Appendix II

SENCKENBERG
world of biodiversity

Centre for Wildlife Genetics

1/1

Genetic Certificate Eurasian Lynx (*Lynx lynx*)

Gelnhausen, 28.01.2022

Individual identification			
ESB#	**DWV ID**	**GAN**	**Transponder**
3262		CHM16-00787	
Local ID	**Animal name**	**Sex**	**Genotype ID**
KA0284	Emily	female	Z_LL065w
Birth date (dd.mm.yyyy)	**Birth location**	**Sire (ESB#)**	**Dam (ESB#)**
17.05.2016	Karlsruhe (Zoologischer Staatgarten), Germany	2911	2678

Samples

Genetic results received from 2 sample(s) collected by Karlsruhe (Zoologischer Stadtgarten), Germany.

Sample type(s): scat ☐ hair ☒ saliva ☐ blood ☒ tissue ☐

Genetic results

Utilised genetic marker system: SNP ☒ STR ☒ mtDNA ☒

Mitochondrial haplotype: 4 → characteristic for *L. lynx carpathicus*, occasionally in Baltic *L. lynx lynx*

Reference: Helborg, L., Walker, C. W., Rueness, E. K., Stacy, J. E., Kojola, I., Valdmann, H., Vila, C., Zimmermann, B., Jakobsen, K. J. & Ellegren, H. (2002). *Differentiation and levels of genetic variation in northern European lynx (Lynx lynx) populations revealed by microsatellites and mitochondrial DNA analysis.* Conservation Genetics, 3(2), 97-111; Rueness, E. K., Naidenko, S., Trosvik, P., & Stenseth, N. C. (2014). *Large-scale genetic structuring of a widely distributed carnivore-the Eurasian lynx (Lynx lynx).* PloS one, 9(4), e93675.

96 SNPs (Single Nucleotide Polymorphisms) genotype (call rate: ?? % successfully genotyped):

Marker#																														
Genotype																														
Marker#																														
Genotype																														
Marker#																														
Genotype																														

References: Mueller, S. A., Prost, S., Anders, O., Breitenmoser-Würsten, C., Kleven, O., Klinga, P., Konec, M., Kopatz, A., Krojerova-Prokesova, J., Middelhoff, T. L., Obber-Ruff, O., Reners, T. R., Schmidt, K., Sindičić, M., Skrbinšek, T., Tám, B., Saveljev, A. P., Naranbaatar, G. & Nowak, C. (2022). *Genome-wide diversity loss in reintroduced Eurasian lynx populations urges immediate conservation management.* Biological Conservation, 266, 109442.

19 STRs (Short Tandem Repeats, microsatellites) genotype (call rate: ?? % successfully genotyped):

Marker#																			
Genotype																			

Reference: Mueller SA, Reiners TE, Middelhoff L, Anders O, Nowak C (2020) The rise of a large carnivore population in Central Europe: Genetic evaluation of lynx reintroduction in the Harz Mountains. Conservation Genetics 21, 577-587

Genetic assignment: ***L. lynx carpathicus*** **(assignment probability: based on SNPs: 1.0; based on STRs: 1.0)**

Population/lineage/subspecies assignments are estimates and dependent i. a. on the predefined reference group. Assignment test were done using the software ADMIXTURE with reference samples from Carpathian, Baltic, Scandinavian and Siberian lynx.
Reference: Alexander DH, Novembre J, Lange K (2009). Fast model-based estimation of ancestry in unrelated individuals. Genome Research, 19:1655-1664, 2009.

Sex determination: female Result based on: SNPs (3 markers) ☒ STR (2 markers) ☒

Additional Comments: _____

Contact:

Senckenberg Research Institute
Center for Wildlife Genetics
Clamecystraße 12
63571 Gelnhausen
Germany

forschung.wildtiergenetik@senckenberg.de

Genetic analyses were conducted by the Center for Wildlife Genetics, Senckenberg Research Institute and Natural History Museum Frankfurt. The Center serves as German reference laboratory for genetic analyses of large carnivores. Samples are permanently stored at Senckenberg. These results were reported to the Eurasian Lynx ESB and DWV.