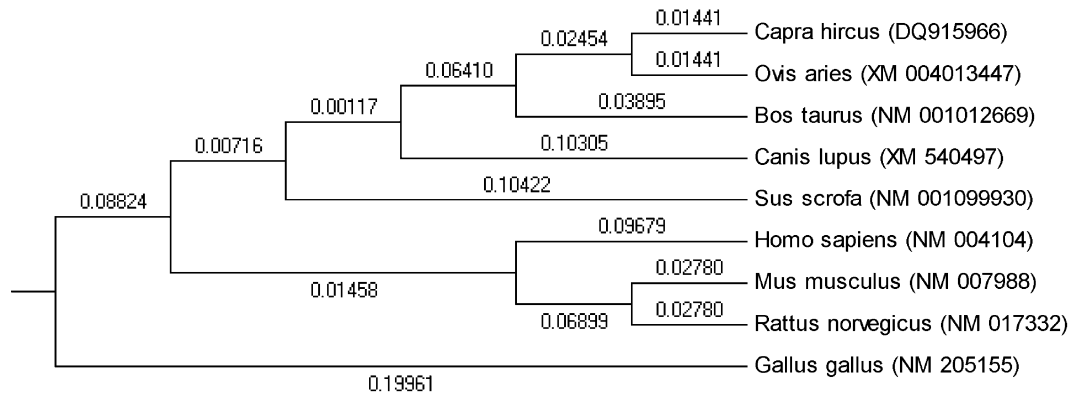


Supplementary table S1 Cloning primers sequences and related information

Fragment name	Primer name	Primer sequence (5' to 3')	Anneal temperature (°C)	Extension time (min)	Size(bp)
KS	KS-F	GAGCAGCCATGGAGGAGGTGGTGA	60°C	1.5	1052
	KS-R	CAGGGACAGCAGCACCTTGGCCAG			
MAT	MAT-F	CTGGCCAAGGTGCTGCTGTCCCTGGAGCACG	72°C	1.5	1449
	MAT-R	CGGGGAGCTGGGAACTCCACAGGTGGGAAC			
DH-ACP	DH-F	GTC AACCCCAACGGGCTGTTCCACCTG	68°C	4.5	4356
	ACP-R	GCTGTGGAACACGGTGGTGGAGCCCTCG			
TE	TE-F	GGGCTCCACCACCGTGTTC	63°C	1	787
	TE-R	AGGCCTAGCCCTCCCGCACGC			
3'-UTR	FN3W	GGGCTCCACCACCGTGTTC	62°C	1.5	1250
	FN3N	GCAGGCCCCAGCAGAGCGCAG	61°C	1.5	
5'-UTR	FN5W	CTCACACCCACCCAGACACCG	60°C	1	360
	FN5N	CCTCGTAGGCGACCTCCAGCA	60°C	1	
	FN5N2	GGCGACCTCCAGCAGCAAGCGG	64°C	1	



Supplementary figure S1. Prediction of Exons and functional domains of FASN cloned from the goat mammary gland. Goat *FASN* gene includes 42 exons represented by 7 function domains, in which three catalytic domains in the N-terminal section (KS, MAT and DH) were separated by a core region from four C-terminal domains (ER, KR, ACP and TE). The sheep FASN gene contains 41 exons (XM004013447).



Supplementary figure S2. Phylogenetic dendrogram obtained by distance matrix analyses of FASN from 9 species. Phylogenetic tree based on FASN amino acid sequences made with MEGA 5.05 software using Neighbor-Joining (NJ) Method. The length of branch indicates evolutionary distance with its scale being 0.05. GenBank accession numbers of *FASN* gene are listed behind corresponding species.