## Analysis of Polycerate Mutants Reveals the Evolutionary Co-option of *HOXD1* to Determine the Number and Topology of Horns in Bovidae

By Aurélie Allais-Bonnet, Aurélie Hintermann et al.

This document contains: Supplementary Figures 1-13, Supplementary Tables 1-16, Supplementary Note 1, and additional references.



**Supplementary Figure 1. Comparison of Pecoran headgear types.** a-c) Pronghorns of *Antilocapra Americana* in adult male (a,b) and female (c) skull specimens. d,e) Antlers of a male *Capreolus capreolus*. f,g) Horns of a male *Rupicapra rupicapra*. h,i) Ossicones of a *Giraffa Camelopardalis* of unknown gender. Note the shared position of the different headgear types on the frontal bones (a, d, f, h) and the change of texture between the frontal bone and their bony core as indicated by arrows (c, e, g, i). Note also the presence of vestigial hairs (marked with arrows) after keratinization of the decidual sheath of the pronghorn in (b). Specimens MNHN-ZM-AC 1964-272, 2007-1354, 1993-280 and 1907-277 belong to the *Collection d'anatomie comparée du Muséum National d'Histoire Naturelle*, Paris, France while Mam-04525 originates from the *Collection d'anatomie du Musée Zoologique de Strasbourg*, France.



**Supplementary Figure 2. Mapping of the** *POLYCERATE* loci in sheep and goat. a) Identical-By-Descent (IBD) mapping of ovine *POLYCERATE* locus around the *HOXD* gene cluster and +/- 5 Mb on Chr2 (see Methods). Fisher's exact test p-values equal to zero were set to 1.0 x 10<sup>-320</sup>; 30 consecutive sliding windows of 50 markers corresponding to an IBD segment shared by all the polycerate sheep are highlighted in red. b) IBD mapping of caprine *POLYCERATE* locus on Chr2. One IBD segment of 10 markers shared by all the polycerate goats is highlighted in green. The intervals indicated are defined by the positions of the most proximal markers outside of the IBD segments (on Oar\_v4.0 and ARS1 assemblies). c) Gene content and relative localization of the mapping intervals of the *POLYCERATE* loci in sheep (minus strand) and goat. Dashed lines indicate that a part of *MTX2* is located outside of the region displayed. Sheep and goat icons were made by "Monkik" from www.thenounproject.com.



Fusion point A:No repeat5'-AAGCAAATTCTTAATATTATTGATAAAAACTTAAATAAGTATGTAG-3'LINE (L1MC5)Fusion point B:No repeat5'-GCTACAGCAGAAAGTAAACCTGCAGTGGGCATGGGTTTGATC-3'SINE (CHRL)Fusion point C:LINE (L1MC5)5'-TTTAAAGACATTGAGAACAAAGCAGGGGAAAGGCAACCCCC-3'LINE (L1MC5)Fusion point D:LINE (L1MC5)5'-AAAGACACACACACACACAAAATTGTACCTGATTGTTCACCTTTTC-3'No repeat



Supplementary Figure 3. Details on the large insertion-deletion at the goat *POLYCERATE* locus. a) Schematic representation of the segments involved in the translocation of 137 kb from Chr5 and the 503-kb deletion on Chr2. Fusion points are coded with letters. Positions refer to ARS1 caprine genome assembly. b) DNA sequences at the four fusion points. Nucleotides in bold highlight microhomologies between the fused segments, whereas nucleotides inserted between the breakpoints are underlined. The existence of repeated elements on each side of fusion points is indicated. c) Integrated Genome Viewer screen-captures showing aligned paired-end reads (~100-bp) around the various breakpoints. Reads from aberrantly mapping pairs are color-coded to indicate the chromosomal segment to which the other pair maps.



Supplementary Figure 4. Genotyping of g.115,652,290\_116,155,699delins137kb in goat using PCR and electrophoresis. a) Schematic representation of the segments involved in the mutation and localization of the PCR primers on wild type (Wt) and mutant chromosomes. The coordinates of primers « Common », « Wt », and « Mut » on ARS1 genome assembly are Chr2:115,652,119-115,652,140, Chr2:115,652,323-115,652,344, and Chr5:48,545,700-48,545,722, respectively. b) Agarose gel electrophoresis of amplicons from wild type (Wt) and polycerate (Poly.) animals.

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**Supplementary Figure 5. Details on eyelid and eyebrow malformation in polycerate goats.** Upper head of a one-week old polycerate (a, b) and a four-week old wild type (c, d) billy-goat before and after shaving. Note the splitting of the eyelid, of the two rows of vibrissae forming the eyebrow and of the horn buds (white arrows), as well as the presence of abnormally long hair forming a tuft (ht) in the polycerate individual. Black arrows point to vibrissae from the upper row of the eyebrow that are orthologous in (b) and (d). e-h) Eyelid malformation of increasing severity in adult polycerate male goats of the Provençale breed. e) absence of eyelid malformation and presence of a small hair tuft marked with arrows, f) notch in the eyelid margin and hair tuft of moderate size, g) eyelid coloboma partially hidden by a hair tuft of important size. h) Details of the eyelid in (g) after cutting the hair tuft.



**Supplementary Figure 6. Details on eyelid and eyebrow malformation in polycerate sheep.** Right and Left eyes of a polycerate (a, b, respectively) and a wild type (c, d, respectively) adult Jacob ewe, after shaving. Note the shortened eyebrows in the polycerate ewe as shown by the white arrows pointing to the two most posterior vibrissae. Note also the asymmetry of the eyelid defect with a large portion of the eyelid missing in (a) and only a small notch (yellow arrow) in (b). No hair tuft was observed before shaving. To our knowledge, the presence of abnormally long hair on the eyelid is only observed in polycerate goats. The white color of the cornea is due to the freezing of head samples after slaughter for conservation purpose.



**Supplementary Figure 7. Histology of split upper eyelids in polycerate goats and sheep.** Longitudinal section of the upper eyelid of an adult heterozygous polycerate billy-goat (a) and a heterozygous polycerate female sheep fetus at 76 dpc (b). Meibomian glands (mg) are either absent or underdeveloped in the vicinity of the eyelid coloboma (ec). Sheep and goat icons were made by "Monkik" from www.thenounproject.com.







**Supplementary Figure 8. Pictures of goat and sheep fetuses.** a,d) General view of goat (a) and sheep (d) fetuses at 70 and 76 dpc, respectively. b, c) Head of polycerate (b) and wild type (c) goat fetuses. e, f) Head of polycerate (e) and wild type (f) sheep fetuses. Arrows indicate horn buds.

**Supplementary Figure 9. cDNA (top) and amino acid (bottom) sequences for ovine wild type (Wt) and polycerate (Mut)** *HOXD1* alleles. Nucleotide sequences are represented in black for exon 1, red for intron 1, and blue for exon 2. Codons are labelled with alternating yellow triplets. The two nucleotides flanking the 4 bp deletion in the polycerate (Mut) allele are bolded and underlined. Boxes correspond to the RT-qPCR amplicons from intron 1 and exon 2 used for confirming intron retention. Finally, the homeobox DNA binding site of the wild type (Wt) protein is highlighted in green.

Wt Mut	1 1	ATG <mark>AGC</mark> TCC <mark>TAC</mark> CTC <mark>GAC</mark> TAC <mark>GTG</mark> TCG <mark>TGC</mark> GGCCGGGACGGCGGC <mark>GAC</mark> TTG <mark>CTG</mark> AGC <mark>TTC</mark> ATG <mark>AGC</mark> TCC <mark>TAC</mark> CTCGACTACGTGTCGTGCGGCCGGGACGGCGACTTGCTGAGCTTC	60 60
Wt	1	-MSSYLDYVSCGRDGGDLLSF-	20
Mut	1	-MSSYLDYVSCGRDGGDLLSF-	20
Wt	61	GCG <mark>CCC</mark> AAG <mark>TTC</mark> TGT <mark>CGC</mark> GCC <mark>GAC</mark> GCC <mark>CGG</mark> CCC <mark>ATG</mark> GTC <mark>CTG</mark> CAG <mark>CCC</mark> GCC <mark>TTC</mark> CCC <mark>CTG</mark>	120
Mut	61	GCG <mark>CCC</mark> AAG <mark>TTC</mark> TGT <mark>CGC</mark> GCC <mark>GAC</mark> GCC <mark>CGG</mark> CCC <mark>ATG</mark> GTC <mark>CTG</mark> CAG <mark>CCC</mark> GCC <mark>TTC</mark> CCC <mark>CTG</mark>	120
Wt	21	-APKFCRADARPMVLQPAFPL-	40
Mut	21	-APKFCRADARPMVLQPAFPL-	40
Wt	121	GGC <mark>AGC</mark> GGC <mark>GAC</mark> GGC <mark>GCG</mark> TTT <mark>GTT</mark> AGC <mark>TGC</mark> CTG <mark>CCC</mark> CTG <mark>GCC</mark> GCG <mark>GCG</mark> CGA <mark>GCG</mark> GGG <mark>CCC</mark>	180
Mut	121	GGC <mark>AGC</mark> GGC <mark>GAC</mark> GGC <mark>GCG</mark> TTT <mark>GTT</mark> AGC <mark>TGC</mark> CTG <mark>CCC</mark> CTG <mark>GCC</mark> GCG <mark>GCG</mark> CGA <mark>GCG</mark> GGGCCC	180
Wt	41	-GSGDGAFVSCLPLAAARAGP-	60
Mut	41	-GSGDGAFVSCLPLAAARAGP-	60
Wt	181	TCG <mark>CCC</mark> CCG <mark>GCC</mark> GCCC <mark>GCGGCAG</mark> CCT <mark>CCC</mark> GGG <mark>CCT</mark> GCC <mark>GCG</mark> CCC <mark>GCG</mark> TAC <mark>GCG</mark> CCC <mark>TGC</mark>	240
Mut	181	TCGCCCCCGGCCCCCGGCGCAGCCTCCCGGGCCTGCCGCGCCCGCGTACGCGCCCTGC	240
Wt	61	-SPAAPAQPGPAAPAYAPC-	80
Mut	61	-SPPAAPAQPGPAAPAYAPC-	80
Wt	241	CCC <mark>CTA</mark> GAG <mark>GGG</mark> GCC <mark>TAC</mark> GAG <mark>CCA</mark> GGC <mark>GCC</mark> GCA <mark>CCT</mark> GTC <mark>CAG</mark> GCC <mark>GGG</mark> GGC <mark>GAG</mark> GAC <mark>TGC</mark>	300
Mut	241	CCCCTAGAGGGGGCCTACGAGCCAGGCGCCGCACCTGTCCAGGCCGGGGGGGG	300
Wt	81	-PLEGAYEPGAAPVQAGGEDC-	100
Mut	81	-PLEGAYEPGAAPVQAGGEDC-	100
Wt	301	TGC <mark>CTG</mark> CCG <mark>GGG</mark> TCT <mark>GCG</mark> CCC <mark>GCA</mark> TAC <mark>GAG</mark> TTA <mark>CCG</mark> TGC <mark>GCG</mark> CTC <mark>GGG</mark> CGG <mark>CCG</mark> GCA <mark>GAC</mark>	360
Mut	301	TGCCTGCCGGGGTCTGCGCCCGCATACGAGTTACCGTGCGCGCTCGGGCGGCCGGC	360
Wt	101	-CLPGSAPAYELPCALGRPAD-	120
Mut	101	-CLPGSAPAYELPCALGRPAD-	120
Wt	361	GAC <mark>AGC</mark> GGG <mark>GCG</mark> CAC <mark>GTC</mark> CAT <mark>TAC</mark> CCG <mark>CCC</mark> CCC <mark>GCC</mark> GTC <mark>TCC</mark> CCC <mark>AAG</mark> TGT <mark>GCG</mark>	420
Mut	361	GACAGCGGGGCGCACGTCCATTACCCGCCCCCGCCCCCGGCGTCTCCCCCAAGTGTGCG	420
Wt	121	-DSGAHVHYPPPAPGVSPKCA-	140
Mut	121	-DSGAHVHYPPPAPGVSPKCA-	140
Wt	421	TCC <mark>CCA</mark> GCC <mark>TCC</mark> GGC <mark>CTC</mark> CCT <mark>GCC</mark> GCC <mark>TTC</mark> AGC <mark>ACG</mark> TTC <mark>GAG</mark> TGG <mark>ATG</mark> AAA <mark>GTG</mark> AAG <mark>AGG</mark>	480
Mut	421	TCCCCAGCCTCCGGCCTCCCGCCTTCAGCACGTTCGAGTGGATGAAAGTGAAGAGG	480
Wt	141	-SPASGLPAAFSTFEWMKVKR-	160
Mut	141	-SPASGLPAAFSTFEWMKVKR-	160
Wt	481	AAC <mark>GCG</mark> CCG <mark>AAG</mark> AAA <mark>AGCAAATTC</mark> GCG <mark>GAGTATGGA</mark> GCC <mark>GCC</mark> ACC <mark>CCC</mark> TCC <mark>AGC</mark> GCGATC	540
Mut	481	AACGCGCCGAAGAAA <mark>AGT<mark>AC</mark>TTGA</mark> GCCTTGGACGGACGGACGCGACTGGGGTTGGGGACG	540
Wt	161	-NAPKKSKFAEYGAATP- <mark>-SSAI-</mark>	180
Mut	161	-NAPKKST*	167
Wt	541	CGC <mark>ACGAATTTC</mark> AGC <mark>ACCAAGCAA</mark> CTG <mark>ACAGAACTG</mark> GAG <mark>AAG</mark> GAG <mark>TTT</mark> CAT <mark>TTC</mark> AATAAG	600
Mut	541	AGCCTGCCCAGCGGAACTGAGCCGAGGGCGCGCGCGCGGGCCCCTGTGGACGGCGGTTT	600
Wt	181	-RTNFSTKQLTELEKEFHFNK-	200
Mut			
Wt	601	TAC <mark>TTA</mark> ACT <mark>CGG</mark> GCC <mark>CGA</mark> CGC <mark>ATC</mark> GAG <mark>ATA</mark> GCC <mark>AAC</mark> TCA <mark>TTG</mark> CAA <mark>CTG</mark> AAT <mark>GAC</mark> ACC <mark>CAA</mark>	660
Mut	601	GGGTCTTATGGGGAACACGCGGCCCCAGGCATTATTAAACCAGGCGAATTGCATTGAGCG	660
Wt	201	-YLTRARRIEIANSLQLNDTQ-	220
Mut			

Wt Mut Wt Mut	661 661 221	GTCAAAATCTGGTTCCAGAACCGCAGGATGAAACAGAAGAAAAGGGAACGGGAAGGGCTT TGCCCCGAATGCCAGGGGTTGAGAAAATTGCCGGAAGGAGC -VKIWFQNRRMKQKKRE--REGL-	720 720 240
Wt Mut Wt Mut	721 721 241	CTGCCCTCGGCCACCCCGTGGCTTCCTTCCAGCTTCCCCTCTCAGGACCGAGCCCTGCC TTGGCACAGCTGTGTTCGGAGGCCCAGAAGGGCCGCTCAGTAACTCTGATTCTAGTGTGG -LPSATPVASFQLPLSGPSPA-	780 780 260
Wt Mut Wt Mut	781 781 261	AAGTCTGGCAAGAACCCGGGGGGGCCCCTCTCAGGCCCAGGAGCCATCCTGA CCCCAAAGCTCTCCCAAGTCGCGTCTCCCGTGTCATCTCGCCACGCTGACGACGCCCTGTC -KSGKNPGSPSQAQEPS*-	831 840 276
Mut Wt	841	TTTACGTTGCAGGCAAATTCGCGGAGTATGGAGCCGCCACCCCTCCAGCGCGATCCGCA	900
Mut Wt	901	CGAATTTCAGCACCAAGCAACTGACAGAACTGGAGAAGGAGTTTCATTTCAATAAGTACT	960
Mut Wt	961	TAACTCGGGCCCGACGCATCGAGATAGCCAACTCATTGCAACTGAATGACACCCAAGTCA	1020
Mut Wt	1021	AAATCTGGTTCCAGAACCGCAGGATGAAACAGAAGAAAAGGGAACGGGAAGGGCTTCTGC	1080
Mut Wt	1081	CCTCGGCCACCCCGTGGCTTCCTTCCAGCTTCCCCTCTCAGGACCGAGCCCTGCCAAGT	1140
Mut Wt	1141	CTGGCAAGAACCCGGGGAGCCCTCTCAGGCCCAGGAGCCATCCTGA	1187



Supplementary Figure 10. Intraspecific three-dimensional geometric morphometric analyses of 61 ovine (a) and 19 caprine (b) skulls. Distribution of specimens along the first two axes of the PCA. The percentages of variance explained by the two main principal components are indicated on each axis. Squares and circles represent skulls from male and female animals, respectively. a) green marks: polycerate sheep with a distance between lateral horns (dlh) larger than the distance between upper horns (duh); light blue: polycerate sheep with a dlh≤duh; and blue: polycerate sheep with at least two lateral horns partially fused at their basis; purple: wild type sheep. b) red: polycerate goats; and black: wild type goats. Specimens are presented to illustrate each cluster and symbols are used to indicate their respective locations in the PCA analyses. Their respective ID in **Suppl. Table 10** are: &: Pachot\_M4C\_Haie; @: MNHN-ZM-AC A-12130; #: Omsr13; £: MNHN-ZM-AC A-12157; €: MNHN-ZM-AC A-12122; and \$: Bresson\_M2C.



Supplementary Figure 11. Localization of selected anatomical landmarks and sliding semilandmarks on the skulls of wild type (a-d) and polycerate (e, f) sheep. Arrows indicate the sense of the numbering of the sliding semi-landmarks around the neck of the cornual process. The definition of the whole landmarks is in **Suppl. Table 11**.



Supplementary Figure 12. Repeatability and reproducibility of landmark placement using PCA. A total of 116 landmarks and sliding semi-landmarks were placed ten times independently on the skulls of two polycerate and two control male sheep sampled between 1852 and 1909 in Tunisia (MNHN-ZM-AC A-12130, A12132 and 1909-4) and neighboring Algeria (MNHN-ZM-AC A12157; see **Suppl. Table 10**). The percentages of variance explained by the two main principal components are indicated on each axis. Each color corresponds to a specimen. For each skull, the inter-specimen variation on the two main axes is lower than the intra-specimen error due to differences between landmark digitalization, showing that our landmark configuration is relevant to describe shape variation within our sample.



MNHN-ZM-AC 1991-1423

MNHN-ZM-AC 1858-26



MNHN-ZM-AC 1927-18



INRAE Bresson\_M4C

INRAE Pachot\_M4C\_Haie

Supplementary Figure 13. Comparison between the skulls of *Tetracerus quadricornis* and polycerate *Capra hircus* and *Ovis aries* individuals. a-c) skulls of males *T. quadricornis* of growing age. d, e) skulls of polycerate goat (*C. hircus*; in mirror view) and sheep (*O. aries*) males, respectively. The ID of each specimen in the MNHN and INRAE collections is indicated on the panel. Two of the three recognized subspecies of *T. quadricornis* have additional anterior horns (Groves, 2003; Leslie and Sharma, 2009), which start to develop at 10–14 months of age in captivity (Sharma *et al.* 2005). Most male *T. quadricornis* have anterior horns 1/4 to 2/3 the length of their posterior horns (Sharma *et al.* 2005). Note the differences in relative placement and relative size of the anterior and posterior pairs of horns in *T. quadricornis* versus polycerate *C. hircus* and *O. aries*. Specimens MNHN-ZM-AC 1991-1423, 1858-26 and 1927-18 belong to the *Collection d'anatomie comparée du Muséum National d'Histoire Naturelle*, Paris, France while specimens Bresson\_M4C and Pachot\_M4C\_Haie originate from the collection of INRAE UMR1313 GABI, Jouy-en-Josas, France.

Supplementary Table 1. Illumina OvineHD Beadchip genotypes used for mapping the *POLYCERATE* locus in sheep. Wt: "wild type" refers to two normal horns or two scurs. "Polycerate" refers to the existence of more than two horns or scurs. \*: In Greyvenstein *et al.* 2016, individual D-003 was mistakenly registered as polycerate while it has only two horns.

No	Breed or	Country of origin	Origin of	Number of animals			
NO	population	of the breed	the samples	All	Wt	Polycerate	
1	Jacob	UK	Kijas <i>et al.</i> 2016	130	57	73	
2	Navajo-Churro	USA	Kijas <i>et al.</i> 2016	27	14	13	
3	Damara	Namibia	Greyvenstein <i>et al.</i> 2016	41	16*	25*	
Total				198	87	111	

**Supplementary Table 2. Details on individuals considered for IBD mapping of the** *POLYCERATE* locus in sheep. Illumina OvineHD Beadchip genotyping data have been downloaded from the Dryad repository (datadryad.org/stash/dataset/doi:10.5061/dryad.1p7sf and datadryad.org/stash/dataset/doi:10.5061/dryad.6t34b) and phenotypic information have been obtained from the corresponding authors of the related articles: Kijas *et al.* 2016 and Greyvenstein *et al.* 2016. Breed : D. =Damara, J.=Jacob, and N.=Navajo-Churro; Ph. :Phenotype.

ID	Breed	Ph.	ID	Breed	Ph.	ID	Breed	Ph.	ID	Breed	Ph.	ID	Breed	Ph.
D-003	D.	0	H102	J.	0	H36	N.	0	H35	J.	1	H115	J.	1
D-008	D.	0	H106	J.	0	H37	N.	0	H47	J.	1	H116	J.	1
D-010	D.	0	H112	J.	0	H42	N.	0	H48	J.	1	H118	J.	1
D-011	D.	0	H114	J.	0	H43	N.	0	H50	J.	1	H121	J.	1
D-014	D.	0	H117	J.	0	H45	N.	0	H51	J.	1	H122	J.	1
D-018	D.	0	H119	J.	0	H52	N.	0	H54	J.	1	H123	J.	1
D-023	D.	0	H120	J.	0	H58	N.	0	H55	J.	1	H124	J.	1
D-076	D.	0	H125	J.	0	Black	D.	1	H57	J.	1	H131	J.	1
D-100	D.	0	H126	J.	0	Brown	D.	1	H59	J.	1	H132	J.	1
D-101	D.	0	H127	J.	0	D-004	D.	1	H61	J.	1	H133	J.	1
D-103	D.	0	H128	J.	0	D-005	D.	1	H62	J.	1	H136	J.	1
D-104	D.	0	H129	J.	0	D-013	D.	1	H64	J.	1	H138	J.	1
DD11	D.	0	H130	J.	0	DD01	D.	1	H71	J.	1	H139	J.	1
DD12	D.	0	H134	J.	0	DD02	D.	1	H72	J.	1	H143	J.	1
DD15	D.	0	H135	J.	0	DD04	D.	1	H76	J.	1	H145	J.	1
DD16	D.	0	H137	J.	0	DD05	D.	1	H77	J.	1	H146	J.	1
H7	J.	0	H140	J.	0	DD06	D.	1	H78	J.	1	H147	J.	1
H17	J.	0	H141	J.	0	DD07	D.	1	H80	J.	1	H151	J.	1
H21	J.	0	H142	J.	0	DD08	D.	1	H83	J.	1	H155	J.	1
H34	J.	0	H144	J.	0	DD09	D.	1	H87	J.	1	H158	J.	1
H40	J.	0	H148	J.	0	DD10	D.	1	H88	J.	1	H159	J.	1
H46	J.	0	H149	J.	0	DD13	D.	1	H90	J.	1	H163	J.	1
H65	J.	0	H150	J.	0	DD14	D.	1	H91	J.	1	H164	J.	1
H66	J.	0	H152	J.	0	DD17	D.	1	H92	J.	1	H167	J.	1
H67	J.	0	H153	J.	0	DD18	D.	1	H93	J.	1	H170	J.	1
H68	J.	0	H154	J.	0	DD20	D.	1	H95	J.	1	H2	N.	1
H69	J.	0	H156	J.	0	DR02	D.	1	H96	J.	1	H8	N.	1
H70	J.	0	H157	J.	0	DR03	D.	1	H97	J.	1	H10	N.	1
H73	J.	0	H160	J.	0	DR04	D.	1	H98	J.	1	H11	N.	1
H74	J.	0	H161	J.	0	DR05	D.	1	H99	J.	1	H12	N.	1
H75	J.	0	H162	J.	0	DS02	D.	1	H100	J.	1	H14	N.	1
H79	J.	0	H166	J.	0	DS03	D.	1	H103	J.	1	H28	N.	1
H81	J.	0	H169	J.	0	H5	J.	1	H104	J.	1	H31	N.	1
H82	J.	0	H1	N.	0	H13	J.	1	H105	J.	1	H38	N.	1
H84	J.	0	H4	N.	0	H16	J.	1	H107	J.	1	H44	N.	1
H85	J.	0	H9	N.	0	H20	J.	1	H108	J.	1	H56	N.	1
H86	J.	0	H15	N.	0	H22	J.	1	H109	J.	1	H60	N.	1
H89	J.	0	H24	N.	0	H26	J.	1	H110	J.	1	H63	N.	1
H94	J.	0	H29	N.	0	H27	J.	1	H111	J.	1			
H101	J.	0	H30	N.	0	H32	J.	1	H113	J.	1			

Supplementary Table 3. Details on animals phenotyped and genotyped for validating the causative mutation of the ovine *POLYCERATE* locus. Wt: "wild type" refers to two normal horns or two scurs. "Polycerate" refers to the existence of more than two horns or scurs. Wt: wild type.

No	Breed or	Origin	Origin of	Number of animals		
NU	Population	of the breed	the samples	All	Wt	Polycerate
1	Hebridean	UK	Two breeders from the Netherlands	3	-	3
2	Jacob	UK	Multiple breeders from France, Switzerland and the USA	106	19	87
3	Manx Loaghtan	UK	Three breeders from the UK and the Netherlands	32	10	22
4	Ouessant admixed with Jacob	France and UK	One breeder from Paris area, France	6	4	2
5	Navajo-Churro	USA	Multiple breeders from the USA	49	32	17
6	Ovino Quadricorna	Italy	One breeder from the Province of Frosinone, Italy	16	6	10
7	Local population from Tunis area	Tunisia	Zoological Park of Tunis, Tunisia	6	2	4
8	Damara	Namibia	Three breeders from South Africa	18	12	6
Total for sheep (Ovis aries)					85	151

Supplementary Table 4. Association between the polycerate phenotype and chromosome 2 g.132,832,249\_132,832,252del allele in 236 sheep. Wt: wild type; Del: deletion of four nucleotides.

Phonotypo	Brood or population	Number of animals per genotype			
Phenotype	Breed of population	Wt/Wt	Wt/Del	Del/Del	
	Jacob	19	-	-	
	Manx Loaghtan	10	-	-	
	Ouessant admixed with Jacob	4	-	-	
Wild type	Navajo-Churro	32	-	-	
	Ovino Quadricorna	6	-	-	
	Local population from Tunis area	2	-	-	
	Damara	12	-	-	
	Total for wild type animals	85	0	0	
	Hebridean	-	2	1	
	Jacob	-	73	14	
	Manx Loaghtan	-	17	5	
Dolycoroto	Ouessant admixed with Jacob	-	2	-	
Folycerate	Navajo-Churro	-	16	1	
	Ovino Quadricorna	-	9	1	
	Local population from Tunis area	-	3	1	
	Damara	-	5	1	
	Total for polycerate animals	0	127	24	
	Grand total	85	127	24	

Supplementary Table 5. Analysis of nucleotide sequence conservation at the *HOXD1* exon 1 –intron 1 junction in sarcopterygians and tetrapods. The 40 last nucleotides of *HOXD1* exon 1, the splice donor site of exon 1 (bolded), and 20 additional nucleotides of intron 1 are presented for 103 species and genome assemblies obtained from the Ensembl (www.ensembl.org; release 98) and UCSC (http://genome.ucsc.edu/) genome browser databases.

Species	Genome Assembly	Nucleotide sequence			
	<b>—</b> 0	TTTGAATGGATGAAAGTGAAAAGAAACGCCC			
Notamacropus eugenii	macEug2	CCAAGAAAA <b>GT</b> AAGTAAACCTTAACCTTGGG			
		TTTGAATGGATGAAAGTGAAAAGAAACGCCC			
Sarcophilus harrisii	SarHarl	CCAAGAAAA <b>GT</b> AAGTAAACCTTAACTTTGGG			
		TTTGAATGGATGAAAGTGAAAAGGAACGCCC			
Monodelphis domestica	monDom5	CCAAGAAAA <b>GT</b> AAGTAAACCTTAACCTTGGG			
	bare-				
Vombatus ursinus	nosed wombat ge				
	nome_assembly	CCAAGAAAAGIAAGIAAGCCIIAACCIIGGG			
Phagoalaratos cinerous	phaCin_unsw_v4.	TTTGAATGGATGAAAGTGAAAAGAAACGCCC			
Fliascolarceos cinereus	1	CCAAGAAAA <b>GT</b> AAGTAAGCCTTAACCTTGGG			
Ostodon dogus	OctDoc1 0	TTTGAGTGGATGAAAGTGAAGAGGAACACCC			
loctodon degus	OctDeg1.0	CGAAAAAAA <b>GT</b> GAGTACATGGACCTGGGAGG			
Chrysomys pists bollii	chrDic1	TTCGAGTGGATGAAAGTGAAAAGAAATGCGC			
Chrysencys picca belli	CHIFICI	CCAAGAAAA <b>GT</b> AAGTGTGAACCTCGGCGAGG			
Conhorus agassizii	7 CM2806/11 TT	TTCGAGTGGATGAAAGTGAAAAGAAATGCGC			
Gopherus agassizii	A3M209041V1	CCAAGAAAA <b>GT</b> AAGTGTGAACCTCGGCGAGG			
Cholopoidis phingdonii	A CM35073011	TTCGAGTGGATGAAAGTGAAAAGAAATGCGC			
cheronordis abinguonir	ASMSSSTSSVI	CCAAGAAAA <b>GT</b> AAGTGTGAACCTCGGCAAGG			
Cania lunua familiaria	ann Form?	TTCGAGTGGATGAAAGTGAGGAGGAGCGCCC			
		CTCGGAAAA <b>GT</b> AAGTGCGGGCCGCGGGCGGG			
Saluator morianao	UI tupMor?	TTCGAGTGGATGAAAGTCAAGAGGAACGCAC			
Salvator merianae	HLCupMers	CTCCGAAAG <b>GT</b> AAGCAGGGCAGCCTCCGGAG			
Alligator		TTCGAGTGGATGAAGGTGAAGAGAAACGCGC			
mississippiensis	alimisi	CCAGGAAAA <b>GT</b> AAGTCTCCAGCCGGGGGAGG			
Crocodylug porogua	CroBor compl	TTCGACTGGATGAAGGTGAAGAGAAACGCGC			
ciocodyius porosus	CIOPOI_COMPI	CCAGGAAAA <b>GT</b> AAGTCTCCAGCCGGGGGGGGT			
Coturnix japonica	Coturnix_japoni	TTCGAGTGGATGCGGATGAAGCGGAGCACGC			
cocuriix Japonica	ca_2.0	CAGGCAGAA <b>GT</b> GAGTGGGGGGGGGGGGGGGGGGG			
Numida meleagris	NumMoll 0	TTCGAGTGGATGCGGATGAAGCGGAGCACGC			
Nulliua mereagris	Numerr. 0	CCGGTAGAA <b>GT</b> GAGTGGGGCGGCGGGGGGCGCG			
Anser brachurhunchus	ASM25921311	TTCGAGTGGATGCGAGTGAAGCGGAGCCCGC			
	1101123921301	CCGGGAGAA <b>GT</b> GAGTGGGGCCGCGGGGCGCG			
Pelodiscus sinensis	Pelsin 1 0	TTCGAGTGGATGAAAGTGAAGCGAAACGCAC			
		CCACGAAAA <b>GT</b> AAGTGTAACCCTCGGGGGGGC			
Meriones unquiculatus	MunDraft-v1 0	TTCGAGTGGATGAAAGTGAAGAGGAACGCCC			
		CCAGGAAAA <b>GT</b> AAGGAGGTGGGCGCCGGGGG			
Dipodomys ordii	dip0rd1	TTCGAATGGATGAAAGTGAAGAGGAACGCCC			
bipedentyb erait	arporar	CTAAGAAGA <b>GT</b> AAGTACTGGGGCGTGGGGTG			
Ornithorhynchus anatinus	ornAna2	TTCGACTGGATGAAAGTGAAAAGAAACGCGC			
	011mma2	CCAGGAAAA <b>GT</b> AAGTAGTCCTCGGGCGACCT			
Fukomys damarensis	DMR v1 0	TTCGAGTGGATGAAAGTAAAGAGGAACGCCC			
		CTAAGAAAA <b>GT</b> AAGTACTTGGGCGAGGGGTG			
Microcebus murinus	micMur2	TTTGAGTGGATGAAAGTGAAGAGGAACGCCC			
		CTAAGAAAA <b>GT</b> AAGTACGTGGGCCTCGGGCC			
Manis pentadactyla	manPen1	TTTGAGTGGATGAAAGTGAAGAGGAACACCC			
		CTAAGAGAA <b>GT</b> AAGTACTTGGGCCCTGGACC			
Otolemur garnettii	otoGar3	TTTGAATGGATGAAAGTGAAGAGGAATGCCC			
		CTAAGAAAA <b>GT</b> AAGTTGTGGGCCTTGGATGG			
Propithecus coquereli	Pcog 1.0	TTTGAGTGGATGAAAGTGAAGAGGAACGCTC			
TTOPTOMOCAD COQUETET		CTAAGAAAA <b>GT</b> AAGTAGTGGGCCTTGGACCG			

#### Supplementary Table 5, continuing

Species	Genome Assembly	Nucleotide sequence
Prolemur simus	Prosim 1 0	TTTGAGTGGATGAAAGTGAAGAGGAACGCCC
	1103111_1.0	CTAAGAAAA <b>GT</b> AAGTCCGTGGGCCTTGGTCG
Mus spretus	SPRET ELT V1	TTCGAGTGGATGAAAGTGAAGAGGAACGCCC
		CCAAGAAAA <b>GT</b> AAGGAGGTGGGCGCTGAGGG
Mus caroli	CAROLT ELT V1 1	TTCGAGTGGATGAAAGTGAAGAGGAACGCCC
		CCAAGAAAA <b>GT</b> AAGGAGGTGGGCGCTGAGGG
Mus musculus	GRCm38.p6	TTCGAGTGGATGAAAGTGAAGAGGAACGCCC
	Gitomoo.po	CCAAGAAAA <b>GT</b> AAGGAGGTGGGCGCTGAGGG
Mus pahari	PAHARI EIJ v1.1	TTCGAGTGGATGAAAGTGAAGAGGAACGCCC
		CCAAGAAAA <b>GT</b> AAGGAGGTGGGCGCTGTGGG
Rattus norvegicus	rn6	TTCGAGTGGATGAAAGTGAAGAGGAACGCCC
		CCAAGAAAA <b>GT</b> AAGGAGGTGGGCGCTGGGGG
Cricetulus griseus	criGriChoV2	TTCGAGTGGATGAAAGTGAAGAGGAACGCCC
		CCAGGAAAA <b>GT</b> AAGGAGGTGGGCGCTGGAGG
Peromyscus maniculatus	HU Pman 2.1	TTCGAGTGGATGAAAGTCAAGAGGAACGCCC
bairdii		CCAAGAAAA <b>GT</b> AAGGAGG'I'GGGCGC'I'GGAGG
Mesocricetus auratus	MesAur1.0	TTCGAGTGGATGAAAGTGAAGAGGAACGCCC
		CCAAGAAAA <b>GT</b> AAGAAGG'I'GGGCGC'I'GGAGG
Microtus ochrogaster	MicOch1.0	
Mus spicilegus	MUSP714	
Cavia porcellus	cavPor3	
-		
Chinchilla lanigera	ChiLan1.0	
Erinaceus europaeus	eriEur2	
Nannospalax galili	S.galili_v1.0	
Tatidomus		
tridecemlineatus	speTri2	
Urocitellus parryii	ASM342692v1	CTAAGAAAA <b>GT</b> AAGTCGCTGGGCTCTGGATG
Spermophilus dauricus	ASM240643v1	CTAAGAAAA <b>GT</b> AAGTCGCTGGGCGCTGGATG
		TTCGAGTGGATGAAAGTGAAGAGGAATGCCC
Heterocephalus glaber	hetGla2	CTAAGAAAA <b>GT</b> AAGTACTTGGGTGCCGGGTG
		TTTGAGTGGATGAAAGTGAAGAGGAATGCCC
Tupaia belangeri	tupBel1	CTAAGAAAA <b>GT</b> AAGTCCTTGGCTTCTGATGC
		TTCGAGTGGATGAAAGTGAAAAGGAACGCTC
Ochotona princeps	ochPri3	CTAAGAAAA <b>GT</b> AAGTGAAGTAGGGTTTAGAC
		TTCGAGTGGATGAAAGTGAAGAGGAACGCCC
Myotis lucifugus	myoLuc2	CCAAGAAAA <b>GT</b> GAGTACTCGAGTCTTGGACG
		TTCGAGTGGATGAAAGTGAAAAGAAACGCCC
Oryctolagus cuniculus	oryCun2	CAAAGAAAA <b>GT</b> AAGTACTGAGCTTTGGATGC
	- 11	TTCGAGTGGATGAAAGTGAAGAGGAACGCCC
Sus scroia	susScr11	CGAAGAAAA <b>GT</b> AAGTACTTGGGCTCTCGACG
		TTCGAGTGGATGAAAGTGAAAAGGAACGCCC
Vicugna pacos	VICPAC2	CGAAGAAAA <b>GT</b> AAGTACTTGGGCCCTGGACC
muundana ta ta ta		TTCGAGTGGATGAAAGTGAAGAGGAACGCCC
Tursiops truncatus	turTru2	CGAAAAAAA <b>GT</b> AAGTGCTTGGGCCTTGGACG
Oni a ani aa		TTCGAGTGGATGAAAGTGAAGAGGAACGCGC
UVIS aries	OVIAT14	CGAAGAAAA <b>GT</b> AAGTACTTGAGCCTTGGACG
Conno hingua	1 D C 1	TTCGAGTGGATGAAAGTGAAGAGGAACGCGC
Capra nircus	AKSI	CGAAGAAAA <b>GT</b> AAGTACTTGAGCCTTGGACG

#### Supplementary Table 5, continuing

Bos taurus     bosTau9     TTCGAGTGAATGAAAGTGAAAGGCACCCCC GAAGAAAAGTAGTAGTAGTGGGCCTTGGACCG TCGAGTGAAGTAAAGTGAAAGTGAAAGGCAAGGC	Species	Genome Assembly	Nucleotide sequence
DescriptionDescriptionBison bison bison bisonBison_UMD1.0TTCGAGTGGATCAANGTGACAGGGACGAGCGCCCAAGAAAAGTAACTACTTGGGCCTTGGACGCAAGAAAAGTAACTACTTGGGCCTTGGACGBalaenoptera acutorostrata scammonibalAculTTCGAGTGGATGAAAGTGACAGGCAACGGCCFelis catusfelCat9TTCGAGTGGATGAAAGTGACGGGCCTTGGACGPanhera pardusPanParl.0TTCGAGTGGATGAAAGTGACGGCCTTGGACGParopus vampyruspteVamlCGAAGAAAGTACTACTGGGCCTTGGACGCPteropus vampyruspteVamlCGAAGAAAGTACTACTGGCCTGGGCCTGGACGNeovison visonNNQGG.v01TTCGAGTGGATGAAAGTGACGGCCCAiluropoda melanoleucaailMel1TTCGAGTGGATGAAAGTACGACGGCCCUrsus americanusASM334442v1TTCGAGTGATGAAAGTACGTGGGCCTGGGACCTrichechus mantustriMan1TTCGAGTGATGAAAGTACGTGGGCCTGGGACCTrichechus mantustriMan1TTCGAGTGATGAAAGTACGTGGGCCTGGGACCProcavia capensisproCap1TTCGAGTGAAAGTAAGTGGAGGAGAGCGCCProcavia capensisproCap1TTCGAGTGGATAAAGTGAGGAGAGGCGCCProcavia capensisproCap1TTCGAGTGGATAAAGTGAGGAGAGGCCCAguus asinusASM303372v1CTGAGGAAAGTACTTGGGCCTTGGACCGCastor canadensisC. can_genome_v1TTCGAGTGGATGAAAGTACGGGCCTGGATGCastor canadensisC. can_genome_v1TTCGAGTGATGAAGGAGAGCGCCCCastor canadensis0TTCGAGTGATGATACTTGGGCCTTGGACGGAGGGCCTCastor canadensis0CTAAGAAAGTAACTACTGGGCGCTGGATGCastor canadensis0TTCGAGTGATGATAGTGGAGGGACGGCCCCatagaaAgtactactactgAGGGAGGGCCCCCTGGATGTTCGAGTGAGAGAGA	Bos taurus	bosTau9	TTCGAGTGGATGAAAGTGAAGAGGAACGCCC
Bison bison     Bison_UMD1.0     TTGGAGTGGATGGAAGGTGGAAGGCCCC       Ralaenoptera acutorostrata scammoni     balAcul     TTGGAGTGGATGGAAGGTGGAGGGACGCCC CGAGGAAAGTGAAAGTGGAGGAAGGCCCC CTAAGGAAAGTAAGTATCTGGGCCTTGGACG       Pelis catus     felCat9     TTGGAGTGGATGAAGTGCAAGGGACGCCC CTAAGAAAGTAAGTATCTGGGCCTTGGACG       Panthera pardus     PanParl.0     TTGGAGTGGATGGAAGGGACGCCC CTAAGAAAGTAAGTATCTGGGCCTTGGACG       Peropus vampyrus     pteVaml     CGAAGAAAGTAAGTATCTGGGCCTGGACG       Mustela putorius furo     musFurl     TTGGAGTGGATGAAAGTGAAGGGACGCCC CTAGGAAAAGTAAGTGCTTGGGCCTGGGACC       Nunogda melanoleuca     ailMell     TTGGAGTGGATGAAAGTGAAGGGACGCCC CTAGGAAAAGTAAGTGCTTGGGCCTGGGACC       Ursus americanus     ASM334442vl     TTGGAGTGGATGAAAGTGAAGGAAGGCCC CTAGGAAAAGTAAGTGCAGGAGGAAGGCCC CTAGGAAAAGTAAGTGCAGGAGGAAGGCCCC Loxodonta africana     loxAfr3     TTGGAGTGGATGAAGGAAGGAAGGACGCCC CTAGGAAAAGTAAGTGCAGGAGGAGGCCCC CTAAGAAAAGTGAAGTG		0051007	CGAAGAAAA <b>GT</b> AAGTACTTGGGCCTTGGACG
Balaenoptera acutorostrata scammoni     -     CHARGAMARATIANGIACITEGAGCAGAGGAGCGCC CGAGGARAAGTAAGTGAGAGAGGAGCGCC CGAGGARAAGTAAGTGAGGAGGAGCGCC Felis catus     felCat9     TTCGAGTGATGAGAGGAGGAGCGCC CTAAGAAAGTAAGTATCTGGGCCTTGGACG       Panthera pardus     PanParl.0     TTCGAGTGATGAGAGGAACGCCC CTAAGAAAGTAAGTATCTGGGCCTTGGACG       Pteropus vampyrus     pteVam1     TTCGAGTGGATGAAGGAACGCAC CTAAGAAAGTAAAGTA	Bison bison bison	Bison UMD1.0	TTCGAGTGGATGAAAGTGAAGAGGAACGCCC
Balaenoptera acutorostrata scammoni     balacul     TTCGADEGATEGATAGTAGATGCADGCCTTGGGCCTTGGGCC CGAGAAAAGTAGATGCTTGGGCCTTGGGCC TCGACGAAAGTGAAAGTGAAGGAACGCCC CTAGGAAAAGTGAAAGTGAAGGGACCCCC CTAGGAAAGTGAAAGTGAAGGGACCCCC CTAGGAAAGTAAGTGCATGGGCCTGGGCC Mustela putorius furo     PueVaml     TTCGAGTGGTGAAAGTGAAGGGACCCCC CTAGGAAAAGTAAGTGAAGGGACCCCC CTAGGAAAAGTAAGTGAAGGGACCCCC CTAGGAAAAGTAAGTGAAGGGACCCCC CTAGGAAAAGTAAGTGAAGGGACCCCC CTAGGAAAAGTAAGTGAAGGGACCCCC CTAGGAAAAGTAAGTGAAGGGACCCCC CTAGGAAAAGTAAGTGAAGGGACCCCC CTAGGAAAAGTAAGTGAAGGGACCCCC CTAGGAAAAGTAAGTGAAGGGACCCCC CTAGGAAAAGTAAGTGAAGGGACCCCC CTAGGAAAAGTAAGTGAAGGGACCCCC CTAGGAAAAGTAAGTGAAGGGACCCCC CTAGGAAAAGTGAAGGAACGCACCCC CTAGGAAAAGTGAAGGAACGCACCCC CTAGGAAAAGTGAAGGAACGCACCCC CTAGGAAAAGTGAAGGAACGCACCCC CTAGGAAAAGTGAAGGAACGCACCCC CTAGGAAAAGTGAAGGAACGCACCCC CTAGGAAAAGTGAAGGAACGCACCCC CTAGGAAAAGTGAAGGAACGCACCCC CTAGGAAAAGTGAAGGAACGCACCCC Actions anatus triMan1     TTCGAGTGGATGAAAGGAACGCCC CTAGGAAAAGTGAAGGAAGGAACCCCC CTAGGAAAAGTGAAGGAAGGAACCCCC CTAGGAAAAGTGAAGGAAGGAACCCCC CTAGGAAAAGTGAAGGAGGACCCCC CTAGGAAAAGTGAAGGAAGGAACCCCC CTAGGAAAAGTGAAGGAAGGAACCCCC CTAGGAAAAGTGAAGGAAGGAACCCCC CTAGGAAAAGTGAAGGAAGGAACCCCC CTAGGAAAAGTGAAGGAAGCGACCCCC CTAGGAAAAGTGAAGGAAGCGACCCCC CCAAGGAAAAGTGAAGGAACGCACCTGGACC CCAAGGAAAAGTGAAGGAAACGGAACCCCC CCAAGGAAAGTGAAAGTGAAGGAACCCCC CCAAGGAAAAGTGAAGGAAACGGAACCCCC CCAAGGAAAGTGAAAGTGAAGGAACCCCC CCAAGGAAAGTGAAAGTGAAGGAACCCCC CCAAGGAAAGTGAAAGTGAAGGAACCCCC CCAAGGAAAGTAAAGT		-	
Felis catus     felCat9     TTCGADTGATAGATAGAAGGAACCCCC CTAAGAAAGTAAGTACTAGGCCTTGGAC       Pantera pardus     PanParl.0     TTCGADTGATGAAGTAGTACTGGCCTTGGAC       Pteropus vampyrus     pteVaml     CGAGAAAGTAAGTATCTGGCCTTGGACG       Mustela putorius furo     musPurl     TTCGAGTGGATGAAAGTAAGGAACCCCC       Neovison vison     NNQGG.v01     TTTGGAGTGGATGAAAGTAAGTACTGGCCTGGGCCTGGACC       Ailuropoda melanoleuca     ailMell     TTCGAGTGGATGAAAGTAAGTCATGGGCCTGGACC       Ursus americanus     ASM334442vl     TTCGAGTGGATGAAAGTAAGTGAGGAGGACCCCC       Loxdonta africana     loxAfr3     TTCGAGTGGATGAAAGTAAGTGAGGAGGACCCCC       Trichechus manatus     triMan1     TTCGAGTGGATGAAAGTGAAGGAACGCCC       Iatirostris     proCap1     TTCGAGTGGATGAAAGTGAAGGAACGCCC       Procavia capensis     proCap1     TTCGAGTGGATGAAAGTGAAGGAACGCCC       Procavia capensis     proCap1     TTCGAGTGGATGAAAGTGAAGGAACGCCC       Procavia capensis     proCap1     TTCGAGTGGATGAAAGTGAAGGAACGCCC       Galeopterus variegatus     galVar1     TTCGAGTGGATGAAAGTGAAGGAAGGACGCCC       Galeopterus variegatus     galVar1     TTCGAGTGGATGAAAGTGAAGGAAGGACGCCC       CatagaAagtGaAAGTGGAAGGAAGGACGCCC     CTAAGAAAAGTAA	Balaenoptera acutorostrata scammoni	balAcul	TTCGAGTGGATGAAAGTGAAGAGGAACGCCC CGAAGAAAA <b>GT</b> AAGTGCTTGGGCCTTGGACG
Peris Calus   Tellaty   CTAAGAAAGTAAGTAAGTAAGGACGCCC     Panthera pardus   PanPari.0   TTCCAGTGGATGAAAGTAAAGGAAAGGACGCCC     Pteropus vampyrus   pteVaml   TTCCAGTGGATGAAAGTAAAGGAAAGGACGCCC     Mustela putorius furo   musFurl   TTCCAGTGGATGAAAGTAAAGGACAGGACCCCC     Neovison vison   NNQGG.v01   TTTGAGTGGATGAAAGTAAGGCATGGACGCCCGGACC     Ailuropoda melanoleuca   ailMel1   CTAGGAAAGTAAGTAAGTGGATGGGCCTGGGACC     Ursus americanus   ASM334442v1   TTCGAGTGGATGAAAGTAAGGCAAGGGCCCCGGACC     Loxodonta africana   loxAfr3   TTCGAGTGGATGAAAGTAAGGGAAGGCCC     Trichechus manatus   triMan1   TTCGAGTGGATGAAAGTAAGGGAAGGCCCC     CTAAGAAAGTAAGTAAGTGAAGGAAAGCCCC   CTAAGAAAGTAAGTGCAAGGGAACGCCC     Procavia capensis   proCapl   TTCGAGTGGATGAAAGTAAGGAGAGACGCCC     CAGAGAAGTAAGTAAGTGAAAGTAAGGAAAGGCCTTGGACG   TTCGAGTGGATGAAAGTAAGTGGAGGACGCCC     CAGAGAAAGTAAGTAAGTGAAAGTAAGTGGAGGAGCCCCC   CCAAGAAAAGTAAGTAAGTGGAGGAGCGCCC     CAGAGAAAGTAAGTAAGTGAAGGAAAGCCCC   CCAAGAAAAGTAAGTGAAGGAAGGACGCCC     CAGAGAAAGTAAGTAAGTGAGAGGAACGCCC   CCAAGAAAAGTAAGTAAGTGGAGGAGGACGCCC     Gaus sinus asinus   ASM30372v1   CTCAGGAGAGAAGTAAGTGGAGGAGGACGCCC     Castor canadensis   C. can_genome_v11 <td< td=""><td>Telie setus</td><td>falCato</td><td>TTCGAGTGGATGAAAGTGAAGAGGAACGCCC</td></td<>	Telie setus	falCato	TTCGAGTGGATGAAAGTGAAGAGGAACGCCC
Panthera pardusPanPar1.0TTCGAGTGATGAAAGTGAAGGGAACGCCC CTAGGAAAGTAAGTAAGTGAGGAACGCCC CGAGAGAAAGTAAGTAAGTGAGCCATGGACGPteropus vampyruspteVamlTTCGAGTGGATGAAAGTGAGGGACGCCC CTAGGAAAGTAAGTGAGGCCTGGACCMustela putorius furomusFur1TTCGAGTGGATGAAGTGAGGCCTGGGACCNeovison visonNNQGG.v01TTGAGGAAAGTAAGTGCATGGGCCTGGGACCAiluropoda melanoleucaailMel1TTCGAGTGGATGAAAGTGAAGGGAACGCCCUrsus americanusASM334442v1TTCGAGTGGATGAAAGTGAAGGGAACGCCCLoxodonta africanaloxAfr3TTCGAGTGGATGAAGTGAAGGGAACGCCCLoxodonta africanaloxAfr3TTCGAGTGGATGAAGTGAAGGGACGCCClatirostrisproCap1TTCGAGTGGATGAAGTGAAGGGACGCCCProcavia capensisproCap1TTCGAGTGGATGAAGTGAAGGGAAGGCCCDasypus novemcinctusdasNov3TTCGAGTGGATGAAGTGAAGGGAAGGCCCGaleopterus variegatusgalVar1TTCGAGTGGATGAAGTGAAGGGAAGCGCCCGaleopterus variegatusgalVar1TTCGAGTGGATGAAGTGAAGGGAACGCCCCataGaaAAGTAAGTAACTACTGGCCTTGGACGCTAAGAAAAGTAACTACTGGGCCTGGGACGGaleopterus variegatuscalJac3TTCGAGTGGATGAAAGTAAGGAGGCCCCCastor canadensisC. can_genome_v1TTCGAGTGGATGAAGTGAAGGGAACGCCCCastor canadensiscalJac3TTCGAGTGGATGAAGTGAAGGGAACGCCCCastor canadensissiBol1CTAAGAAAGTAACTACTCGCGGCCTTGGATGAhun_2.0CTAAGAAAGTAAGTGCCCGGGCCTTGGATGAhun_2.0CTAAGAAAGTAAGTGCCCGGGCCTTGGATGAhuno sapienshg38TTCGAGTGGATGAAGTGAAGGGAAGCCCCNotus nancymaeAna_2.0CTAAGAAAGTAAGTGCCCGGGCCTTGGATG <td>Feils Calus</td> <td>Telcaly</td> <td>CTAAGAAAA<b>GT</b>AAGTATCTGGGCCTTGGACG</td>	Feils Calus	Telcaly	CTAAGAAAA <b>GT</b> AAGTATCTGGGCCTTGGACG
Paintieta pirudisPaintietaPteropus vampyruspteVamlCTAGGARAAGTAAGTAAGGACCGCCPteropus vampyrusmusFurlTTCCACTGGATGAAAGTAAGGAAGCGCCMustela putorius furomusFurlTTCCACTGGATGAAAGTGAAGGAAGCGCCNeovison visonNNQGG.v01TTCCACTGGATGAAAGTGAAGGAAGCCCCAiluropoda melanoleucaailMellCTAGGAAAGTAAGTGATGAGGACGCCCUrsus americanusASM334442v1CTCGACTGGATGAAGTGAAGGAAGCGCCLoxdonta africanaloxAfr3TTCCACTGGATGAAAGTAAGGAAGCGCCCTAAGAAAGTAAGTACTTGGGCCTTGGACCCTAAGAAAGTAAGTACTTGGGCCTTGGACCLoxdonta africanaloxAfr3TTCCACTGGATGAAAGTAAGGAAGCGCCProcavia capensisproCaplTTCCACTGGATGAAAGTAAGGAAGCGCCCProcavia capensisproCaplTTCCACTGGATGAAAGTAAGGGAACGCCCCCAAGAAAGTAAGTAAGTAAGGAAGCGCCTCTAAGAAAAGTAAGTAAGTGAAGGAACGCCCCCAAGAAAGTAAGTAAGTAAGGAAGCGCCTCCAAGAAAGTAAGTAAGTGAGGAACGCCCGaleopterus variegatusgalVarlTTCCACTGGATGAAAGTAAGGGAACGCCCCastor canadensisC.c.an_genome_vlTCCAGTGGATGAAAGTAAGGGAACGCCCCallithrix jacchuscalJac3TTCCAGTGGATGAAAGTAAGTGAGGGAACGCCCCastor canadensissaiBol1TTCCAGTGGATGAAAGTAAGTGAGGGAACGCCCCallithrix jacchuscalJac3TTCCAGTGGATGAAAGTAAGTGGAGGGACGCCTColos capucinus imitatorCebus initatorTTCCAGTGGATGAAAGTAAGTGGAGGAACGCCC1.0CTAAGAAAGTAAGTGCCCGGGCCTTGGATGAotus nancymaaeAna_2.0CTAAGAAAGTAAGTGCCGGGCCTTGGATGAotus nancymaaeAna_2.0CTAAGAAAGTAAGTGCCCGGGCCTTGGATGPongo abeli	Panthora pardus	PapPar1 0	TTCGAGTGGATGAAAGTGAAGAGGAACGCCC
Pteropus vampyruspteVam1TTCGACTGGATGAAAGTGAAGGGAGCACCAGGGCC CGAGAAAGTAAGTATTTGAGCCAGGGCC GGAAAGTAAGTAAGTGATGGCTGGGCCC CTAGGAAAAGTAAGTGAAGGGCCCGGGACCMustela putorius furomusFur1TTCGAGTGGATGAAGTGAAGGGAAGGCCC CTAGGAAAAGTAAGTGACGCCCGGGCCCCGGACCNeovison visonNNQGG.v01TTCGAGTGGATGAAGTGAAGGGAAGGCCC CTAGGAAAAGTAAGTGATGGCCTGGGACCAiluropoda melanoleucaailMel1TTCGAGTGGATGAAGTGAAGGGAAGGCCC CTAGGAAAAGTAAGTACTTGGGCCTGGGACCUrsus americanusASM334442v1TTCGAGTGGATGAAGTGAAGGGAAGGCCC CTAGGAAAGTAAGTGAAGGGAAGGCCC CTAGGAAAGTAAGTGAAGGGAAGGCCCC Loxodonta africanaloxAfr3Trichechus manatus triMan1TTCGAGTGGATGAAAGTGAAGGGAAGCCCC CTAGGAAAGTAAGTGAAGGGAAGCCCCProcavia capensisproCap1CTAGGAGAAAGTAAGTGAAGGGAGCCCC CTAGGAAAGTAAGTGAAGGGAGGCCCC CTAGGAAAAGTAAGTAAGTGAGGGACGCCC CCAGGAAAAGTAAGTGATGGCCTTGGACABaypus novemcinctusdasNov3TTCGAGTGGATGAAAGTGAAGGGAGCCCC CCAGGAAAAGTAAGTGAAGGGAGGCCCC CCAGGAAAAGTAAGTAAGTGAGGGACGCCC CCAGGAAAAGTAAGTGAAGGCAGGCCCC GGaleopterus variegatusASM303372v1Castor canadensisC.c.an_genome_v1 TTCGAGTGGATGAAAGTGAAGGGAAGCCCC CTAAGAAAAGTAAGTCAGGCAGGGAAGCCCC CTAAGAAAAGTAAGTCAGCGGCCTTGGATC 1.0TTCGAGTGGATGAAAGTGAAGGGAAGCCCCC CTAAGAAAAGTAAGTCAGCGGCCTTGGATC CTAAGAAAAGTAAGTCCCCGGGCCTTGGATG Galisini boliviensissaiBol1TTCGAGTGGATGAAAGTGAAGGGAAGCCCC CTAAGAAAAGTAAGTCCCGCGGGCCTTGGATG CTAAGAAAGTAAGTCCCCGGGCCTTGGATG CTAAGAAAGTAAGTCCCCGGGCCTTGGATG CTAAGAAAGTAAGTCCCCGGGCCTTGGATG CTAAGAAAGTAAGTCCCCGGGCCTTGGATG CTAAGAAAGTAAGTCCCCGGGGCCTTGGATG Fongo abeliiponAbe3TTCCGAGTGGATGAAGTGAAGGGAATGCCT CTAAGAAAGTAAGTCCCCCGGGCCTTGGATG CTAAGAAAGTAAGTCCCCGCGGCCTTGGATG <b< td=""><td>ranchera pardus</td><td>railrail.0</td><td>CTAAGAAAA<b>GT</b>AAGTATCTGGGCCTTGGACG</td></b<>	ranchera pardus	railrail.0	CTAAGAAAA <b>GT</b> AAGTATCTGGGCCTTGGACG
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Aotus nancymaaeAnan_2.0TTCGAGTGGATGAAAGTGAAGAGGAACGCCC CTAAGAAAGTAAGTCCGCGGGCCTTGGATGHomo sapienshg38TTCGAGTGGATGAAAGTGAAGAGGGAAGGCT CTAAGAAAGTAAGTCCGCGGGCCTTGGATGGorilla gorilla gorillagorGor5TTCGAGTGGATGAAAGTGAAGAGGAATGCCT CTAAGAAAGGTAAGTCCGCGGGCCTTGGATGPongo abeliiponAbe3TTCGAGTGGATGAAAGTGAAGAGGAATGCCT CTAAGAAAGGTAAGTCCGCGGGCCTTGGATGPan troglodytespanTro6TTCGAGTGGATGAAAGTGAAGAGGAATGCCT CTAAGAAAGGTAAGTCCGCGGGCCTTGGATAPan paniscuspanPan2TTCGAGTGGATGAAAGTGAAGAGGAATGCCT CTAAGAAAGGTAAGTCCACGCGGGCCTTGGATANomascus leucogenysnomLeu3TTCGAGTGGATGAAAGTGAAGAGAGAGGAATGCCT CTAAGAAAGGTAAGTGAAGAGGAATGCCT	boliviensis	5412011	CTAAGAAAA <b>GT</b> AAGTCCGCGGGCCTTGGATG
Homo sapienshg38TTCGAGTGGATGAAAGTCCGCGGGGCCTTGGATGHomo sapienshg38TTCGAGTGGATGAAAGTGAAGAGGAATGCCT CTAAGAAAG <b>T</b> AAGTCCGCGGGCCTTGGATGGorilla gorilla gorillagorGor5TTCGAGTGGATGAAAGTGAAGAGAGAGAGAATGCCT CTAAGAAAG <b>T</b> AAGTCCGCGGGGCCTTGGATGPongo abeliiponAbe3TTCGAGTGGATGAAAGTGAAGAGGAATGCCT CTAAGAAAG <b>T</b> AAGTCCGCGGGCCTTGGATGPan troglodytespanTro6TTCGAGTGGATGAAAGTGAAGAGAGAATGCCT CTAAGAAAG <b>T</b> AAGTCCGCGGGCCTTGGATAPan paniscuspanPan2TTCGAGTGGATGAAAGTGAAGAGAGAATGCCT CTAAGAAAG <b>T</b> AAGTCCGCGGGCCTTGGATANomascus leucogenysnomLeu3TTCGAGTGGATGAAAGTGAAGAGAAGGCAACGCT	Aotus nancymaae	Anan 2.0	TTCGAGTGGATGAAAGTGAAGAGGAACGCCC
Homo sapienshg38TTCGAGTGGATGAAAGTGAAGAGAGAATGCCT CTAAGAAAGGTAAGTCCGCGGGCCTTGGATGGorilla gorilla gorillagorGor5TTCGAGTGGATGAAAGTGAAGAGAGAGAATGCCT CTAAGAAAGGTAAGTCCGCGGGCCTTGGATGPongo abeliiponAbe3TTCGAGTGGATGAAAGTGAAGAGGAATGCCT CTAAGAAAGGTAAGTCCGCGGGCCTTGGATGPan troglodytespanTro6TTCGAGTGGATGAAAGTGAAGAGGAATGCCT CTAAGAAAGGTAAGTCCACGCGGGCCTTGGATAPan paniscuspanPan2TTCGAGTGGATGAAAGTGAAGAGAATGCCT CTAAGAAAGGTAAGTCCGCGGGCCTTGGATANomascus leucogenysnomLeu3TTCGAGTGGATGAAAGTGAAGAGAGAGAATGCCT CTAAGAAAGGTAAGTGAAGAGAGAGAATGCCT			CTAAGAAAA <b>GT</b> AAGTCCGCGGGCCTTGGATG
Image: ConstructionConstructionGorilla gorilla gorillagorGor5TTCGAGTGGATGAAAGTGAAGAGGAATGCCT CTAAGAAAGGTAAGTCCGCGGGCCTTGGATGPongo abeliiponAbe3TTCGAGTGGATGAAAGTGAAGAGGAATGCCT CTAAGAAAGGTAAGTCCGCGGGCCTTGGATGPan troglodytespanTro6TTCGAGTGGATGAAAGTGAAGAGGAATGCCT CTAAGAAAGGTAAGTCCGCGGGCCTTGGATAPan paniscuspanPan2TTCGAGTGGATGAAAGTGAAGAGGAATGCCT CTAAGAAAGGTAAGTCCGCGGGCCTTGGATANomascus leucogenysnomLeu3TTCGAGTGGATGAAAGTGAAGAGGAATGCCT CTAAGAAAGGTAAGTGAAGAGGAATGCCT	Homo sapiens	hq38	TTCGAGTGGATGAAAGTGAAGAGGAATGCCT
Gorilla gorilla gorillagorGor5TTCGAGTGGATGAAAGTGAAGAGGGAATGCCT CTAAGAAAGGTAAGTCCGCGGGCCTTGGATGPongo abeliiponAbe3TTCGAGTGGATGAAAGTGAAGAGGGAATGCCT CTAAGAAAGGTAAGTCCGCGGGCCTTGGATGPan troglodytespanTro6TTCGAGTGGATGAAAGTGAAGAGGAATGCCT CTAAGAAAGGTAAGTCCGCGGGCCTTGGATAPan paniscuspanPan2TTCGAGTGGATGAAAGTGAAGAGGAATGCCT CTAAGAAAGGTAAGTCCGCGGGCCTTGGATANomascus leucogenysnomLeu3TTCGAGTGGATGAAAGTGAAGAGGAATGCCT CTAAGAAAGGTAAGTCGAGGGATGCCTCCTTGGATG		<u> </u>	CTAAGAAAG <b>GT</b> AAGTCCGCGGGGCCTTGGATG
Pongo abeliiponAbe3TTCGAGTGGATGAAAGTGAAGAGGAATGCCT CTAAGAAAGGTAAGTCCGCGGGCCTTGGATGPan troglodytespanTro6TTCGAGTGGATGAAAGTGAAGAGGAATGCCT CTAAGAAAGGTAAGTCCGCGGGCCTTGGATAPan paniscuspanPan2TTCGAGTGGATGAAAGTGAAGAGGAATGCCT CTAAGAAAGGTAAGTCCGCGGGCCTTGGATANomascus leucogenysnomLeu3TTCGAGTGGATGAAAGTGAAGAGAGAGGAATGCCT CTAAGAAAGGTAAGTCAAGAGAGAGGAATGCCT CTAAGAAAGGTAAGTCGAGGGATGAAGAGGAATGCCT	Gorilla gorilla gorilla	gorGor5	TTCGAGTGGATGAAAGTGAAGAGGAATGCCT
Pongo abeliiponAbe3TTCGAGTGGATGAAAGTGAAGGGAATGCCT CTAAGAAAGGTAAGTCCGCGGGCCTTGGATGPan troglodytespanTro6TTCGAGTGGATGAAAGTGAAGAGGGAATGCCT CTAAGAAAGGTAAGTCCGCGGGCCTTGGATAPan paniscuspanPan2TTCGAGTGGATGAAAGTGAAGAGAGAATGCCT CTAAGAAAGGTAAGTCCGCGGGCCTTGGATANomascus leucogenysnomLeu3TTCGAGTGGATGAAAGTGAAGAGAGAGGAATGCCT CTAAGAAAGGTAAGTCAAGAGGAATGCCT CTAAGAAAGGTAAGTCAAGAGGAATGCCT		5	CTAAGAAAG <b>GT</b> AAGTCCGCGGGGCCTTGGATG
Pan troglodytes panTro6 TTCGAGTGGATGAAAGTGAAGAGGAATGCCT CTAAGAAAGGTAAGTCCGCGGGCCTTGGATA   Pan paniscus panPan2 TTCGAGTGGATGAAAGTGAAGAGGAATGCCT CTAAGAAAGGTAAGTCCGCGGGCCTTGGATA   Nomascus leucogenys nomLeu3 TTCGAGTGGATGAAAGTGAAGAGGAATGCCT CTAAGAAAGGTAAGTCCGCGGGCCTTGGATA	Pongo abelii	ponAbe3	
Pan troglodytes panTro6 TTCGAGTGGATGAAGGGAAGGGAATGCCT   Pan paniscus panPan2 TTCGAGTGGATGAAGGGAAGGGAATGCCT   Nomascus leucogenys nomLeu3 TTCGAGTGGATGAAGGGAAGGGAATGCCT			
Pan paniscus panPan2 TTCGAGTGGATGAAGTGAAGAGGAATGCCT CTAAGAAAGGTAAGTCCGCGGGCCTTGGATA   Nomascus leucogenys nomLeu3 TTCGAGTGGATGAAAGTGAAGAGGAATGCCT CTAAGAAAGGTAAGTCCGCGGCCTTGGATG	Pan troglodytes	panTro6	
Pan paniscus panPan2 IICGAGTGGATGAAGTGAAGGGAATGCCT   Nomascus leucogenys nomLeu3 TTCGAGTGGATGAAGGGAAGGGAATGCCT			
Nomascus leucogenys     nomLeu3     TTCGAGTGGATGAAGGGAAGGGAATGCCT CTAAGAAAGGTAAGTCCGCGGTCCTTGGATG	Pan paniscus	panPan2	
Nomascus leucogenys nomLeu3 CTAAGAAAGGTAAGGGGTCCTTGGATG			
	Nomascus leucogenys	nomLeu3	CTAAGAAAG <b>GT</b> AAGTCCGCGGGTCCTTGGATG

#### Supplementary Table 5, continuing

Species	Genome Assembly	Nucleotide sequence
Cercocebus atys	Caty_1.0	TTCGAGTGGATGAAAGTGAAGAGGAACGCCT CTAAGAAAA <b>GT</b> AAGTCCGCGGGCCTTGGATG
Piliocolobus tephrosceles	ASM277652v2	TTCGAGTGGATGAAAGTGAAGAGGAACGCCT CTAAGAAAA <b>GT</b> AAGTCCGCGGGCCTTGGATG
Theropithecus gelada	Tgel_1.0	TTCGAGTGGATGAAAGTGAAGAGGAACGCCT CTAAGAAAA <b>GT</b> AAGTCCGCGGGCCTTGGATG
Mandrillus leucophaeus	Mleu.le_1.0	TTCGAGTGGATGAAAGTGAAGAGGAACGCCT CTAAGAAAA <b>GT</b> AAGTCCGCGGGCCTTGGATG
Rhinopithecus bieti	ASM169854v1	TTCGAGTGGATGAAAGTGAAGAGGAACGCCT CTAAGAAAA <b>GT</b> AAGTCCGCGGGCCTTGGATG
Colobus angolensis palliatus	Cang.pa_1.0	TTCGAGTGGATGAAAGTGAAGAGGAACGCCT CTAAGAAAA <b>GT</b> AAGTCCGCGGGCCTTGGATG
Rhinopithecus roxellana	rhiRox1	TTCGAGTGGATGAAAGTGAAGAGGAACGCCT CTAAGAAAA <b>GT</b> AAGTCCGCGGGCCTTGGATG
Nasalis larvatus	nasLarl	TTCGAGTGGATGAAAGTGAAGAGGAACGCCT CTAAGAAAA <b>GT</b> AAGTCCGCGGGCCTTGGATG
Chlorocebus sabaeus	chlSab2	TTCGAGTGGATGAAAGTGAAGAGGAACGCCT CTAAGAAAA <b>GT</b> AAGTCCGCGGGCCTTGGATG
Macaca fascicularis	Macaca_fascicul aris 5.0	TTCGAGTGGATGAAAGTGAAGAGGAACGCCT CTAAGAAAA <b>GT</b> AAGTCCGCGGGCTTGGATGG
Macaca mulatta	 Mmul_10	TTCGAGTGGATGAAAGTGAAGAGGAACGCCT CTAAGAAAA <b>GT</b> AAGTCCGCGGGCTTGGATGG
Macaca nemestrina	Mnem_1.0	TTCGAGTGGATGAAAGTGAAGAGGAACGCCT CTAAGAAAA <b>GT</b> AAGTCCGCGGGCTTGGATGG
Papio anubis	papAnu4	TTCGAGTGGATGAAAGTGAAGAGGAACGCCT CTAAGAAAA <b>GT</b> AAGTCCGCAGGCCTTGGATG
Papio hamadryas	papHaml	TTCGAGTGGATGAAAGTGAAGAGGAACGCCT CTAAGAAAA <b>GT</b> AAGTCCGCAGGCCTTGGATG
Sorex araneus	sorAra2	TTCGAGTGGATGAAAGTGAAGAGGAACGCTC CGAAGAAAA <b>GT</b> AAGTACTTGGCCCGTGGACT
Jaculus jaculus	JacJac1.0	TTCGAGTGGATGAAAGTGAAGAGGAACGCCC CGAGGAAAA <b>GT</b> GAGTGGTGGGCGATGGATGG
Thamnophis sirtalis	thaSir1	TTCGACTGGATGAAAGTCAAGAGGAACGCAC CCCCTAAAA <b>GT</b> AAGTGCCGGGGCTTGGTCAA
Notechis scutatus	TS10Xv2-PRI	TTCGAGTGGATGAAAGTCAAGAGGAACGCGC TCCAGAAAA <b>GT</b> AAGTGCGGGGGCTTCGTCGGC
Xenopus tropicalis	xenTro9	TTTGATTGGATGAAAGTTAAAAGGAACCCAC CTAAGAAAA <b>GT</b> AAGTCCTGCCAAGCTTGATA
Xenopus laevis	xenLae2	TTTGATTGGATGAAAGTTAAAAGGAACCCTC CTAAGAAAA <b>GT</b> AAGTTTTTATTAGCGCGAAA
Latimeria chalumnae	LatCha1	TTCGATTGGATGAAGGTTAAAAGAAATCCTC CCAAAACAT <b>GT</b> AAGTCTCGGTACAACAATAA
Nanorana parkeri	nanPar1	TTTGATTGGATGAAAGTTAAACGGAACGCTC CTAAGAAAA <b>GT</b> AAGTACAAAGAGATCCCATT
Conservation		** ** ***** * * * * * * * ** **

Supplementary Table 6. Illumina GoatSNP50 BeadChip genotypes generated for mapping the *POLYCERATE* locus in goat. Wt : "wild type" refers to the presence of two normal horns while "polycerate" refers to the existence of more than two horns. a: in these admixed populations the polycerate phenotype originates from local ancestry.

No	Breed or	Origin of	Origin of	Number of animals		
NO	population	the breed	the samples	All	Wt	Polycerate
1	Local population of Massif Central admixed with African dwarf goat <sup>a</sup>	France	One breeder from the St Etienne area, France	1	-	1
2	Local population of Normandy admixed with Nubian goat <sup>a</sup>	France	Parc Animalier du Beauquet Marais, Normandy, France	5	2	3
3	Provençale	France	One breeder from Moustiers- Sainte-Marie, France	44	31	14
4	Provençale crossbred with Alpine and Saanen	France	UCEA Bressonvilliers, INRAE experimental farm, France	16	11	5
5	Rove admixed with Provençale	France	One breeder from Moustiers-Sainte-Marie, France	3	-	3
6	Population from the German Alps admixed with other breeds <sup>a</sup>	Germany	Tierpark Hamm, North Rhine- Westphalia and one breeder from Asendorf, Lower Saxony, Germany	5	2	3
7	Local population	Italy	One breeder from the Osimo locality, Italy	8	4	4
8	Local population	Macedonia	Two breeders from Radovis and Strumica municipalities, Macedonia	3	1	2
Tota	l			86	51	35

Supplementary Table 7. Informatin on candidate variants for polyceraty in goat and primers used for genotyping. Genotyping was done by PCR and Sanger sequencing on a 5 case-control pairs the panel of for all variants except g.115,652,290 116,155,699delins137kb. For the latter, the genotyping was done on a panel of 77 case and 355 control animals by PCR and electrophoresis, using two primers specific of the wild type (Wt) and mutant (Mut) alleles, respectively and one primer in common. The expected size of the wild type and mutant amplicons are 226 and 197 bp respectively (see Supplementary Fig. 4). Positions refer to ARS1 goat genome assembly. Conservation : "Yes" indicates that the variant affects at least one nucleotide located within a constrained element among 103 eutherian mammals genomes according to Ensembl (www.ensembl.org; release 98) EPO-Low-Coverage track and that this nucleotide is entirely conserved among the 103 species. Genotyping : "Eliminated" refers to variants for which the derived allele was not perfectly associated with polyceraty in the panel studied. \*) Despite five trials with distinct primer pairs we failed to genotype these variants because of lack of PCR amplification or amplification of multiple segments. Therefore these variants are considered as retained by default. NC: not communicated. Cons. : conservation.

Variant	Primer sequences	Cons.	Genotyping
g.115,143,545G>A	CCTTGGCTTGCCTGAATCTC CCAGCCGTATCACAGTCAGA	No	Eliminated
g.115,166,967_115,166,968insT	CGGGAGCAAAAGCCTACATG CTGGAGATGGACGGTCATGA	No	Eliminated
g.115,186,815G>A	CCCGGTTTGATTCCTAGGTT CTTGCAAGATCCTCCGTTTC	No	Eliminated
g.115,213,759G>C	CCTGGCTTGGAGAATTTTGA TGAAGGAACAAGGCTGACCT	No	Retained
g.115,221,938C>T	ATCACAGCGCTATGAGGGTT ACCCTTATTGTGAAATAGGCAGA	No	Retained
g.115,223,871_115,223,871insA	ACTCCAGTAAGTGCAGTCTTCA AGAAAGGAGGCAGCTGTTCT	No	Eliminated
g.115,232,184T>C	CCTGCAGTGTTATTTGGGCA GGCATACATGTGTCAGGCTG	No	Retained
g.115,269,955A>G	TCAGTGCTCAGCCTTCTTCA GTGCCACAACAGCTATCTTCT	No	Retained
g.115,283,205G>A	GCCTGTTCAGAGAATGCCTG TTCTCCCTTCTGGCTCTGTG	No	Eliminated
g.115,285,788C>T	AAGGGCTGCTGTGTCACTAT AATCAACAGTCTCGGCTCCA	No	Eliminated
g.115,319,352A>G	TGAACAAATCCATCAGATGAGTC TCCCTTTCTTTTGTTTCAGCA	No	Eliminated
g.115,337,441C>T	TCGTGTCCAGTCCTAAGCAT GCCATTGACGGATTGAGGAA	No	Retained
g.115,343,411del*	NC	No	Retained by default
g.115,349,841G>T	TTACAAGCCCAACAGTAACTC ATGGGCCGTGTGGGATCA	No	Eliminated
g.115,378,261G>A	TCCTTGTTTCATAATGAGTACT ATAATTTGACCAAAGTCAATGCA	No	Retained
g.115,393,837A>G	GTCTCAGTTCAAAATGGCGGA GTCCCTTTGTCAGATCCCCA	No	Retained
g.115,401,255C>A	ACTTGGAATGCAGAGACAGC TTCCCGTTTGATCTTTCCGC	No	Retained
g.115,406,825A>T	CGCTAACTTCGAAACACTTTGAC CCCAGCGTCCTAAGTGAACT	No	Eliminated
g.115,409,283A>G	GTCCACAACCAGTCAACACC AATCTTCCCTCCCCAGTCAC	No	Retained
g.115,417,698C>A	CTGGGGAAGGTGTTATGGGT TGGGAATCTTTGAGGGCCAT	No	Eliminated

#### Supplementary Table 7, continued

Variant	Primer sequences	Cons.	Genotyping
g.115,422,038T>G	GGAGTCTAGAACCCTGAACCC TCTCCAGCCGTTATCCCTTC	No	Eliminated
g.115,459,737A>G	GGCCTGAGATCCTGTGGTAA CCCTGCGCTATTCAGTAGGA	No	Eliminated
g.115,462,622del	GGCAGCTATAGAATACACTGTGC TGCCATTCTTGTAGGTCCGT	No	Eliminated
g.115,465,345T>A	TAGCACCATGACACCACACT CCTCCATACACAACACAGCG	No	Eliminated
g.115,474,151A>C	CCATTGCTTTTCTGTGCCCT GGGAAAGCTTGGACACGTTT	No	Eliminated
g.115,560,482T>A*	NC	No	Retained by default
g.115,566,277G>A	ATCAGTGTGACAATTGCCCG AGATTTCCAGCACACTCCGA	No	Retained
g.115,570,129_115,570,130 delinsCG	TCTTTGCTTTCCCCTTCCCA CCAGTCAGTACCCACCACAT	No	Eliminated
g.115,620,572A>C	GTTGTATGCGCTGACCTGAG TCCTAGCCAAGTGATCCTGG	No	Eliminated
g.115,621,441C>T	AAGGGCAGTGGACAACATCA AACTCCAAGGTCCTCTGTGC	No	Eliminated
g.115,629,515G>T	CTGGGTCCTTGGGCTCTTTA GTCGCCGTGAGATTCAGTTC	No	Retained
g.115,639,463G>C*	NC	No	Retained by default
g.115,643,117C>T	TTCTGTCCCCTGCATGTCTT GGCTTACATTGTCCCACTGG	No	Eliminated
g.115,644,117T>A*	NC	No	Retained by default
g.115,646,033T>C	GAACAACAAGAACGTGGGCT TTGGCTGGAGAGTTGGATTT	No	Eliminated
g.115,652,290_116,155,699 delins137kb	CTTTCAAAGCAGTGTAATAGGA(Wt) GCATGTCTACATACTTATTTAAG(Mut) AGATATAACAAGAGCAAGACTG(Common)	Yes	Retained

Supplementary Table 8. Details on wild type and polycerate goats phenotyped and genotyped for candidate mutations. Wt: "wild type" refers to the presence of two normal horns while "polycerate" refers to the existence of more than two horns. a: In these admixed populations the polycerate phenotype originates from local ancestry. The whole panel was genotyped for mutation g.115,652,290\_116,155,699delins137kb while numbers between brackets refer to individuals genotyped for the other candidate mutations detailed in Suppl. table 7.

No	Breed or	Origin of	Origin of	Number of animals		
NO	population	the breed	the samples	All	Wt	Polycerate
1	Alpine	France	Multiple breeders from France	30	30	-
2	Corse	France	Multiple breeders from France	30	30	-
3	Local population of Massif Central admixed with African dwarf goat <sup>a</sup>	France	One breeder from the St Etienne area, France	5	-	5
4	Local population of Normandy admixed with Nubian goat <sup>a</sup>	France	Parc Animalier du Beauquet Marais, Normandy, France	7 (2)	2 (1)	5 (1)
5	Poitevine	France	Multiple breeders from France	30	30	-
6	Provençale	France	One breeder from Moustiers- Sainte-Marie, France	76 (2)	45 (1)	31 (1)
7	Provençale admixed with Alpine and Saanen	France	UCEA Bressonvilliers, INRAE experimental farm, France	16	11	5
8	Pyrénéenne	France	Multiple breeders from France	30	30	-
9	Rove admixed with Provençale	France	One breeder from Moustiers- Sainte-Marie, France	4	-	4
10	Population from the German Alps admixed with other breeds <sup>a</sup>	Germany	Tierpark Hamm, North Rhine- Westphalia and one breeder from Asendorf, Lower Saxony, Germany	20 (2)	9 (1)	11 (1)
11	Appenzell	Switzerland	Multiple breeders from the canton of Appenzell, Switzerland	5	5	-
12	Booted goat	Switzerland	Multiple breeders from the canton of St. Gallen, Switzerland	10	10	-
13	Capra grigia	Switzerland	Multiple breeders from the canton of Ticino, Switzerland	10	10	-
14	Grisons striped	Switzerland	Multiple breeders from the canton of Grisons, Switzerland	10	10	-
15	Nera verzasca	Switzerland	Multiple breeders from the canton of Ticino, Switzerland	10	10	-
16	Peacock goat	Switzerland	Multiple breeders from the canton of St. Gallen, Switzerland	10	10	-
17	Saanen	Switzerland	Multiple breeders from France	30	30	-

#### Supplementary Table 8, continued

Breed or		Breed or Origin of Origin of		Nur	of animals	
NO	population	the breed	the samples	All	Wt	Polycerate
18	Toggenburg	Switzerland	Multiple breeders from the canton of St. Gallen, Switzerland	10	10	-
19	Valais blackneck	Switzerland	Multiple breeders from the canton of Valais, Switzerland		10	-
20	Local population	Italy	One breeder from the Osimo locality, Italy	23 (2)	10 (1)	13 (1)
21	Local population	Croatia	Four breeders from the Benkovac municipality, Croatia		22	-
22	Local population	Macedonia	Two breeders from Radovis and Strumica municipalities, Macedonia		4 (1)	3 (1)
23	Angora	Turkey	Multiple breeders from France and Germany	17	17	-
24	Boer	South Africa	Multiple breeders from Switzerland	10	10	-
Total				432 (10)	355 (5)	77 (5)

Supplementary Table 9. Association between the polycerate phenotype and chromosome 2 g.115,652,290\_116,155,699delins137kb in 432 goats. Wt: wild type; Indel: deletion of 503 kb and insertion of 137 kb. a: In these admixed populations the polycerate phenotype originates from local ancestry.

Phonotypo	Brood/Population	Number of animals per genotype			
Flienotype	Breed/F opulation	Wt/Wt	Wt/Indel	Indel/Indel	
	Alpine	30	-	-	
	Corse	30	-	-	
	Local population of Normandy admixed with Nubian goat <sup>a</sup>	2	-	-	
	Poitevine	30	-	-	
	Provençale	45	-	-	
	Provençale admixed with Alpine and Saanen	11	-	-	
	Pyrénéenne	30	-	-	
	Population from the German Alps admixed with other breeds <sup>a</sup>	9	-	-	
	Appenzell	5	-	-	
	Booted goat	10	-	-	
Wild type	Capra grigia	10	-	-	
	Grisons striped	10	-	-	
	Nera verzasca	10	-	-	
	Peacock goat	10	-	-	
	Saanen	30	-	-	
	Toggenburg	10	-	-	
	Valais blackneck	10	-	-	
	Local population from Italy	10	-	-	
	Local population from Croatia	22	-	-	
	Local population from Macedonia	4	-	-	
	Angora	17	-	-	
	Boer	10	-	-	
	Total for wild type animals	355	0	0	
	Local population of Massif Central admixed with African dwarf goat <sup>a</sup>	-	5	-	
	Local population of Normandy admixed with Nubian goat <sup>a</sup>	-	5	-	
	Provençale	-	31	-	
Polycerate	Provençale admixed with Alpine and Saanen	-	5	-	
	Rove admixed with Provençale	-	4	-	
	Population from the German Alps admixed with other breeds <sup>a</sup>	-	11	-	
	Local population from Italy	-	13	-	
	Local population from Macedonia		3	-	
	Total for polycerate animals	0	77	0	
	Grand total	355	77	0	

Supplementary Table 10. Details on caprine and ovine skull specimens considered in the morphometric analyses. "ID" corresponds to the reference of the skull in its collection of origin. ENVA: Musée Fragonard, Ecole Nationale Vétérinaire de Maisons-Alfort, France; Halle: Domestic Animal Collections from the Central Natural Science Collections, Martin Luther University Halle-Wittenberg, Halle, Germany; INRAE: collection of INRAE UMR1313 GABI, Jouy-en-Josas, France; MNHN-ZM-AC: Collection d'anatomie comparée du Muséum National d'Histoire Naturelle, Paris, France; MZS: collection d'anatomie du Musée Zoologique de Strasbourg, France; ONIRIS : collection d'anatomie d'ONIRIS, Nantes, France. The horn formula provides information on the number and localisation of the horns on the left and right sides of the skulls, respectively, separated by a ";". Each "1" designate a horn while brackets indicate fusions between the bases of neighbouring horns. Year: Year of death or of entry in the collection. Juv.: juvenile individuals have between 6 and 12 months of age approximately. Ad.: Adult. Scan: method used for the digitization of the skull, with A: Artec Eva structured-light scanner, B: Breuckmann StereoScan structured light scanner, and P: photogrammetry (see Methods). ND: missing information.

Phenotype, sex & species	Collection-ID	Scan	Horn formula	Breed or population	Year	Age
	MNHN-ZM-AC-1845-266	В	(111);11	ND	1845	Ad.
	ENVA A-IV-N23	В	11;11	Jacob	1903	Ad.
	ENVA A-IV-N25	В	11;11	Jacob	1903	Ad.
	MNHN-ZM-AC-A-12126	В	11;11		1884	Ad.
	MNHN-ZM-AC-A-12127	В	11;11		1884	Ad.
	MNHN-ZM-AC-A-12128	В	11;11		1884	Ad.
	MNHN-ZM-AC-A-12130	В	11;11	Local population	1884	Ad.
	MNHN-ZM-AC-A-12131	В	11;11		1884	Ad.
	MNHN-ZM-AC-A-12132	В	11;11	TUTIISIA	1884	Ad.
	MNHN-ZM-AC-A-12133	В	11;11		1884	Ad.
	MNHN-ZM-AC-A-12195	В	11;111		1902	Ad.
	MNHN-ZM-AC-A-12196	В	11;11		1902	Ad.
	MNHN-ZM-AC-ae781	В	11;11	ND	ND	Ad.
	MZS-Mam-03721	В	11;11	Local population from Erzurum, Turkey	1910	Ad.
Delveerete	MZS-Mam-01566	В	11;11	Unknown	1907	Ad.
Polycerale	MZS-Az15	В	11;11	Jacob	2001	Ad.
male sheep	MZS-Ovi015	В	11;11	Jacob	2003	Juv.
	INRAE-Pachot_M4C_Haie	В	11;11	Jacob	2017	Ad.
	Halle-Ofswi1	A	11;11	Indian fat-tailed	1882	Ad.
	Halle-Ofswi3	A	11;(11)	Indian fat-tailed	1885	Ad.
	Halle-Ofswi8	A	11;(11)	Indian fat-tailed	1888	Ad.
	Halle-Ofswi9	Р	11;11	Indian fat-tailed	1888	Juv.
	Halle-Oprs1	A	11;11	Persian	1899	Juv.
	Halle-Osom72	A	11;11	Somali	ND	Ad.
	Halle-Opru1	A	11;11	Local population from Peru	1883	Ad.
	Halle-Omsr13	A	(111);11	Local population from Masuria, Poland	1894	Ad.
	Halle-Opmm1	A	11;11	Pommeranian sheep	1909	Ad.
	Halle-O20b	A	11;11	German sheep	1888	Ad.
	Halle-Omf183	A	(11);(11)	Mufflon cross	1889	Ad.
	Halle-Our53	P	(11);(11)	Urial x Rambouillet	1891	Juv.
Polycerate	INRAE-Pachot_F4C	В	11;11	Jacob	2017	Ad.
female sheep	Halle-Ojak2	A	11;11	Jacob	1995	Ad.

#### Supplementary Table 10, continued

Phenotype, sex & species	Collection-ID	Scan	Horn formula	Breed or population	Year	Age
	MNHN-ZM-AC-1909-4	В	1;1	Local population from Tunis, Tunisia	1909	Ad.
	MNHN-ZM-AC-1904-200	В	1;1	ND	1904	Ad.
	MNHN-ZM-AC-1945-88	В	1;1	Corsican mouflon	1945	Ad.
	MNHN-ZM-AC-2000-438	В	1;1	Corsican mouflon	1989	Ad.
	MNHN-ZM-AC-A-12151	В	1;1	Corsican mouflon	ND	Ad.
	MNHN-ZM-AC-A-12157		1;1	Local population from Algeria	1852	Ad.
	MNHN-ZM-AC-A-12177	В	1;1	Scottish blackface	1891	Ad.
	MNHN-ZM-AC-A-12187	В	1;1	Local population from Gascony, France	1902	Ad.
	MNHN-ZM-AC-A-12188	В	1;1	Local population from France	ND	Ad.
Wild type	MNHN-ZM-AC-A-12193	В	1;1	Local population from France	1884	Ad.
male sheep	MNHN-ZM-AC-A-12194 B 1;1 from the Mo Massif, Fra		Local population from the Morvan Massif, France	1884	Ad.	
	MNHN-ZM-AC-Astrakan2	В	1;1	Astrakhan	ND	Ad.
	ONIRIS-ENVN_Ouessant	В	1;1	Ouessant	1990	Ad.
	Halle-Ofswi7	A	1;1	Indian fat-tailed	1886	Ad.
	Halle-Okar22	A	1;1	Karakul	1923	Ad.
	Halle-Omf116	A	1;1	Mouflon cross	1888	Ad.
	Halle-Omf138	A	1;1	Mouflon cross	1887	Ad.
	Halle-Omsr15	A	1;1	Mauritian	1895	Ad.
	Halle-Ongr11	A	1;1	Negretti	1882	Ad.
	Halle-Orbag288	А	1;1	Rambouillet x Argali	1906	Ad.
	Halle-Oshl10	A	1;1	Shetland	1904	Ad.
	Halle-Osom71	A	1;1	Somali	1924	Ad.
	Halle-Okar153	A	1;1	Karakul	1930	Ad.
	MNHN-ZM-AC-A-12173	В	1;1	Astrakhan	1884	Ad.
	MNHN-ZM-AC-A-12179	В	1;1	Local population from Iceland	1891	Ad.
Wild type	MNHN-ZM-AC-A-12224	В	1;1	Local population from Mycenae,		Ad.
temale sheep	INRAE-Pachot F2C	В	1;1	Jacob	2017	Ad.
	MNHN-ZM-AC-A-12172	В	1;1	Astrakhan	1884	Ad.
	Halle-O14	А	1;1	Local population from Germany	1899	Ad.

#### Supplementary Table 10, continued

Phenotype, sex & species	Collection-ID	Scan	Horn formula	Breed or population	Year	Age
-	MNHN-ZM-AC-1875-630	В	11;11	ND	1875	Ad.
	MNHN-ZM-AC-1906-141	В	11;11	ND	1906	Ad.
	MNHN-ZM-AC-A-12122	В	11;11	ND	1884	Ad.
	INRAE-Bresson_M4C	В	11;11	Provençale X Alpine	2017	Ad.
Polycerate male goats	MZS-Mam-03727	В	11;11	Unknown, animal raised in the Zoological Garden of Strasbourg	1896	Ad.
	Halle-Csom3	Р	11;11	Somali x German spotted goat	1913	Juv.
	Halle-CSom2	A	11;11 Somali x German spotted goat		1914	Ad.
	Halle-C10	A	11;11	German white goat	2013	Ad.
Delveerete	Halle-C11	A	11;11	German spotted goat	2013	Ad.
female goats	Halle-CohneNr10	A	11;11	German goat	ND	Juv.
lemale goals	MNHN-ZM-AC-A12124	В	11;11	ND	<1884	Ad.
	Halle-Cbz40	Р	11;11	crossbreed#: Bezoar multicross	1991	Juv.
	MNHN-ZM-AC-1884-2144	В	1;1	ND	1884	Ad.
Wild type	MNHN-ZM-AC-1905-276	В	1;1	ND	1905	Ad.
male goats	INRAE-Bresson_M2C	В	1;1	Provençale X Saanen, France	2017	Ad.
	ONIRIS-ENVN_PIS	В	1;1	Saanen	1990	Ad.
	Halle-C15	А	1;1	House goat, Germany	ND	Ad.
Wild type female goats	Halle-C16	А	1;1	House goat, Germany	ND	Ad.
iennane geene	Halle-C19	А	1;1	House goat, Germany	ND	Ad.

Supplementary Table 11. Definition and designation on each side of the skull of the anatomical landmarks and sliding semi-landmarks used in the analyses. Landmarks placement is illustrated in Suppl. Fig. 11.

Landmarks		Definition		
left	right	Definition		
s0	s5	Most dorsal point of the Foramen infraorbitale		
s1	s6	<i>Processus lacrimalis caudalis</i> (Process on Margo supraorbitalis of the lacrimal bone)		
s2	s7	Most dorsal point of the lateral Foramen supraorbitale		
s3	s8	Most caudal point of the fronto-zygomatic suture (sutura frontozygomatica)		
s4	s9	Caudo-lateral point of the temporo-zygomatic suture ( <i>sutura temporozygomatica</i> )		
s10	s11	Most caudal point of the horizontal plate ( <i>lamina horizontalis</i> ) of the palatine bone		
s12	s13	Most caudal point of the <i>Margo interalveolaris</i> , connection with the first premolar tooth		
s14	s64	Neck of the cornual process (collum processus cornualis)		
s15 to s63	S65 to s113	Points s15-s63 (resp. s65-s113) were placed round the suture line between the <i>processus cornualis</i> and the frontal bone, starting with point s14 (resp. s64) and turning in a dextral rotation (resp. sinister rotation) from the orbit and towards the back of the skull. Point s63 (resp. s113) overlays with point s14 (resp. s64) to close the loop. When the animal had four separated horns, landmarks were positioned for the two horns located on the same side as follows: the frontal half circle of the upper horn was made between landmarks s14 (resp. s64) and s29 (resp. s79) ; the latter being ventral on the upper horn and closest to the lower horn. Then landmark s30 (resp. s80) was placed just opposite, on the lower horn (at the most dorsal level of it). Landmarks s31 (resp. s81) to s50 (resp. s100) were positioned on the lower horn, turning forward and downward, then coming back up. Landmark s50 (resp. s100) was set to landmark s30 (resp. s80) to close the loop. Then Landmark s51 (resp. s81) was positioned on landmark s29 (resp. s79) of the upper horn and the last half circle was completed on the caudal part of the upper horn with landmarks s51 (resp. s101) to s63 (resp. s113).		
s114	s115	Most medial point of the fronto-nasal suture (sutura frontonasalis)		

Supplementary Table 12. List of four-horned polycerate male sheep genotyped for the causative mutation and phenotyped for the distance between the lateral horns on the left side (dlhl) and for the distance between the upper horns (duh).

		Hetero Polyc	zygous :erate	Homoz Polyc	zygous erate	Total
No	Breed or population	Dlhl ≤ duh	Dlhl > duh	Dlhl ≤ duh	Dlhl > duh	
1	Jacob	11	-	1	6	18
2	Manx Loaghtan	2	-	-	4	6
3	Ouessant admixed with Jacob	2	-	-	-	2
4	Ovino Quadricorna	2	-	-	1	3
	Total	17	0	1	11	29

Supplementary Table 13. Details on whole genome sequences considered in the present study. Ovine and caprine control individuals collected for the present analyses originate from all around the world. a) 401 individuals from the original dataset were not considered : one Navajo-Churro and two Tibetan animals with unknown phenotypes were eliminated because of the occurrence of polycerate animals in these breeds, as well as 398 animals of unknown or composite breeds. b) These animals belong to the Chinese Sishui Fur sheep breed.

Species	ecies NCBI Bioproject or url		Nb of cases	Nb of controls
Goat	www.goatgenome.org/vargoats_data_access.html	VCF	-	1160
Guat	PRJEB39341	FASTQ	1	-
Total for	goat		1	1160
	PRJEB6025	VCF	-	180
	PRJEB6495	VCF	-	14
	PRJEB9911	FASTQ	-	3
	PRJEB14098	FASTQ	-	7
	PRJEB14418	FASTQ	-	24
	PRJEB15642	VCF	-	10
	PRJEB23437	VCF	-	99
Sheep	PRJEB31241	VCF	-	535ª
	PRJEB31930	FASTQ	-	6
	PRJEB32110	FASTQ	-	26
	PRJEB35553	FASTQ	-	2
	PRJEB35682	FASTQ	-	20
	PRJEB37460	FASTQ	-	3
	PRJNA624020	FASTQ	10 <sup>b</sup>	250
	PRJEB39341	FASTQ	1	-
Total for	sheep		11	1179

**Supplementary Table 14. Information on transgenic mouse strains and details on PCR primers used for genotyping purpose.** Mut: amplicon encompassing Chr2 g.74,768,587\_75,133,794del (mutant allele) ; Wt: segment encompassing the proximal breakpoint of Chr2 g.74,768,587\_75,133,794del (wild type allele).

Name of the strain	Name in original publication	Reference	Primer sequences
Hoxd1 <sup>Lac</sup>	Hoxd1 <sup>tm1Ddu</sup>	Zákány <i>et al.</i> , 2001	GAGTTTCTCTTTGCTGTAATGAAGAGCT TCACATTCTCCACGGGCAAGCC
BAC <sup>HoxD</sup>	TgBAC <sup>HoxD</sup>	Schep <i>et al.</i> , 2016	ACAGCTGCCTCTGTGGCCTC ATTACGCCAGCTGGCGAAAGGG
BAC <sup>Mtx2</sup>	-	This work	ACAGCTGCCTCTGTGGCCTC ATTACGCCAGCTGGCGAAAGGG
HoxD <sup>Del(151kb)la</sup> c	Del(tpSB2-attP)	Andrey <i>et al.</i> , 2013	ACTAGCCAGATCCAATGGACC CTATTACGCCAGCTGGCGAAAGG
HoxD <sup>Del(365kb)</sup>	-	This work	GCCTGCACCTATGCAGTTTGAAAGG CTCACAGAGTTCCTTAAACACTCCGAG (Mut) CTGTTGAGTACATCCTATCATCAGGAGC CTCAAAGTTGGGAGAAAGCAACAGTGC (Wt)

Supplementary Table 15. Details on PCR primers used for confirming the nucleotide sequence at the fusion points of variant g.115,652,290\_116,155,699delins137kb. See Supplementary Fig. 3 for a scheme of the segments involved in the mutation and the corresponding fusion points identified with letters A to D.

Fusion point	Primer sequences
A	GTTTAAAAGGTGGGGGAAGG/GTTTCAGGCATGCAACACAG
B,C,D	CATCCTGCAGCCTGTGAGTA/GGTGTCATCCCCTGTCTCAG

#### Supplementary Table 16. Details on primers used for quantitative RT-PCR analyses.

Species	Name of gene and primer pairs	Primer sequences	Amplicon size in bp
Sheep	OAR_HOXD1_exon2	GTTGGCTATCTCGATGCGTC GATCCGCACGAATTTCAGCA	100
Sheep	OAR_HOXD1_intron1	GCTCCTTCCGGCAATTTTCT CGGTTTGGGTCTTATGGGGA	107
Goat	CHI_HOXD1_exon2	CCCTTCCCGTTCCCTTTTCT GACGCATCGAGATAGCCAAC	101
Sheep	OAR_HPRT1	GCCACCCATCTCCTTCATCA TGCTGAGGATTTGGAGAAGGT	94
Goat	CHI_HPRT1	TGGACTAATTATGGACAGGACCG TATAGCCCCCCTTGAGCACA	101
Sheep	OAR_H2AFZ	TAAAGCGTATTACCCCTCGTCA CACCACCAGCAATTGTAGCC	90
Goat	CHI_H2AFZ	GCGTATTACCCCTCGTCACTTG CAGCAATTGTAGCCTTGATGAGA	80
Both	GAPDH	CACTACCATGGAGAAGGCTGG GTGGTTCACGCCCATCACA	106
Both	YWHAZ	GGAGCCCGTAGGTCATCTTG CTCGAGCCATCTGCTGTTTTT	85
Both	RPLP0	TCTCCTTCGGGCTGGTCAT AGGAAGCGGGAATGCAGAGT	100

### **Supplementary Note 1**

# Absence of homozygous mutants at variant g.115,652,290\_116,155,699delins137kb amongst 77 polycerate goats.

Despite a continuous selection for polyceraty in most of the sampled herds, homozygous polycerate observed amongst mutants were never 77 animals for variant g.115,652,290 116,155,699delins137kb. Based on breeders' records, 14 of these goats were born from two polycerate parents while the other individuals were born from wild type x polycerate mating or from unknown sire with polycerate dam (i.e. when several mature males of different phenotypes are present in the same herd). Assuming that all the parents were heterozygous for variant g.115,652,290 116,155,699delins137kb, a Mendelian transmission would have generated 33% (i.e. 25%/(50% + 25%)) of homozygous mutant animals amongst the 14 polycerate goats born from polycerate parents. Considering a binomial law with parameters n=14 and p=0.33, the probability of not observing any homozygote is:  $3.4 \times 10^{-3}$ .

This strong presumption of homozygous lethality was supported by the analysis of a 365-kb deletion in mouse (g.74,768,587\_75,133,794del on Chr2; murine genome assembly mm10), largely overlapping the orthologous 503-kb genomic segment absent in polycerate goats (g.115,652,290\_116,155,699delins137kb on Chr2; **Fig. 1** of this note). Genotyping this variant at birth, in 42 animals derived from heterozygous parents did not identify any homozygous condition for the mutant allele, while at least 25% were expected (binomial p=5.7 x  $10^{-6}$  with parameters n=42 and p=0.25; **Table 1** of this note).

Mtx2 is the only protein-coding gene affected by the two deletions and morpholino knockdown of this gene in zebrafish is lethal at gastrulation (Wilkins et al. 2008). Altogether, these results indicate that the lack of Mtx2 causes early embryonic death, which explains the absence of live homozygous mutants amongst the caprine and murine panels studied.



**Fig. 1 of Suppl. Note 1. Details on the 365-kb deletion encompassing** *Mtx2* **in mouse.** Murine and caprine orthologous segments of chromosome 2 with relative localizations of mouse g.74,768,587\_75,133,794del and goat g.115,652,290\_116,155,699delins137kb variants. Mouse and goat icons were made by "Monkik" from www.thenounproject.com.

Number			
Wt/Wt	Wt/Del	<b>Del/Del</b>	Total
12	30	0	42

**Table 1 of Suppl. Note 1.** Results of the genotyping at birth of 42 mice born from mating between animals that were heterozygous for a 365-kb deletion encompassing Mtx2.

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