66.8 ± 9.21	62.3 ± 7.33	76.7 ± 15.8	73.6 ± 6.26	68.2 ± 7.38	70.0 ± 7.84	80.2± 4.85	72.1± 6.35	90.0± 8.75	82.4± 6.85	
	A	299												
			t-test			*	***	***	***	***	***	***	***	**
LOC 101507442 <i>VRN1</i> -like	C	2654	90.5 ± 5.91	64.2 ± 8.27	57.3 ± 7.98	66.9 ± 16.2	71.3 ± 6.67	63.9 ± 8.24	66.2 ± 8.85	79.2 ± 4.58	70.9 ± 5.82	86.1 ± 8.92	82.5 ± 6.28	
			90.8 ± 5.94	65.9 ± 9.88	57.0 ± 8.00	67.7 ± 17.3	72.5 ± 7.06	64.0 ± 9.46	66.2 ± 10.7	79.0 ± 5.80	71.7 ± 6.57	85.8 ± 8.99	82.5 ± 6.46	
	T	275												
			t-test			ns	*	ns	ns	*	ns	ns	ns	ns
Mean ± SD				90.5 ± 5.96	64.3 ± 8.39	57.2 ± 7.98	66.9 ± 16.24	71.4 ± 6.70	63.9 ± 8.34	66.2 ± 8.99	79.2 ± 4.66	70.9 ± 5.83	86.1 ± 8.95	82.5 ± 6.33

Significant difference Student's t-test (ns: non-significant, $*0.01 < P \leq 0.05$, $**0.001 < P \leq 0.01$, $***P \leq 0.001$).

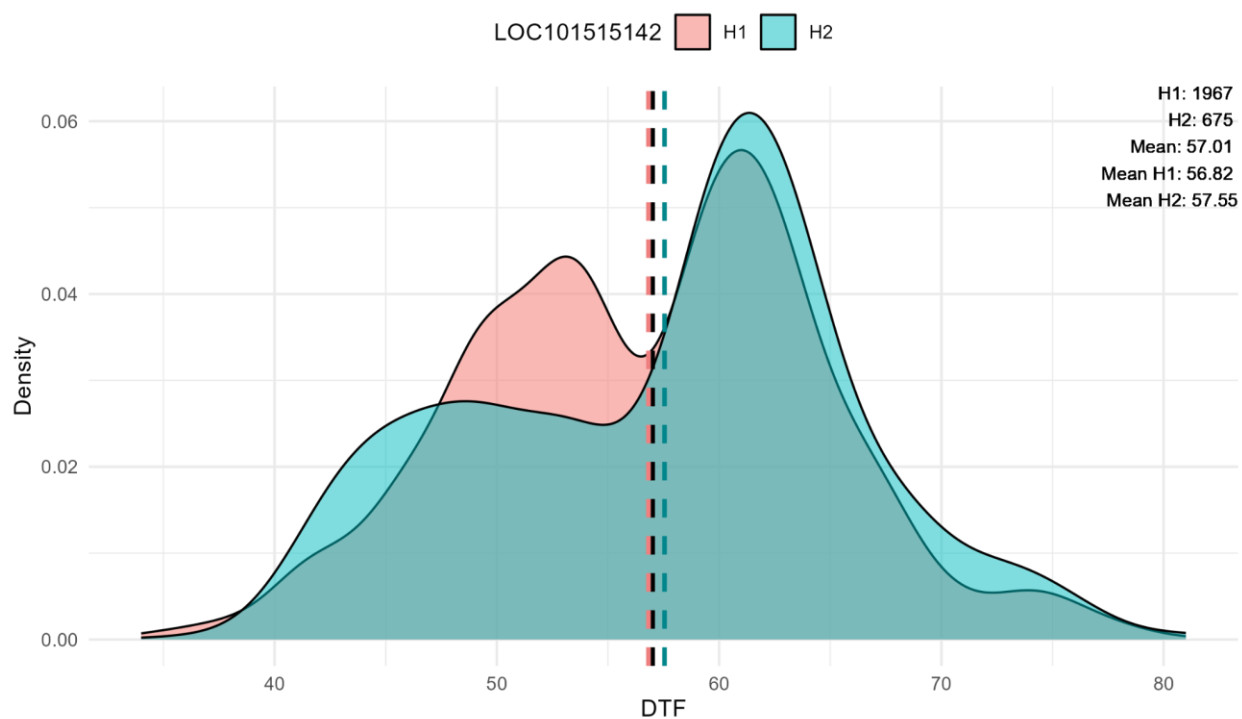
a LOC101515142 haplotypes



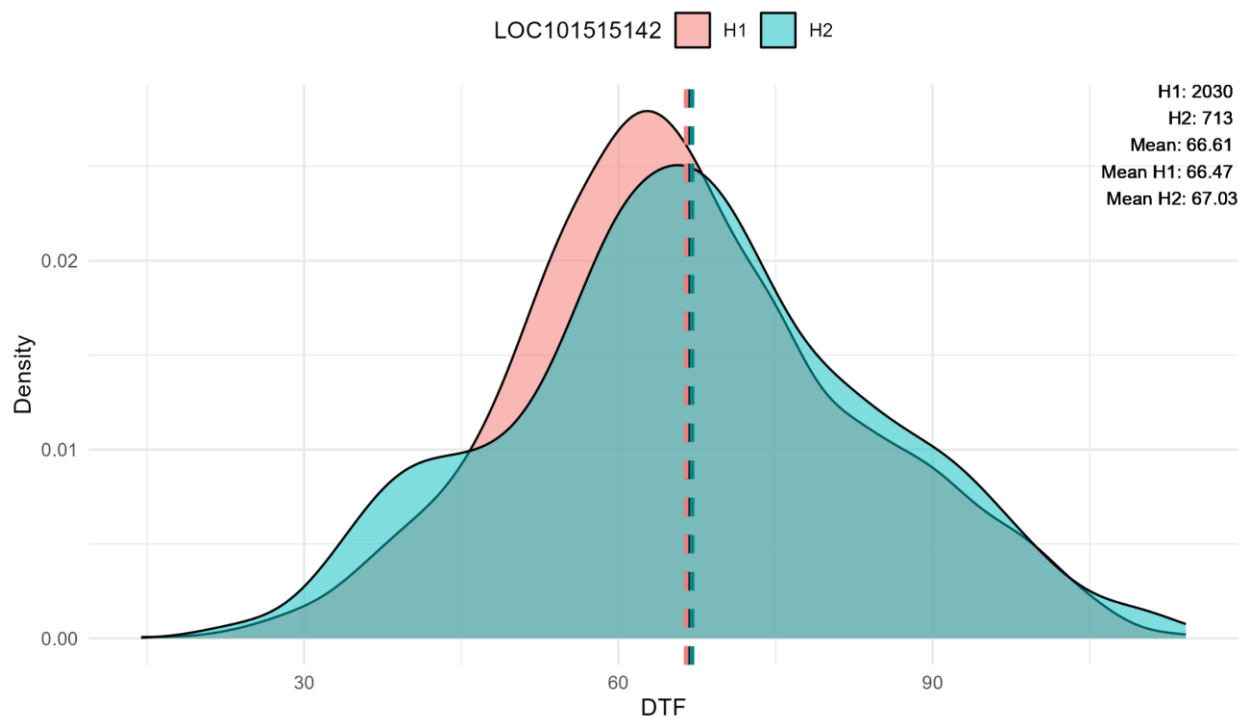
Density plot ICARDA_2015_16



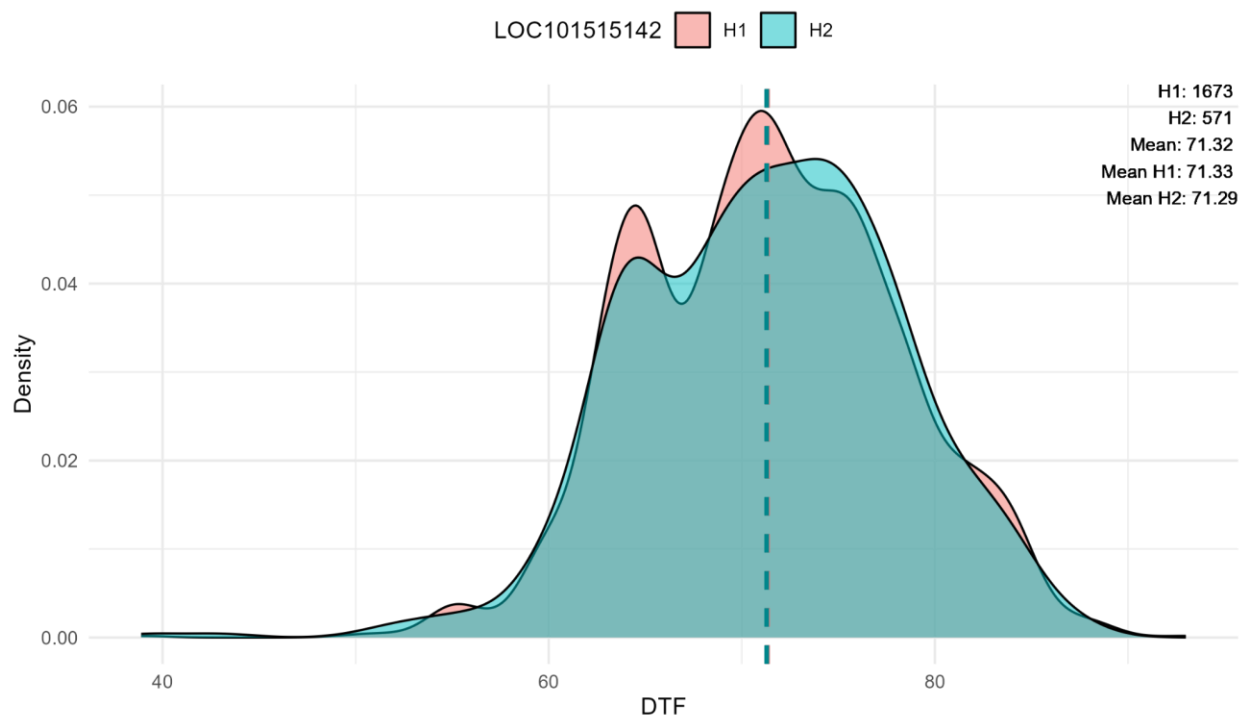
Density plot ICRISAT_2014_15



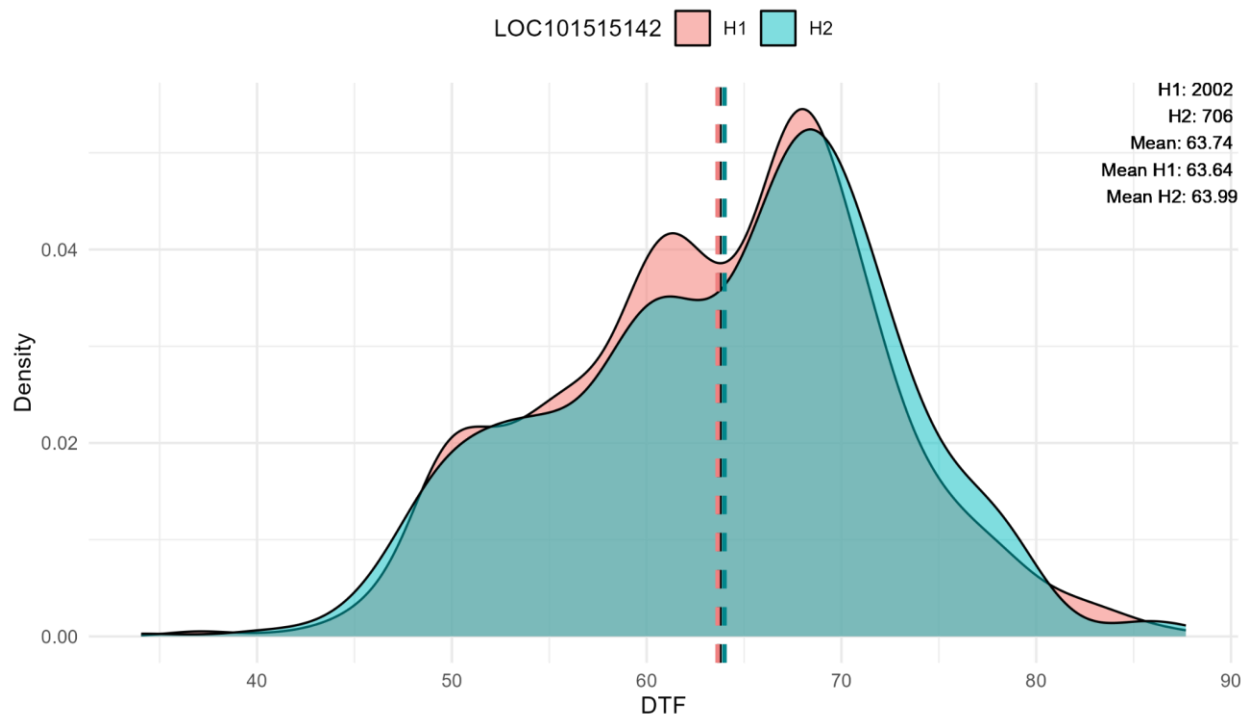
Density plot ICRISAT_2015_16



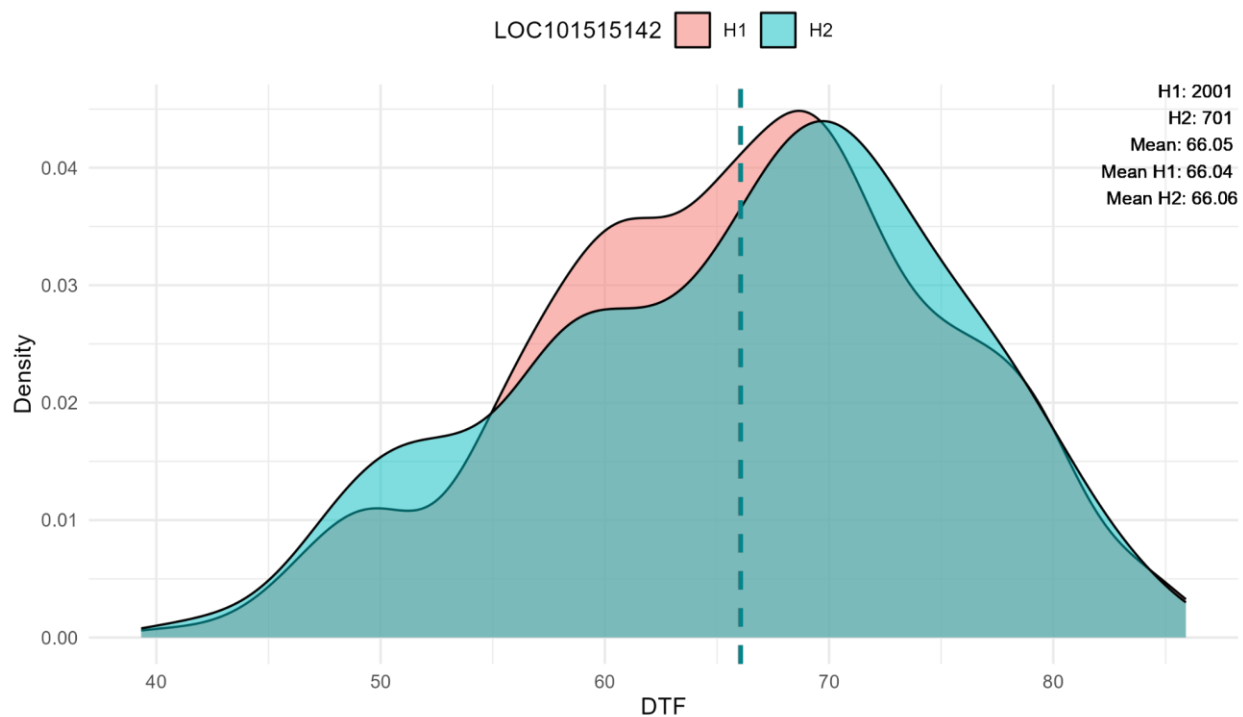
Density plot IIPR_2015_16



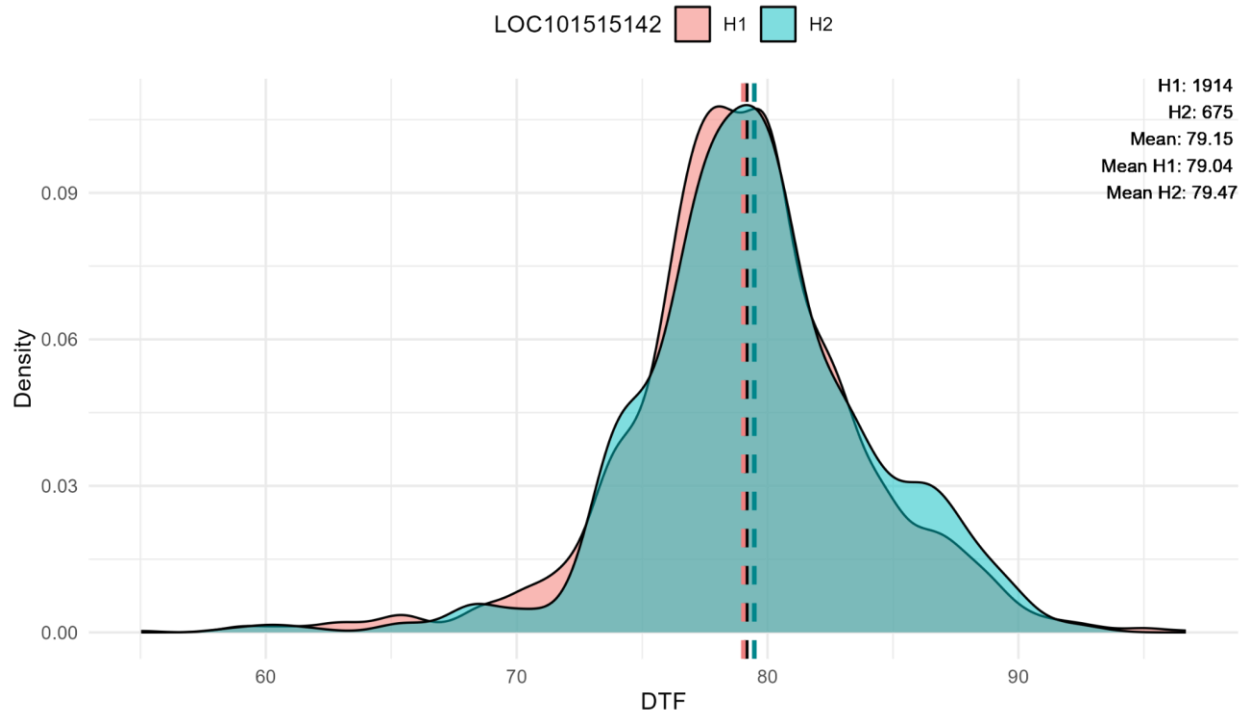
Density plot JAU_2014_15



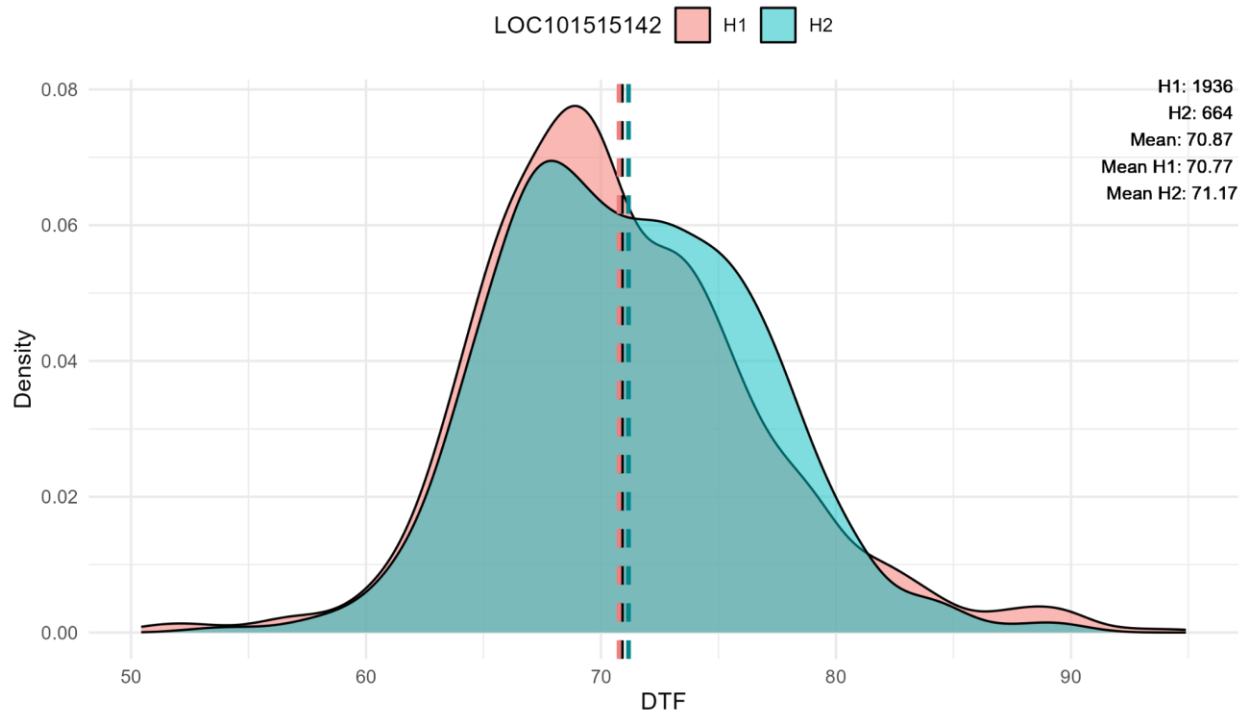
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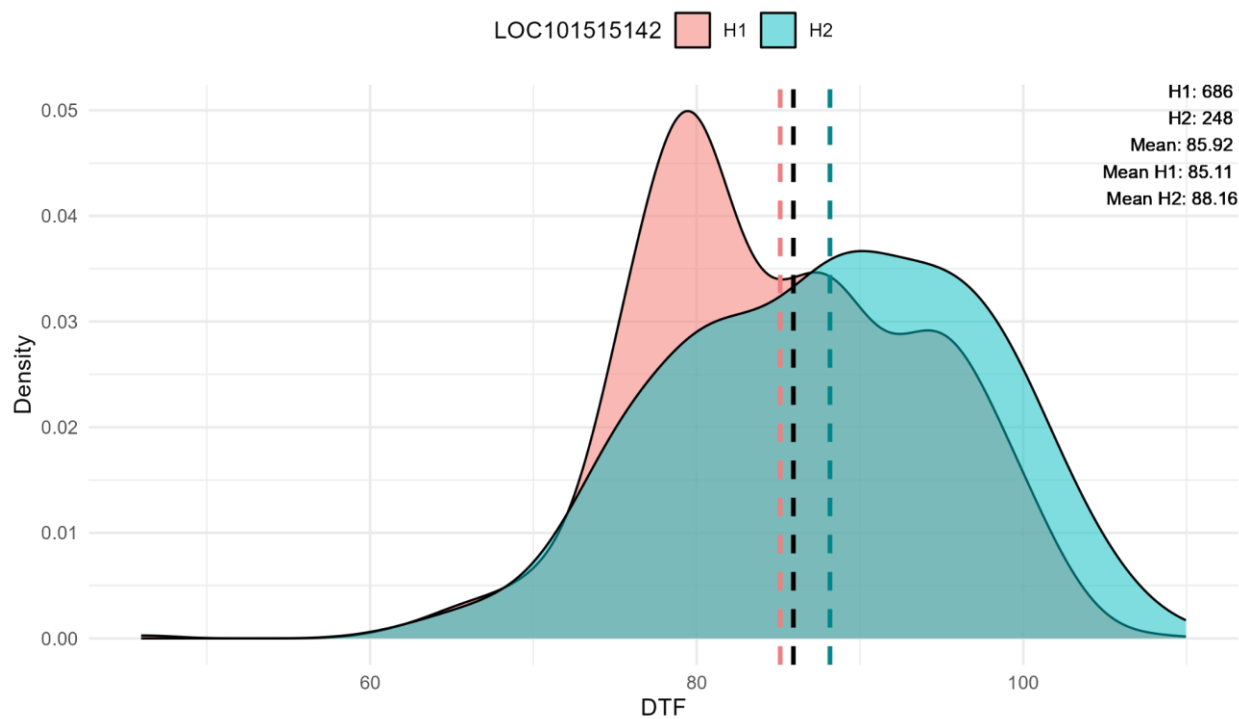
Density plot RAKCA_2014_15



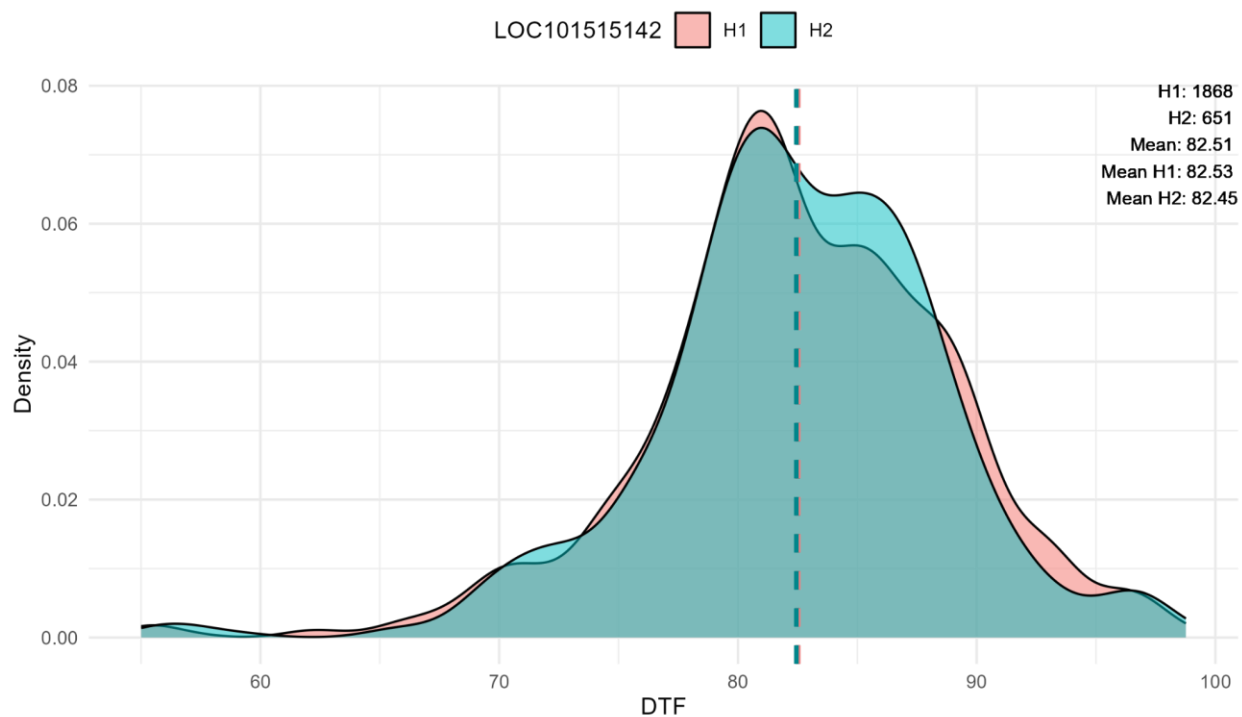
Density plot RAKCA_2015_16



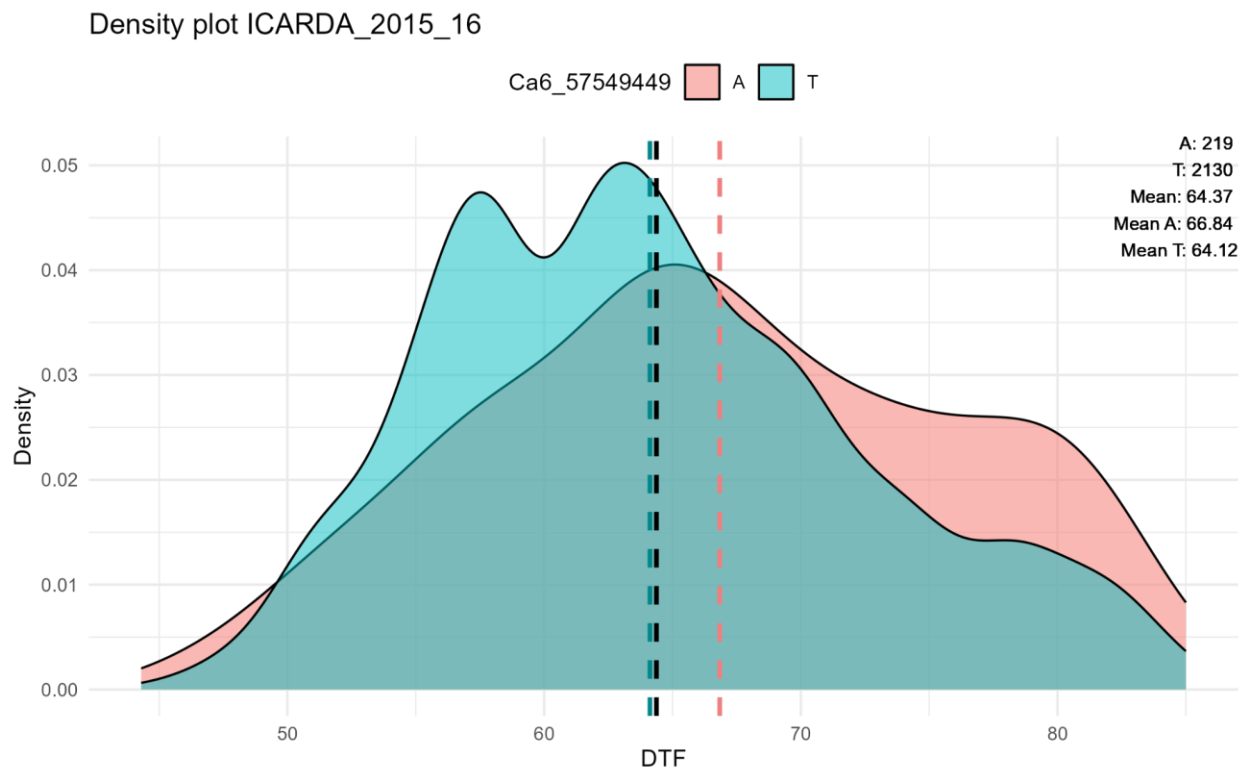
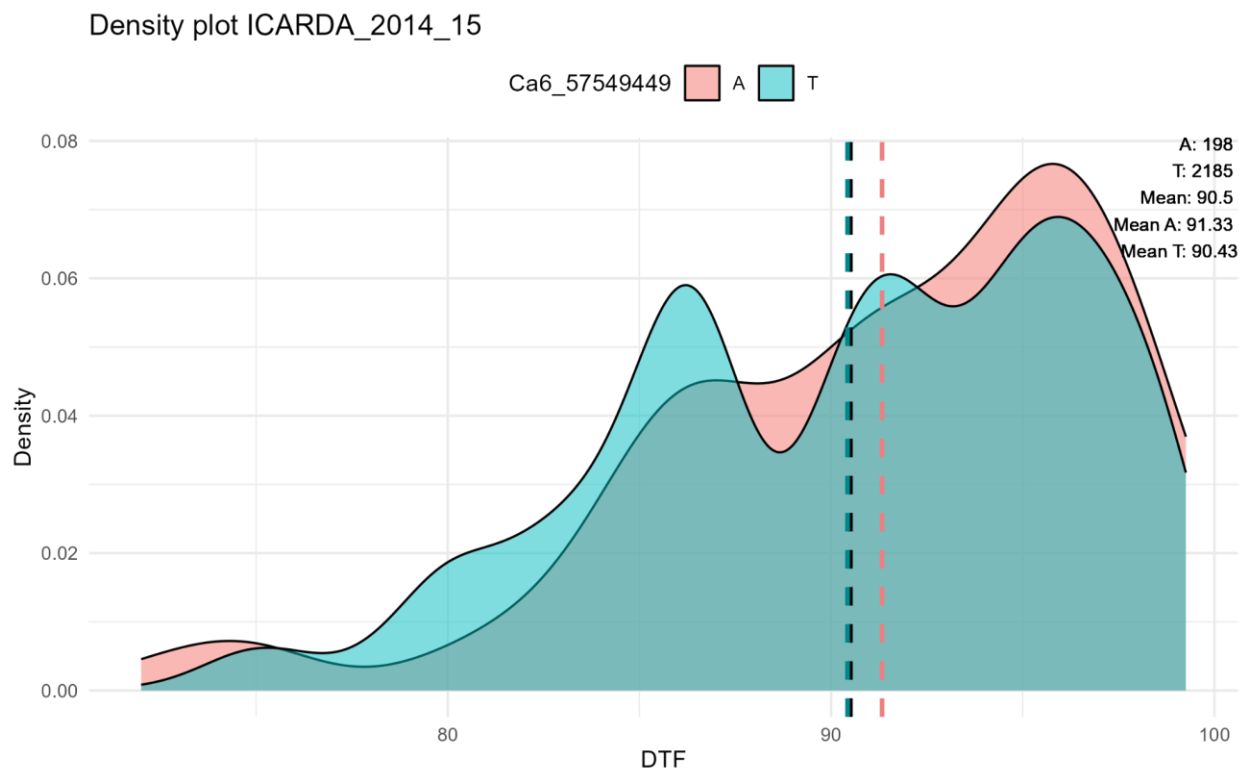
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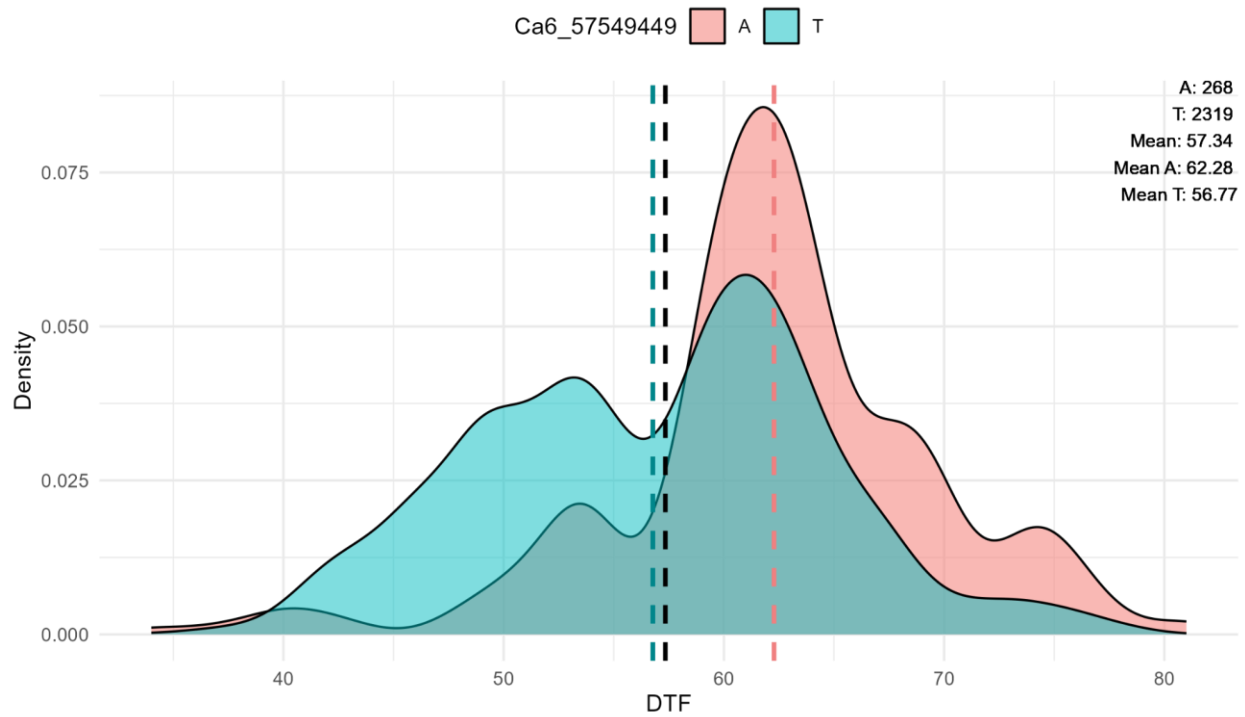
Density plot RARI_2015_16



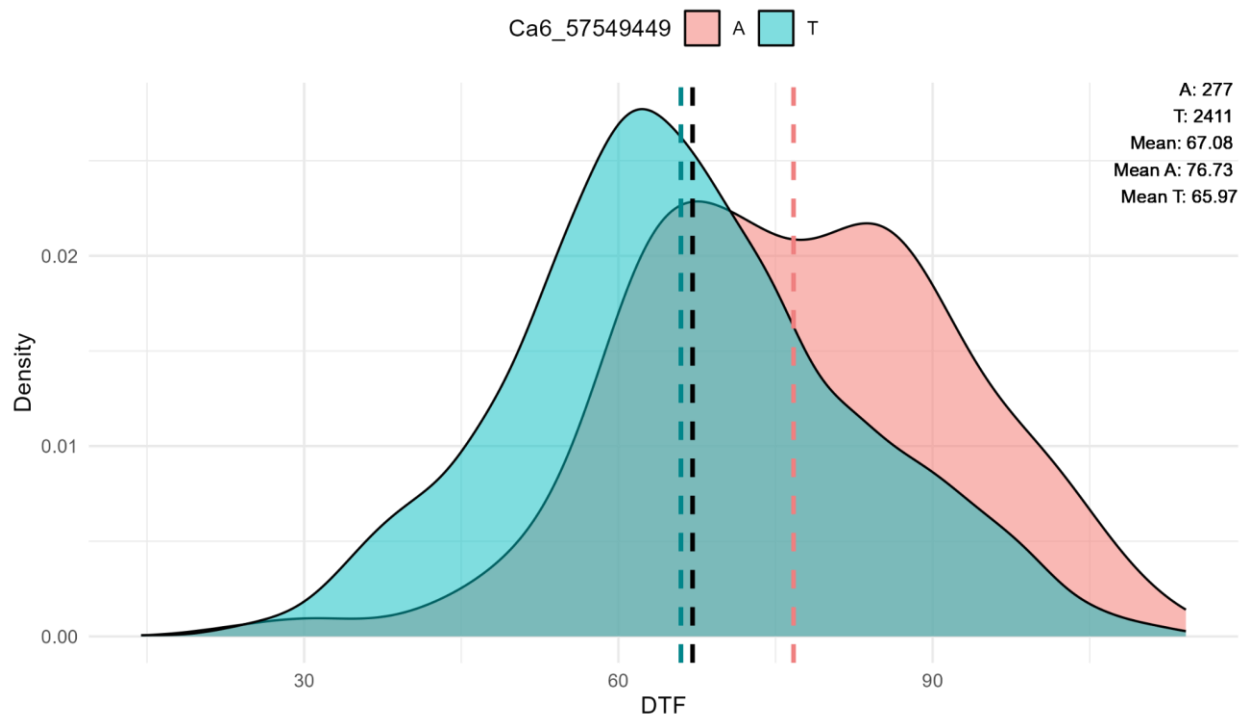
b LOC101499101 SNP (Ca6: 57,549,449)



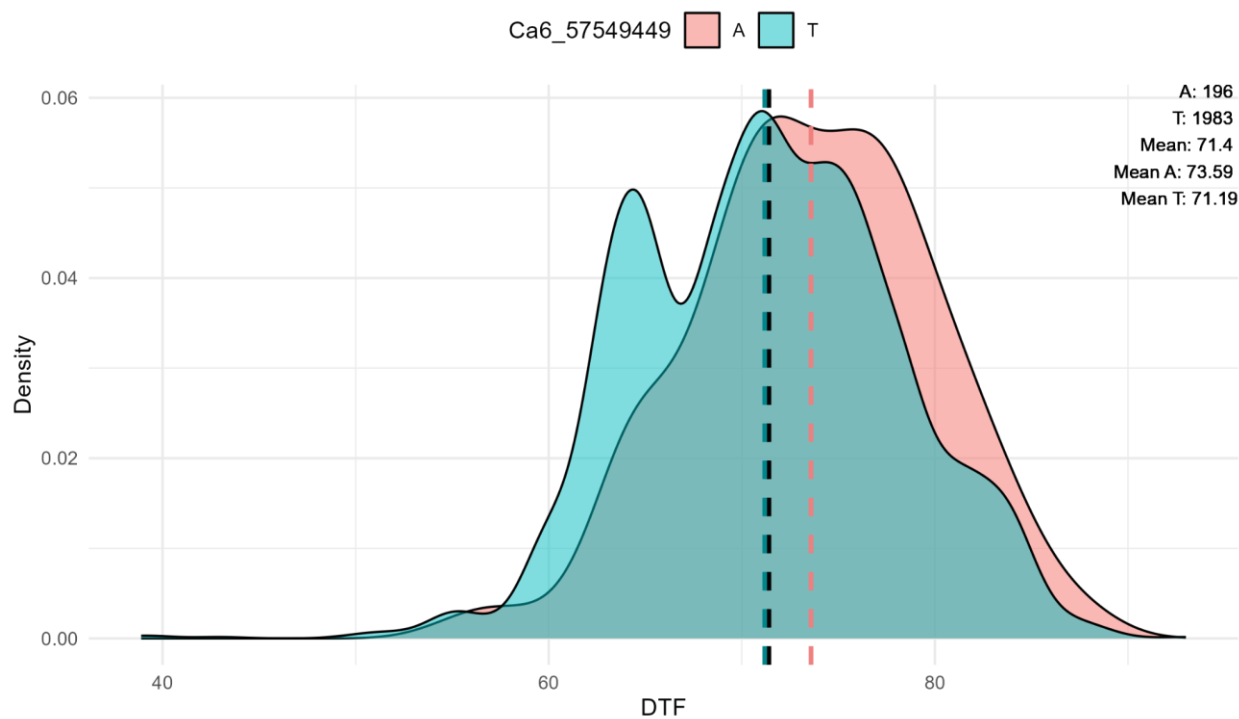
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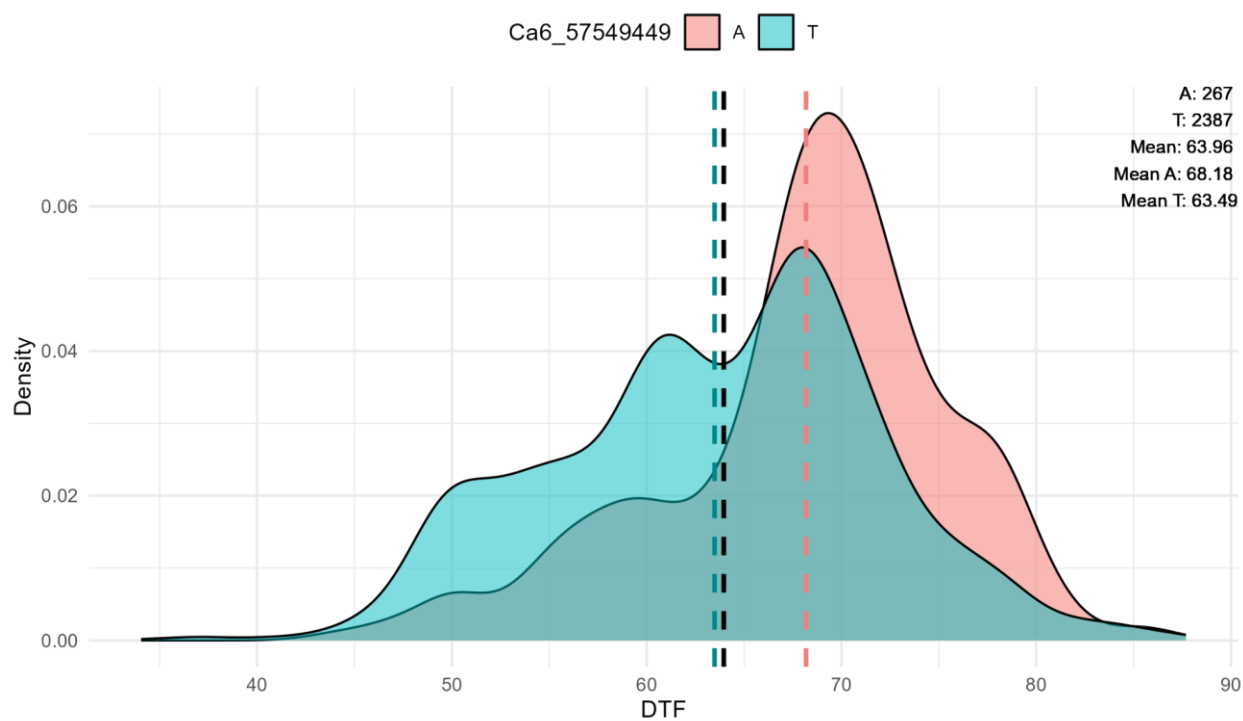
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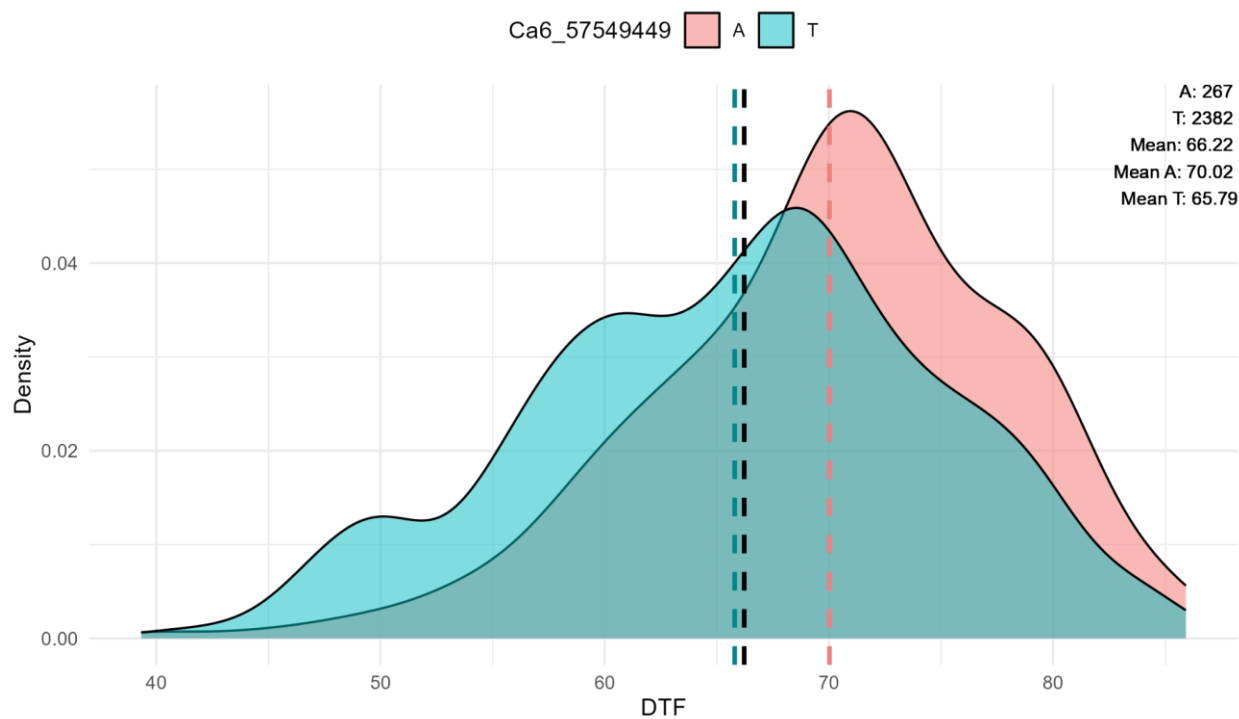
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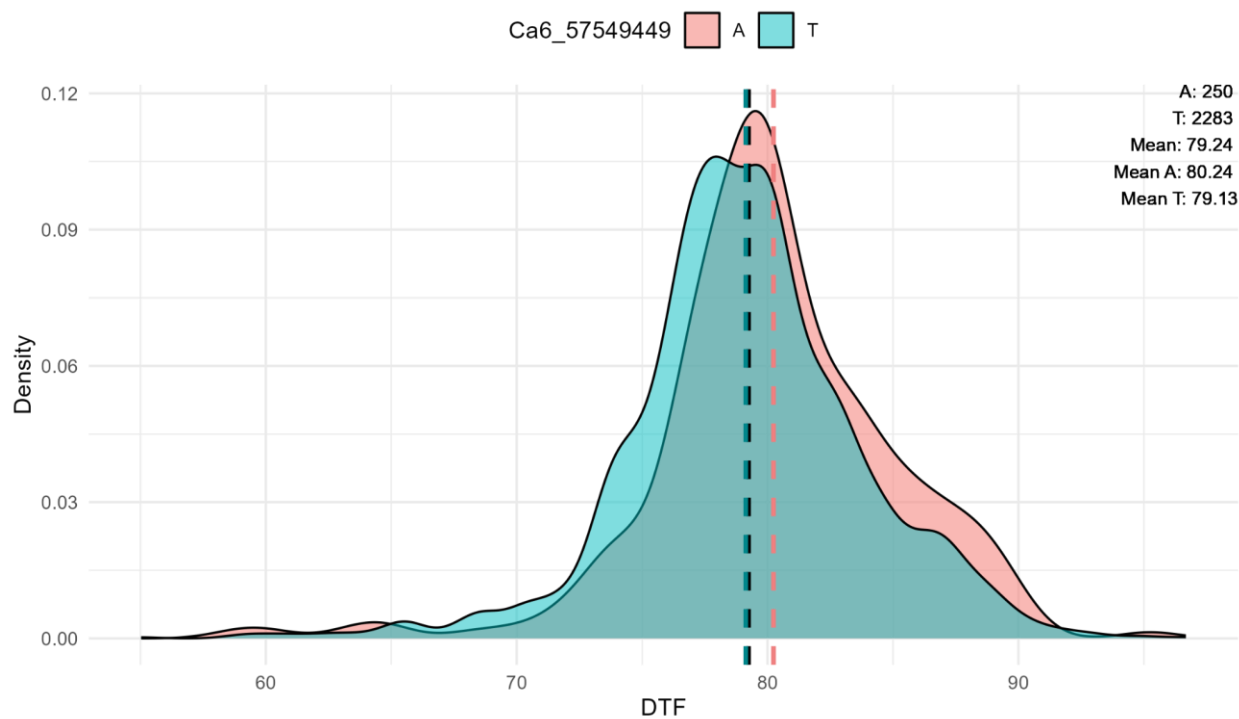
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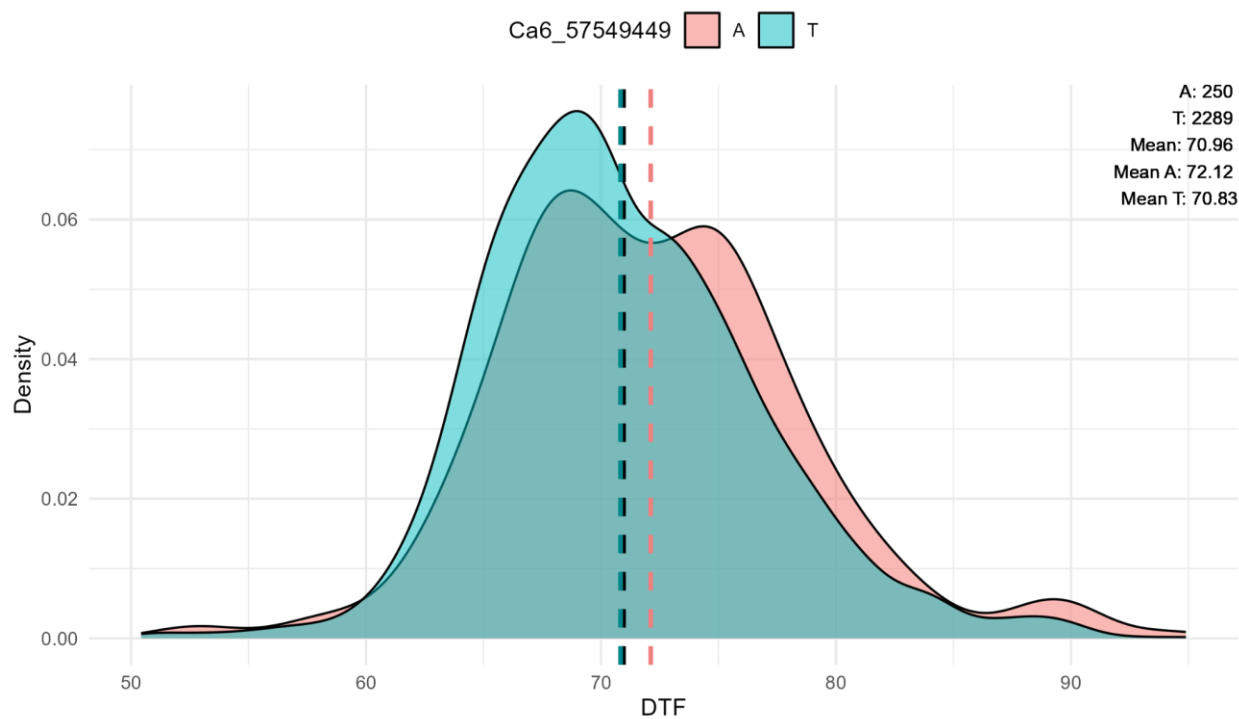
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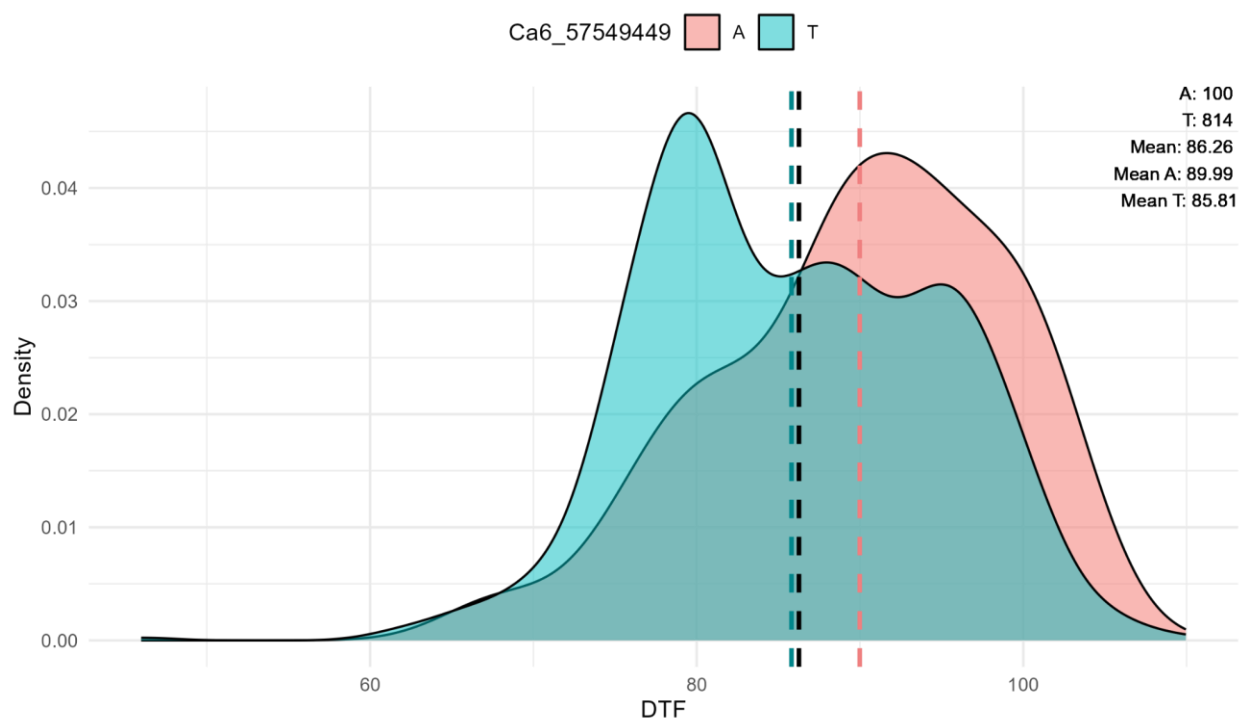
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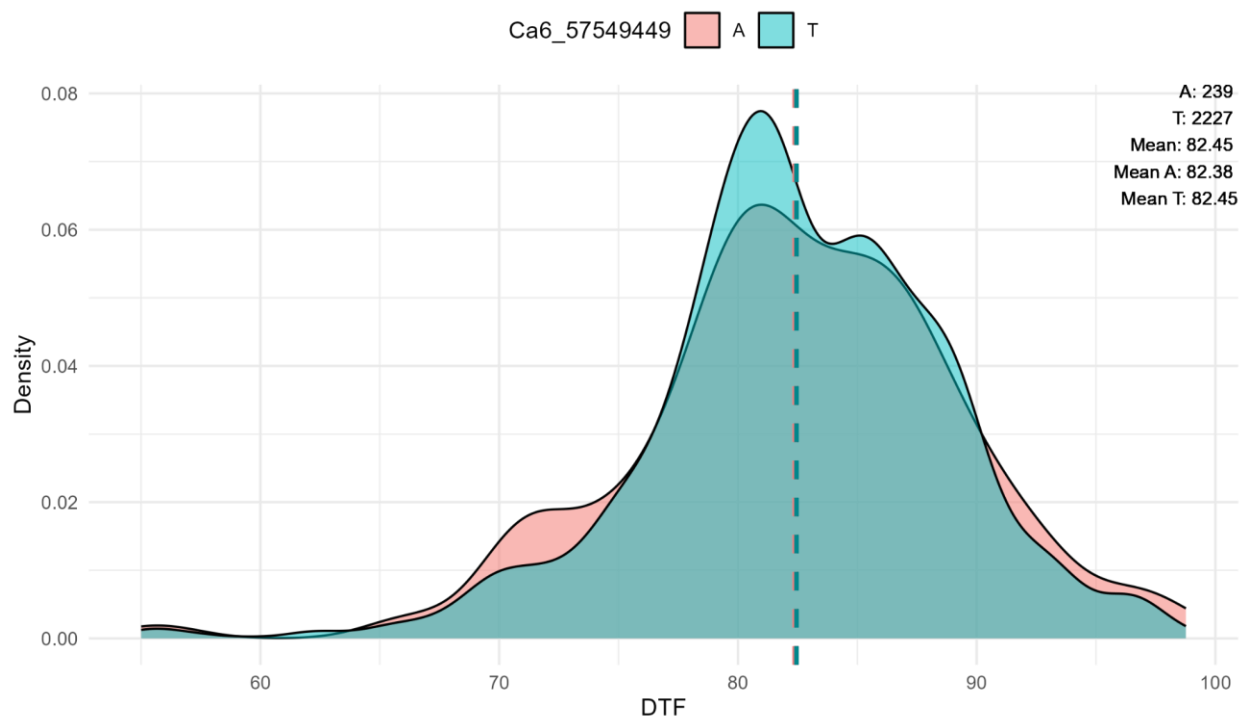
Density plot RAKCA_2015_16



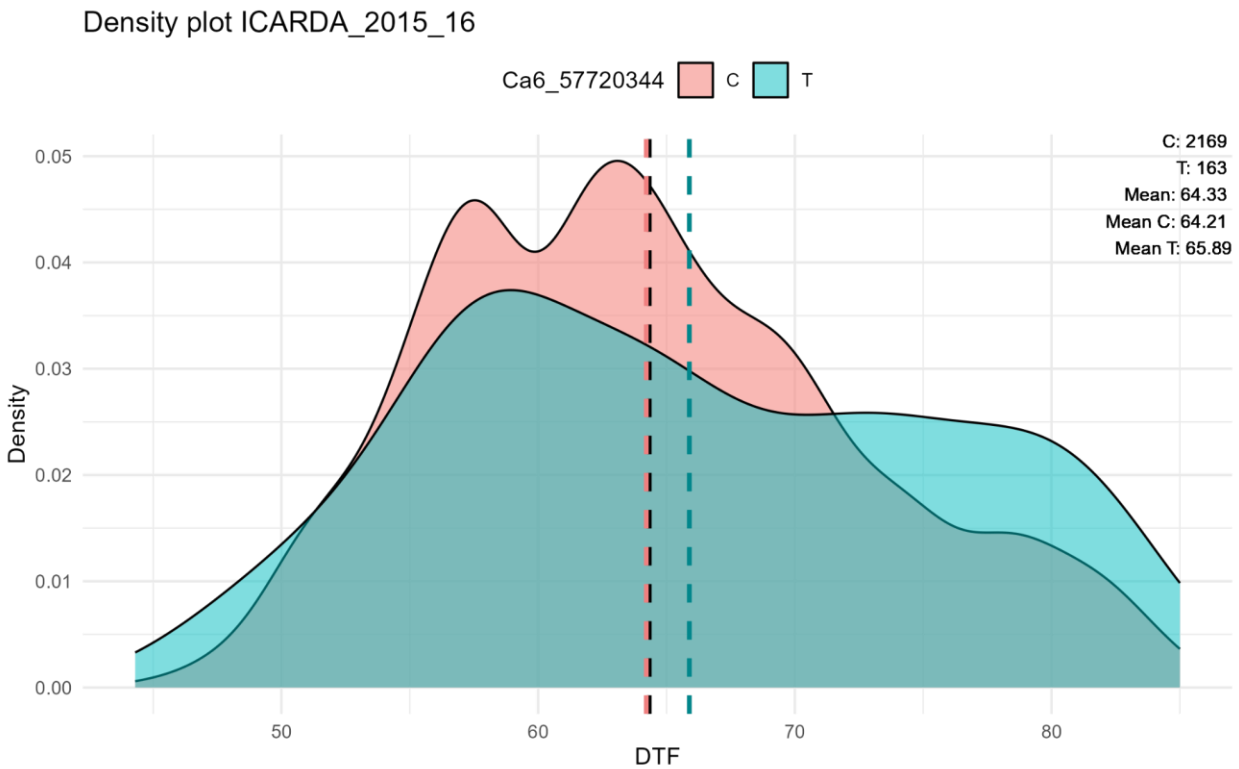
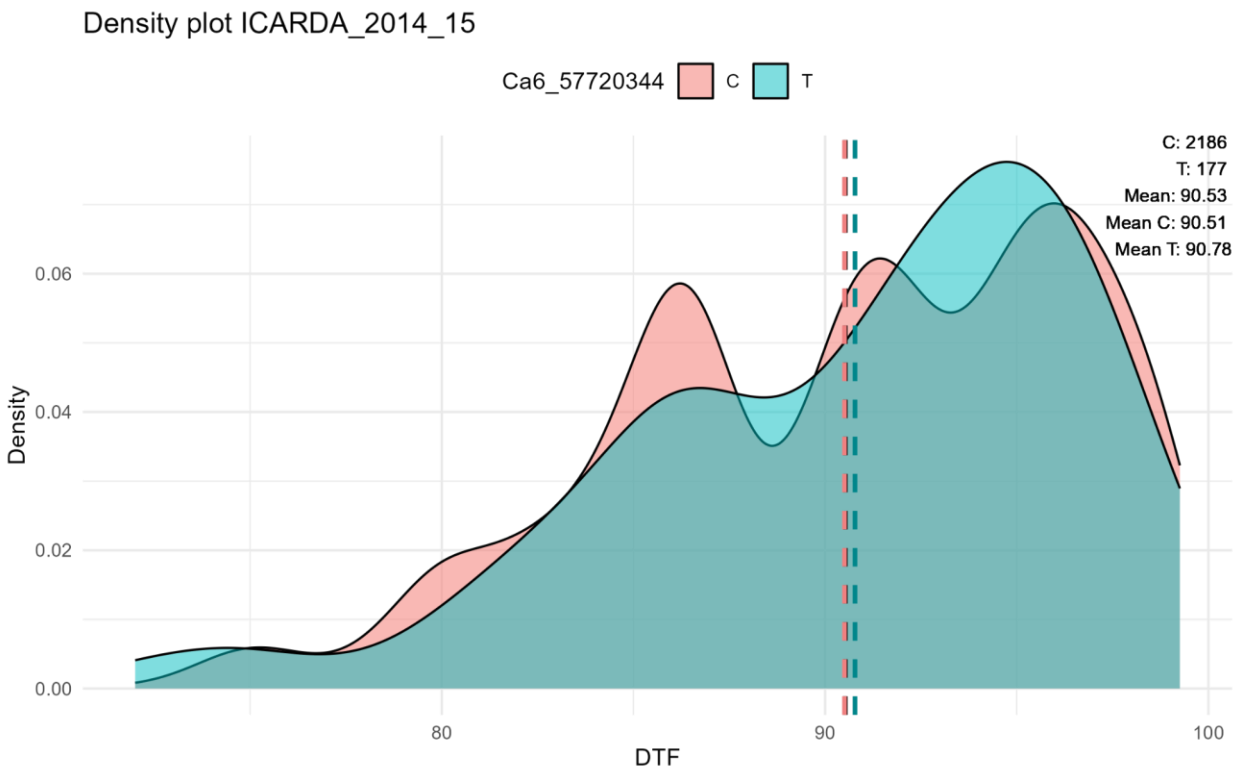
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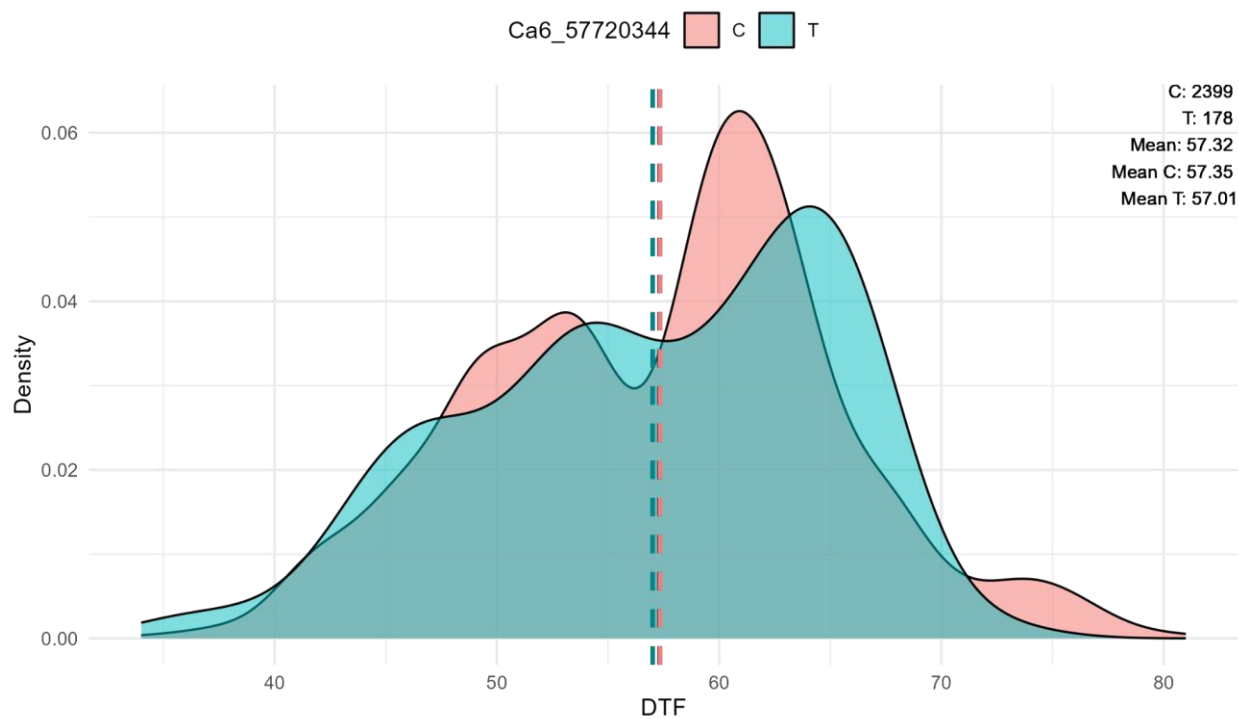
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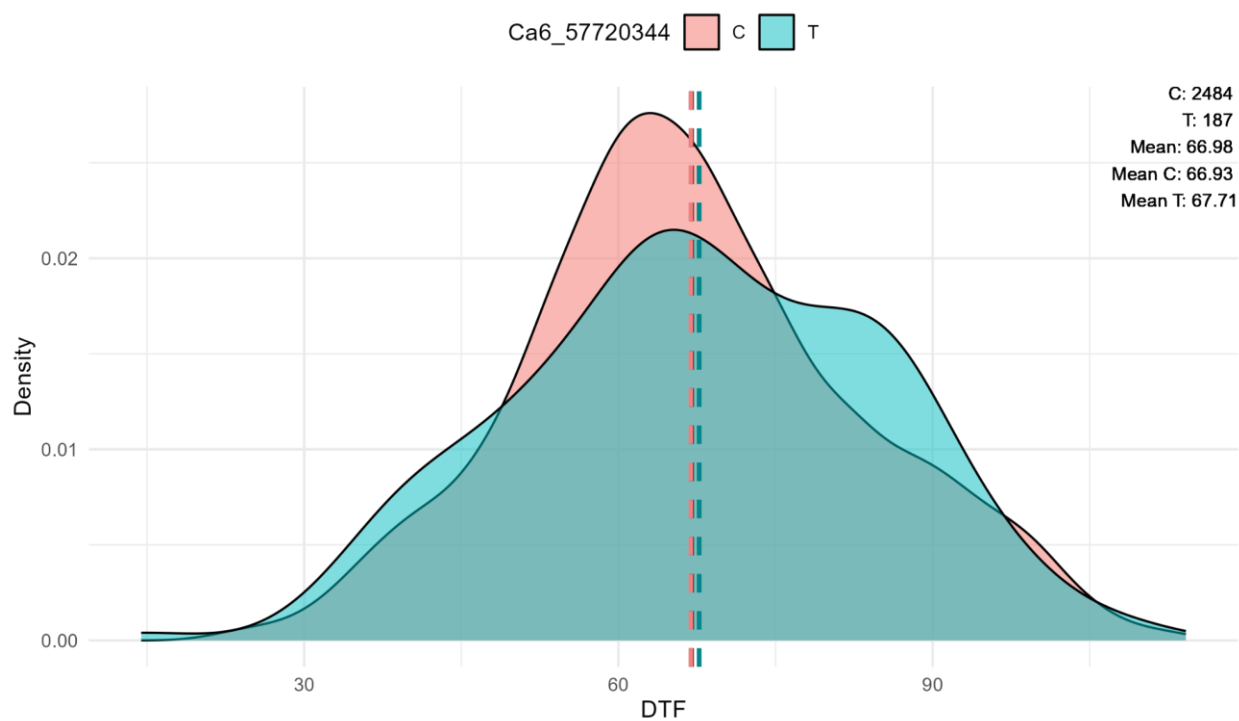
c LOC101507442 SNP (Ca6: 57,720,344).



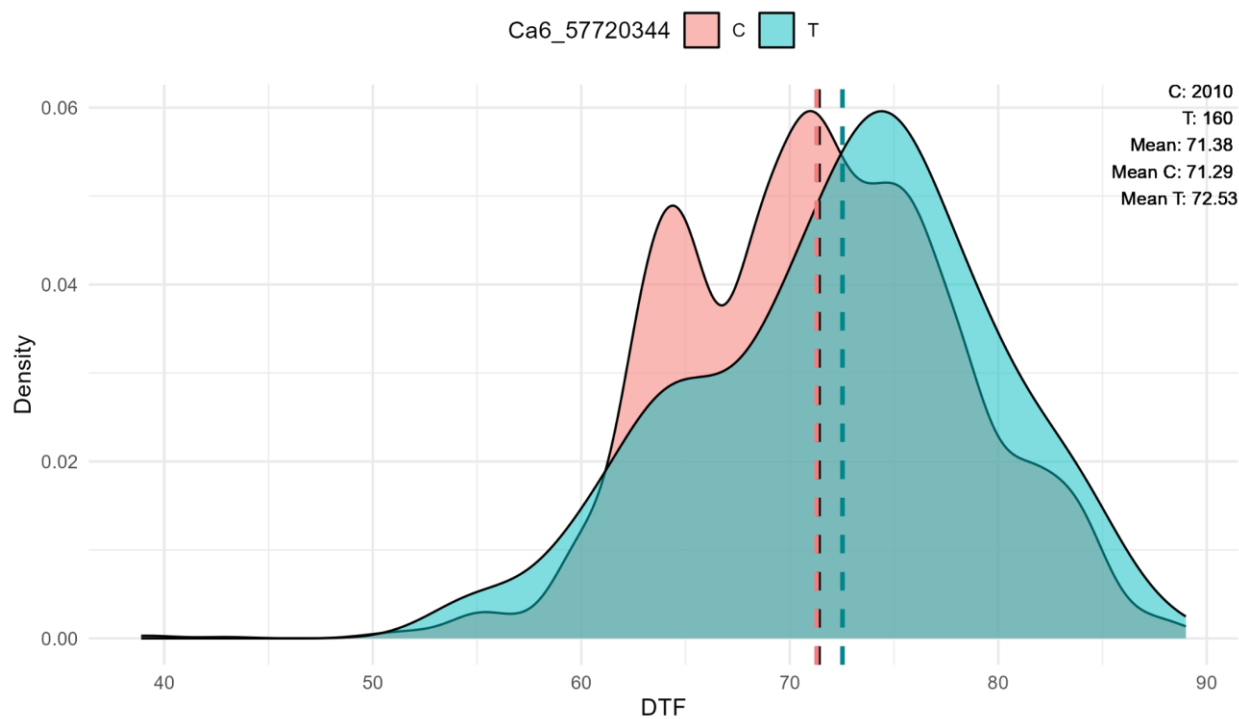
Density plot ICRISAT_2014_15



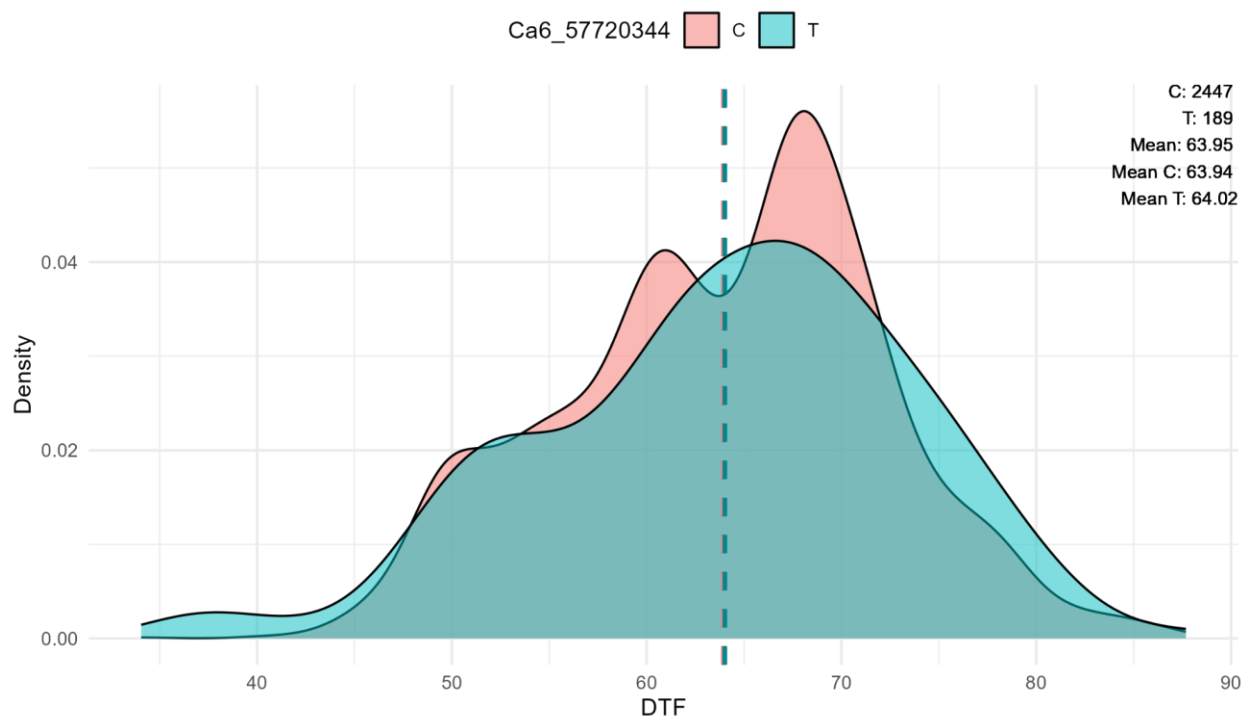
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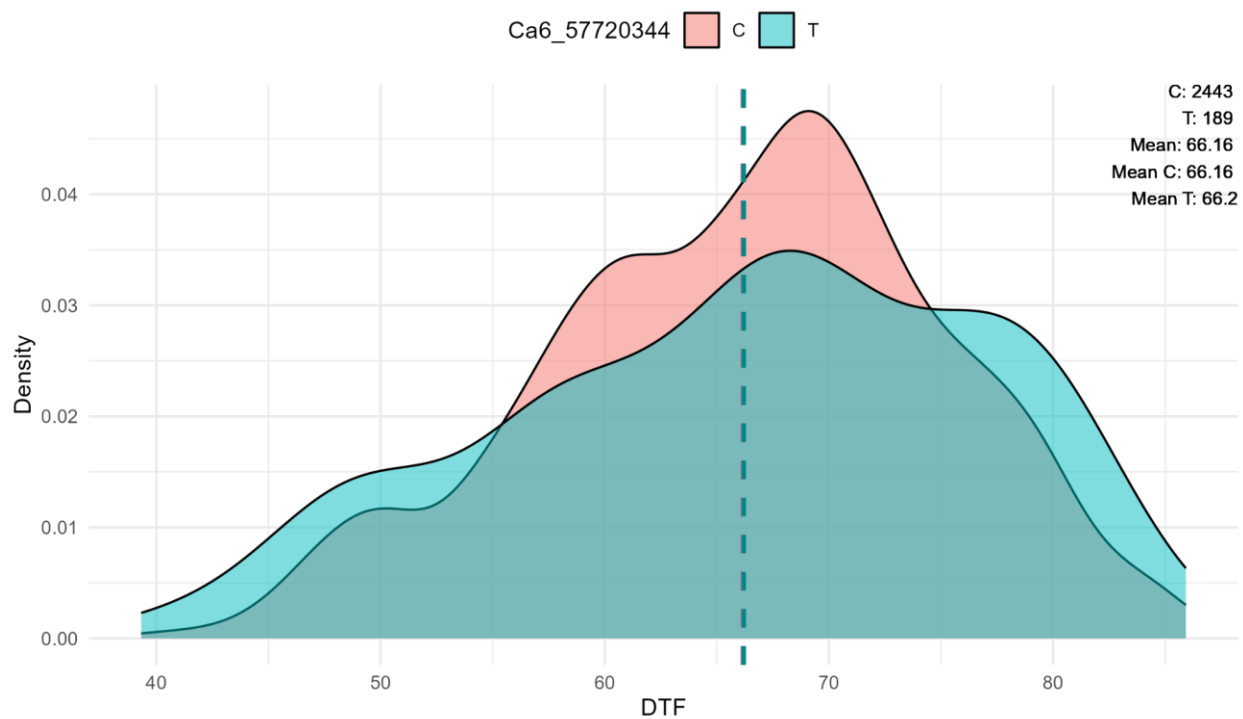
Density plot IIPR_2015_16



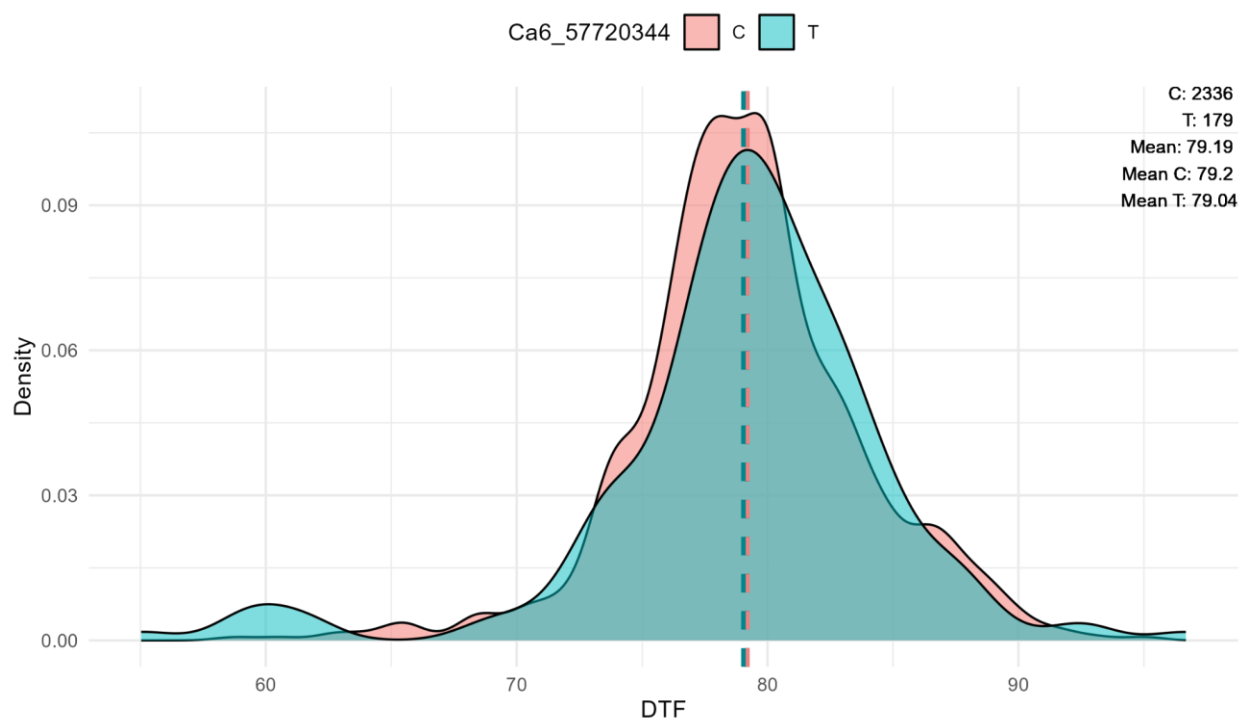
Density plot JAU_2014_15



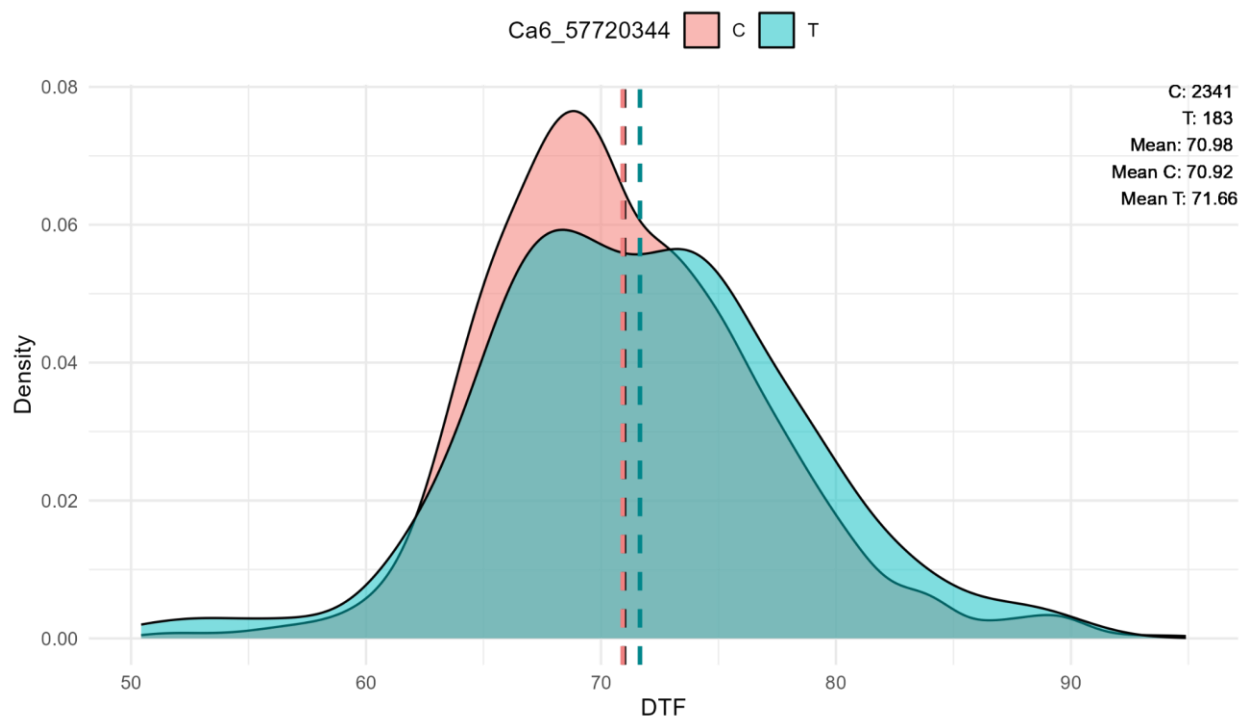
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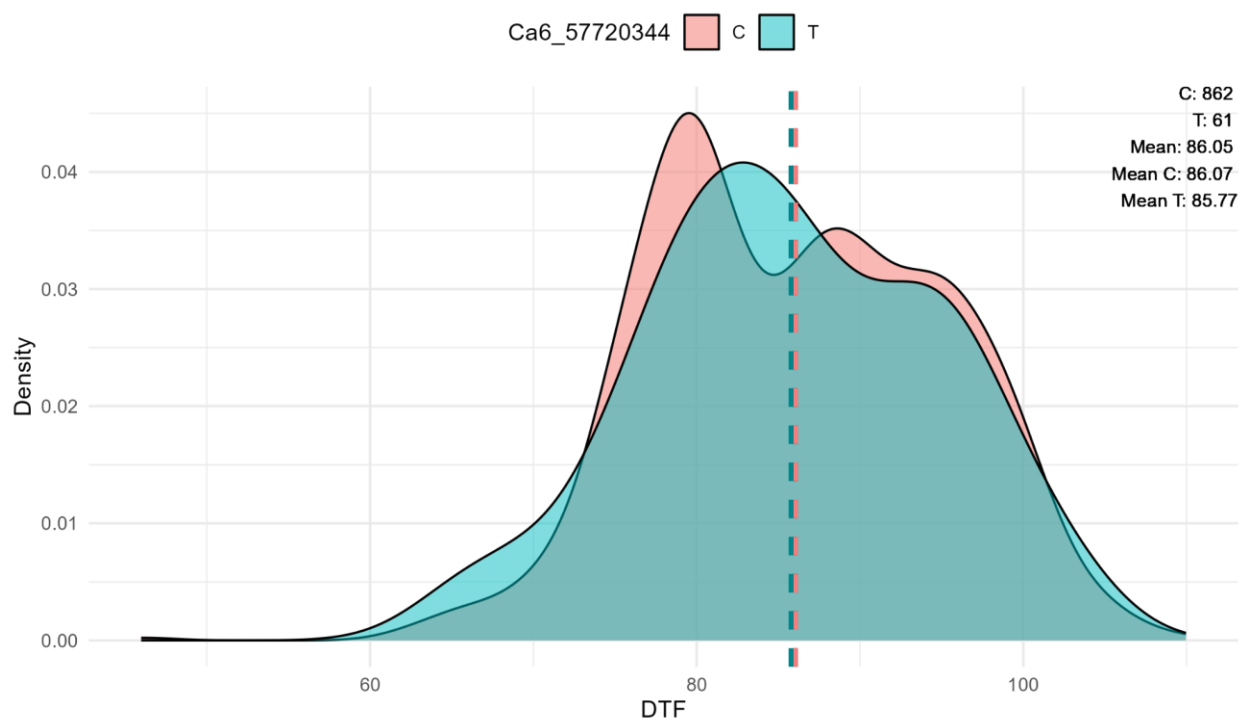
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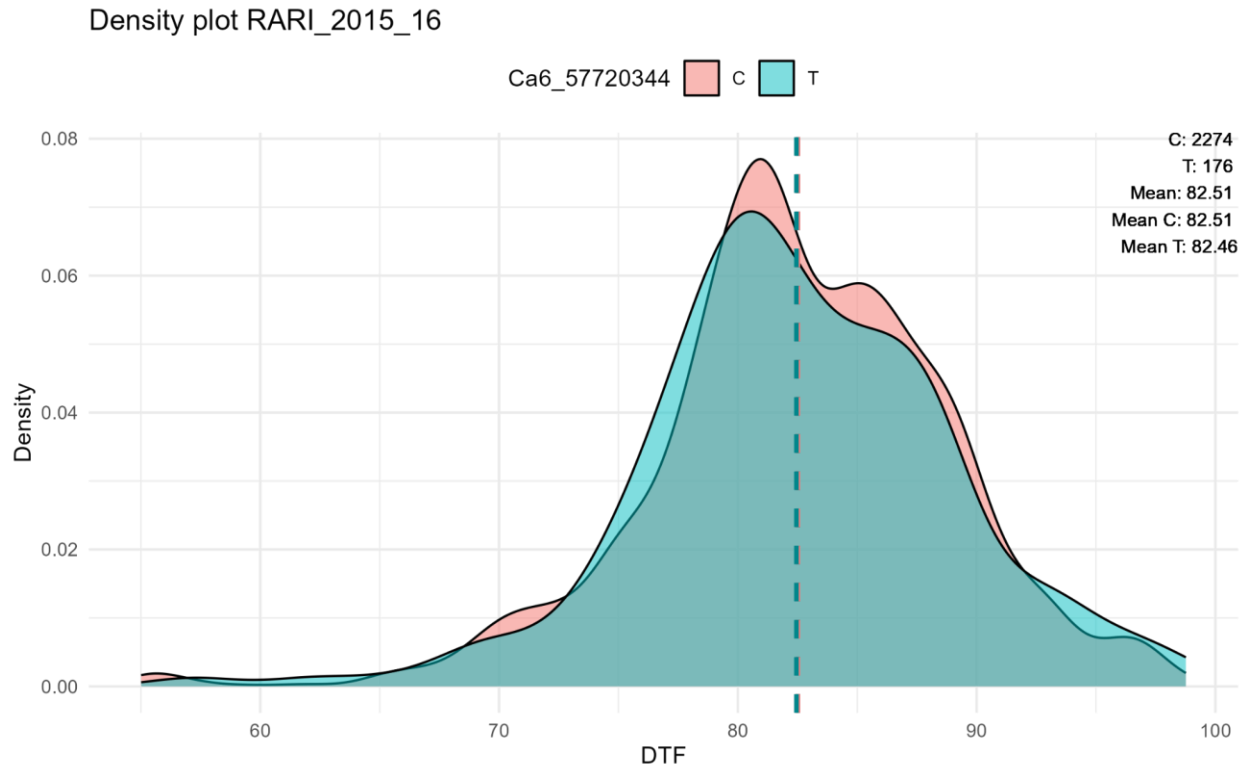


Density plot RAKCA_2015_16



Density plot RARI_2014_15





Additional file 10. Fig. S1 Density plot of cultivated chickpea accessions distribution based on days to flowering (DTF) according to **(a)** LOC101515142 Haplotype, **(b)** LOC101499101 SNP (Ca6: 57,549,449), and **(c)** LOC101507442 SNP (Ca6: 57,720,344). Vertical lines represent the global mean (black) and the means for each group (salmon and turquoise). The number of individuals taken into account for each location/year depending on the SNPs they present is indicated in the upper left corner of each of the plots.