**Supplementary Figures**

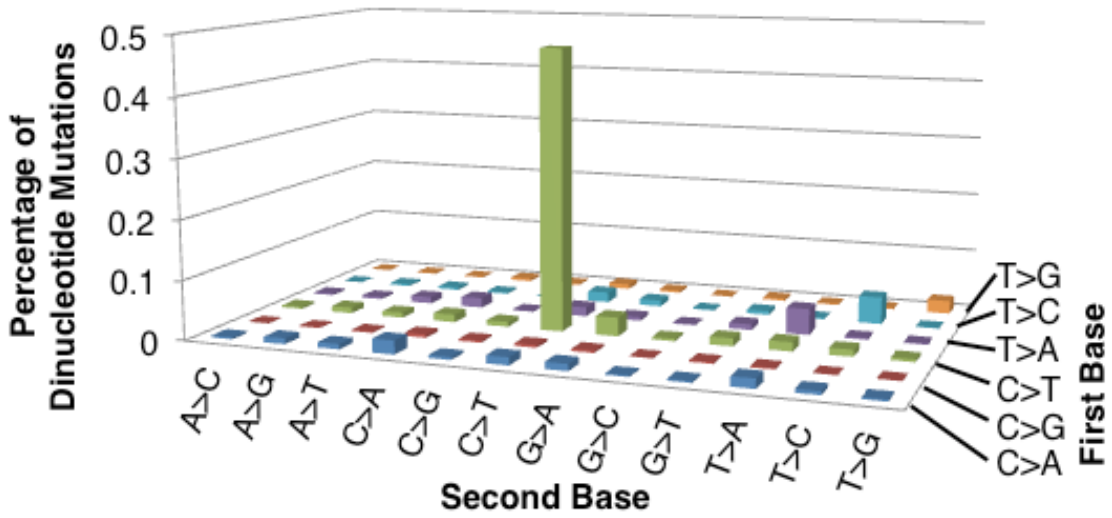
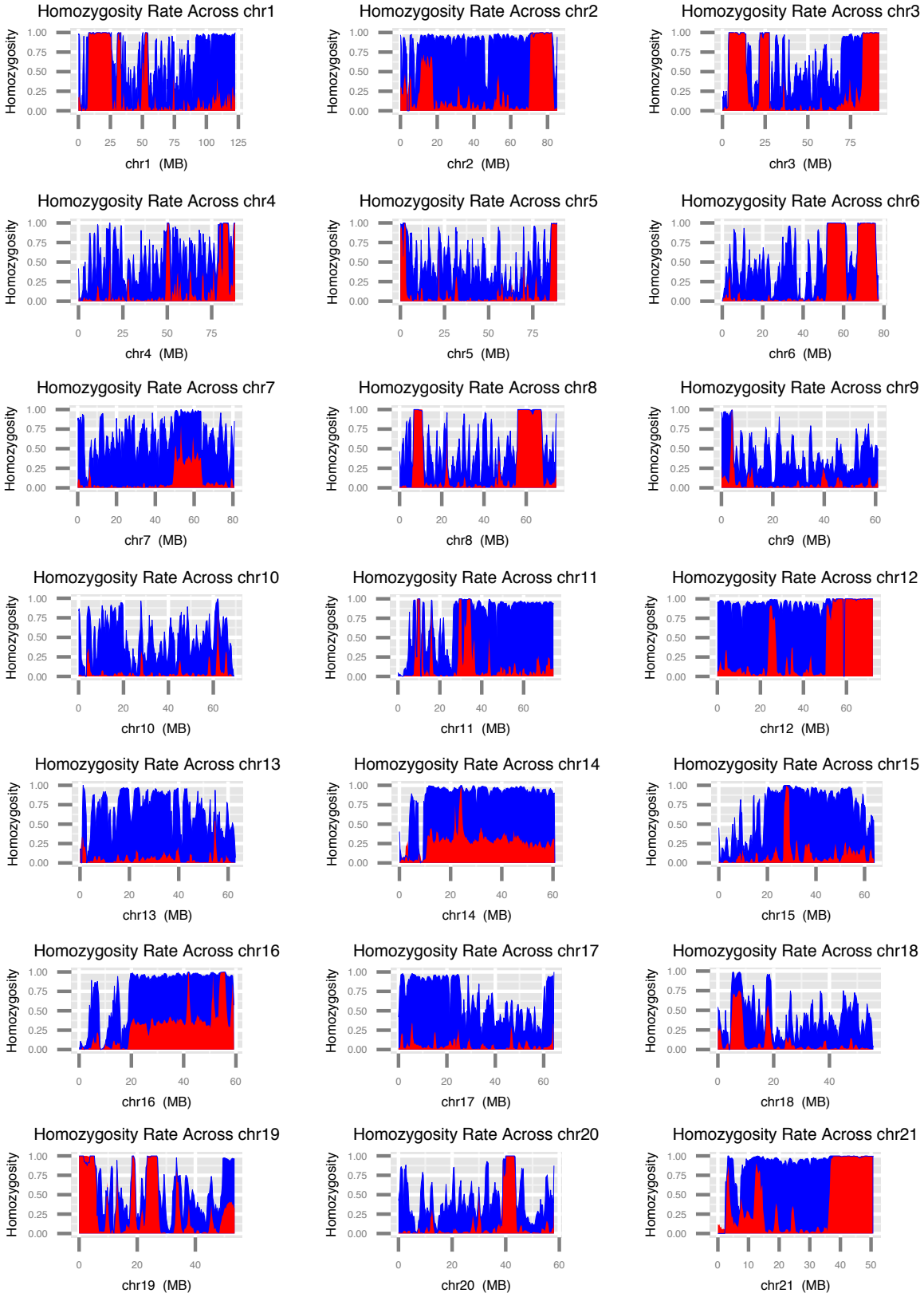



**Fig. S1.** Dinucleotide substitution profile among CTVT somatic mutation candidates. The first base has the lower coordinate in the reference sequence, and strandedness was determined using the first base pyrimidine context. CC>TT/GG>AA dinucleotide substitutions predominated, accounting for 47.2% of the 4,758 somatic events shared by both tumors. This phenomenon is seen in human melanoma tumors, and results from exposure to UV radiation (Alexandrov et al. 2013). This signal is very similar, but somewhat stronger than previously observed for these tumors (Murchison et al. 2014), which supports our hypothesis that our candidate somatic mutations are enriched for true somatic variants.


Homozygosity Rate Across chr1
Homozygosity
1.00
0.75
0.50
0.25
0.00
0
25
50
75
100
125
chr1 (MB)
Homozygosity Rate Across chr2
Homozygosity
1.00
0.75
0.50
0.25
0.00
0
20
40
60
80
chr2 (MB)
Homozygosity Rate Across chr3
Homozygosity
1.00
0.75
0.50
0.25
0.00
0
25
50
75
chr3 (MB)
Homozygosity Rate Across chr4
Homozygosity
1.00
0.75
0.50
0.25
0.00
0
25
50
75
chr4 (MB)
Homozygosity Rate Across chr5
Homozygosity
1.00
0.75
0.50
0.25
0.00
0
25
50
75
chr5 (MB)
Homozygosity Rate Across chr6
Homozygosity
1.00
0.75
0.50
0.25
0.00
0
20
40
60
80
chr6 (MB)
Homozygosity Rate Across chr7
Homozygosity
1.00
0.75
0.50
0.25
0.00
0
20
40
60
80
chr7 (MB)
Homozygosity Rate Across chr8
Homozygosity
1.00
0.75
0.50
0.25
0.00
0
20
40
60
chr8 (MB)
Homozygosity Rate Across chr9
Homozygosity
1.00
0.75
0.50
0.25
0.00
0
20
40
60
chr9 (MB)
Homozygosity Rate Across chr10
Homozygosity
1.00
0.75
0.50
0.25
0.00
0
20
40
60
chr10 (MB)
Homozygosity Rate Across chr11
Homozygosity
1.00
0.75
0.50
0.25
0.00
0
20
40
60
chr11 (MB)
Homozygosity Rate Across chr12
Homozygosity
1.00
0.75
0.50
0.25
0.00
0
20
40
60
chr12 (MB)
Homozygosity Rate Across chr13
Homozygosity
1.00
0.75
0.50
0.25
0.00
0
20
40
60
chr13 (MB)
Homozygosity Rate Across chr14
Homozygosity
1.00
0.75
0.50
0.25
0.00
0
20
40
60
chr14 (MB)
Homozygosity Rate Across chr15
Homozygosity
1.00
0.75
0.50
0.25
0.00
0
20
40
60
chr15 (MB)
Homozygosity Rate Across chr16
Homozygosity
1.00
0.75
0.50
0.25
0.00
0
20
40
60
chr16 (MB)
Homozygosity Rate Across chr17
Homozygosity
1.00
0.75
0.50
0.25
0.00
0
20
40
60
chr17 (MB)
Homozygosity Rate Across chr18
Homozygosity
1.00
0.75
0.50
0.25
0.00
0
20
40
chr18 (MB)
Homozygosity Rate Across chr19
Homozygosity
1.00
0.75
0.50
0.25
0.00
0
20
40
chr19 (MB)
Homozygosity Rate Across chr20
Homozygosity
1.00
0.75
0.50
0.25
0.00
0
20
40
60
chr20 (MB)
Homozygosity Rate Across chr21
Homozygosity
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0.50
0.25
0.00
0
10
20
30
40
50
chr21 (MB)

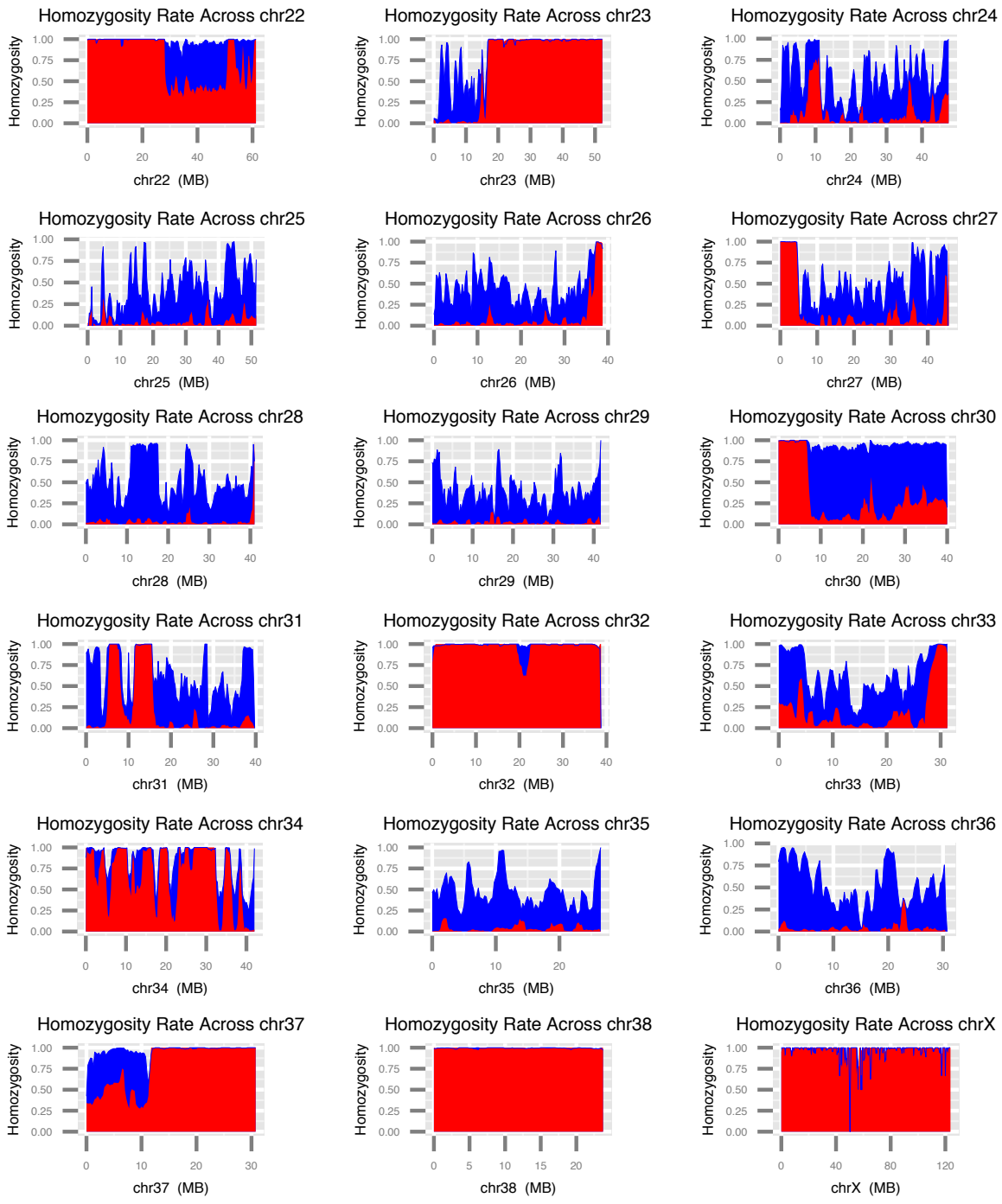


**Fig. S2.** Germline (blue) and somatic (red) homozygosity in CTVT across all canine chromosomes.

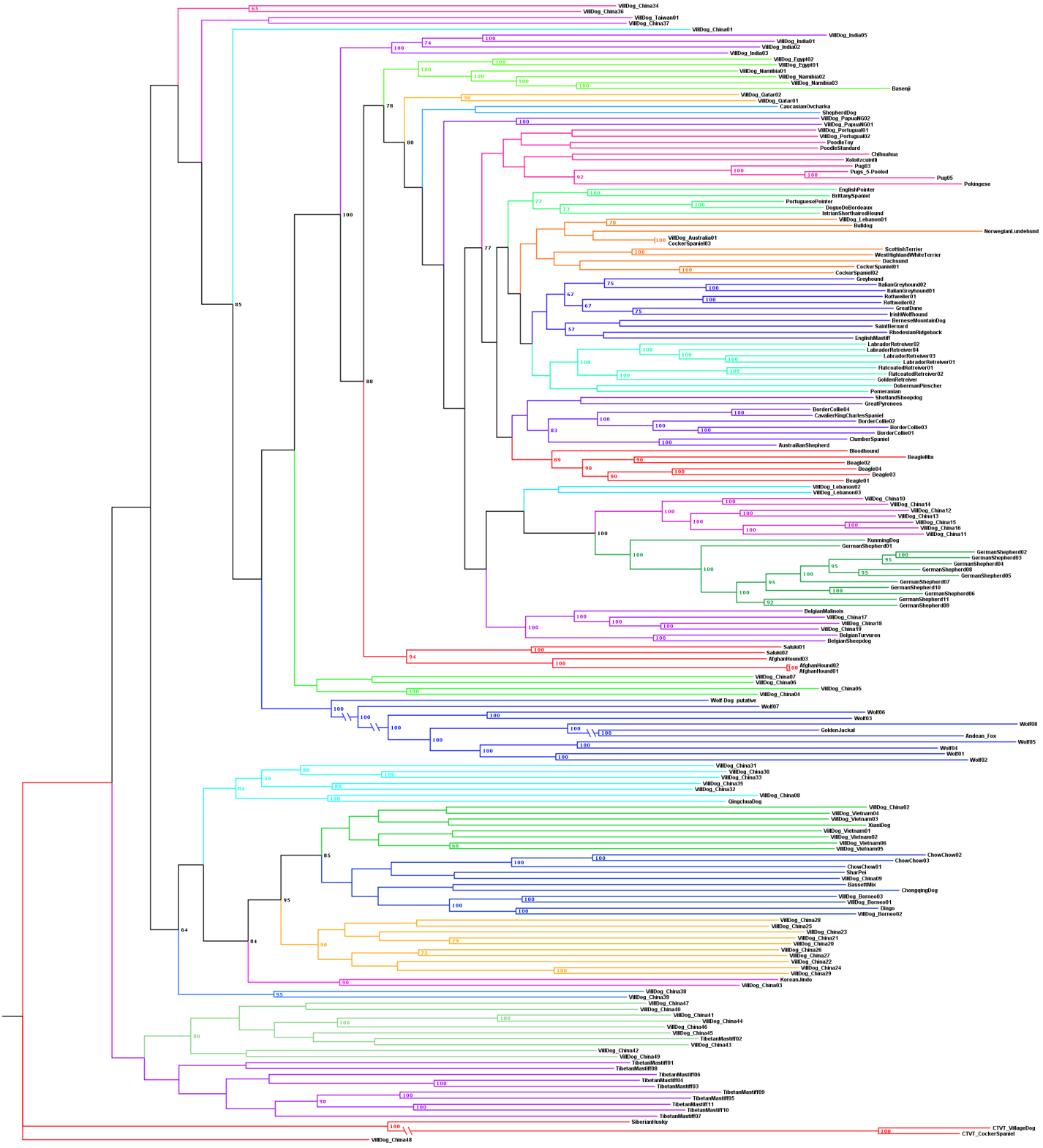
VillDog_China34
VillDog_China36
VillDog_Taiwan01
VillDog_China37
VillDog_China01
VillDog_India05
VillDog_India01
VillDog_India02
VillDog_India03
VillDog_Egypt02
VillDog_Egypt01
VillDog_Namibia01
VillDog_Namibia02
VillDog_Namibia03
Basenji
VillDog_Qatar02
VillDog_Qatar01
CaucasianOvcharka
ShepherdDog
VillDog_PapuaNG02
VillDog_PapuaNG01
VillDog_Portugual01
VillDog_Portugual02
PoodleToy
PoodleStandard
Chihuahua
XoloitzcuintliI
Pug03
Pugs_5-Pooled
Pug05
Pekingese
EnglishPointer
BrittanySpaniel
PortuguesePointer
DogueDeBordeaux
IstrianShorthairedHound
VillDog_Lebanon01
Bulldog
NorwegianLundehund
VillDog_Australia01
CockerSpaniel03
ScottishTerrier
WestHighlandWhiteTerrier
Dachsund
CockerSpaniel01
CockerSpaniel02
Greyhound
ItalianGreyhound02
ItalianGreyhound01
Rottweiler01
Rottweiler02
GreatDane
IrishWolfhound
BerneseMountainDog
SaintBernard
RhodesianRidgeback
EnglishMastiff
LabradorRetreiver02
LabradorRetreiver04
LabradorRetreiver03
LabradorRetreiver01
FlatcoatedRetreiver01
FlatcoatedRetreiver02
GoldenRetreiver
DobermanPinscher
Pomeranian
ShetlandSheepdog
GreatPyrenees
BorderCollie04
CavalierKingCharlesSpaniel
BorderCollie02
BorderCollie03
BorderCollie01
ClumberSpaniel
AustrallianShepherd
Bloodhound
BeagleMix
Beagle02
Beagle04
Beagle03
Beagle01
VillDog_Lebanon02
VillDog_Lebanon03
VillDog_China10
VillDog_China14
VillDog_China12
VillDog_China13
VillDog_China15
VillDog_China16
VillDog_China11
KunmingDog
GermanShepherd01
GermanShepherd02
GermanShepherd03
GermanShepherd04
GermanShepherd08
GermanShepherd05
GermanShepherd07
GermanShepherd10
GermanShepherd06
GermanShepherd11
GermanShepherd09
BelgianMalinois
VillDog_China17
VillDog_China18
VillDog_China19
BelgianTurvuren
BelgianSheepdog
Saluki01
Saluki02
AfghanHound03
AfghanHound02
AfghanHound01
VillDog_China07
VillDog_China06
VillDog_China05
VillDog_China04
Wolf-Dog_putative
Wolf07
Wolf06
Wolf03
Wolf08
GoldenJackal
Andean_Fox
Wolf05
Wolf04
Wolf01
Wolf02
VillDog_China31
VillDog_China30
VillDog_China33
VillDog_China35
VillDog_China32
VillDog_China08
QingchuaDog
VillDog_China02
VillDog_Vietnam04
VillDog_Vietnam03
XiansDog
VillDog_Vietnam01
VillDog_Vietnam02
VillDog_Vietnam06
VillDog_Vietnam05
ChowChow02
ChowChow03
ChowChow01
SharPei
VillDog_China09
BassettMix
ChonggingDog
VillDog_Borneo03
VillDog_Borneo01
Dingo
VillDog_Borneo02
VillDog_China28
VillDog_China25
VillDog_China23
VillDog_China21
VillDog_China20
VillDog_China26
VillDog_China27
VillDog_China22
VillDog_China24
VillDog_China29
KoreanJindo
VillDog_China03
VillDog_China38
VillDog_China39
VillDog_China47
VillDog_China40
VillDog_China41
VillDog_China44
VillDog_China46
VillDog_China45
TibetanMastiff02
VillDog_China43
VillDog_China42
VillDog_China49
TibetanMastiff01
TibetanMastiff08
TibetanMastiff06
TibetanMastiff04
TibetanMastiff03
TibetanMastiff09
TibetanMastiff05
TibetanMastiff11
TibetanMastiff10
TibetanMastiff07
SiberianHusky
CTVT_VillageDog
CTVT_CockerSpaniel
VillDog_China48

**Figure S3.** Unrooted maximum likelihood phylogenetic tree for all individuals in our canine variation catalog. Bootstrap support greater than 50 is noted on each corresponding node. Clade coloration corresponds to major monophyletic groups. Lengths of the CTVT tumor branch and the wild canid branch have been abbreviated for display area considerations.

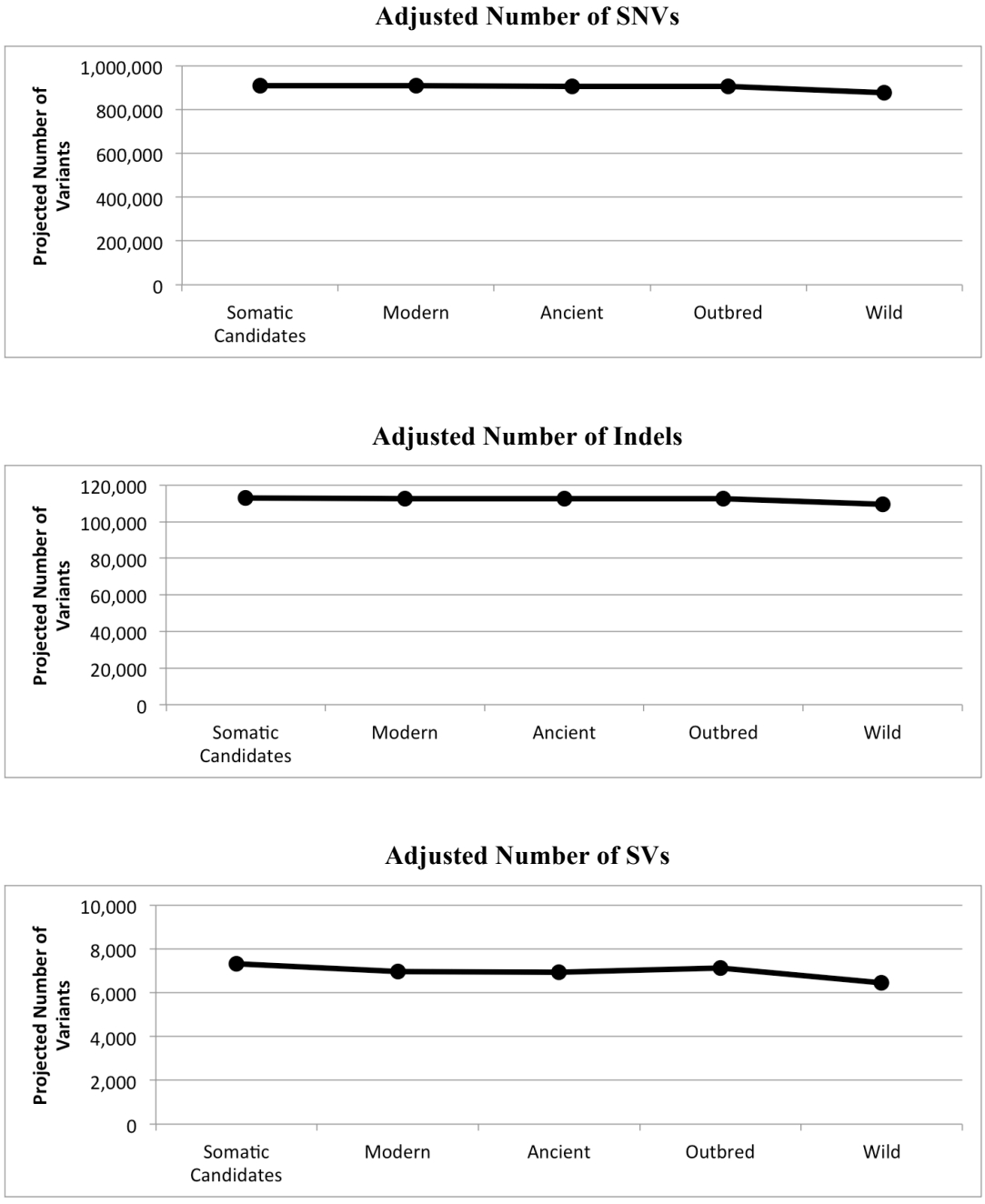


**Fig. S4.** Estimated number somatic SNVs, indels, and SVs, adjusted for average fraction of variants from one individual found in other canids, evaluated by canid group. Since wolves harbored more private variation than other canids, lower somatic mutation estimates result from wolf-based projections. If the founder had diversity similar to wolves, the total number of somatic mutations is likely ~3.7% lower than our raw number of somatic mutation candidates.

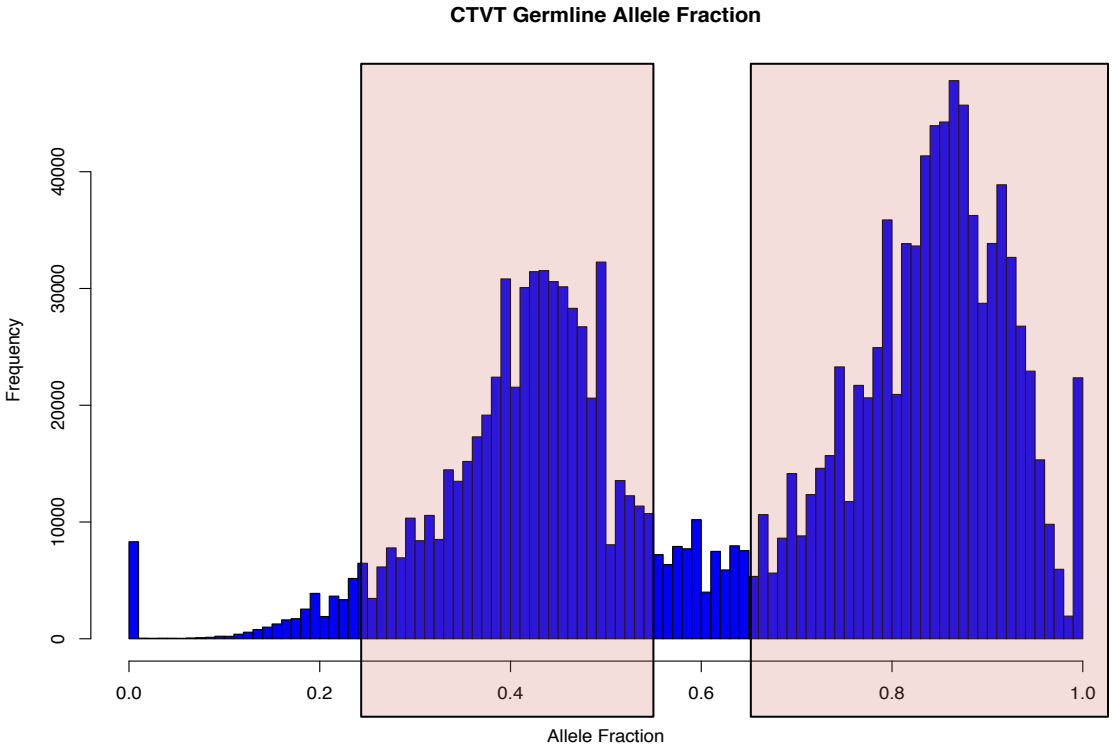


**Fig. S5.** Somatic allele fraction for putative CTVT founder inherited alleles, excluding positions where either of the host dogs also carried an alternate allele. The bimodal distribution enabled confident classification of homozygous versus heterozygous genotypes, as indicated by the boxes.