

**Table S5. Summary of the number of reads and sequence capture efficiency.**

Sample ID	Species/Subspecies	Number of reads after mapping and duplicate removal	Percentage of reads mapping to targets <sup>a</sup>	Mean read depth among targeted positions	Percentage of targeted positions with at least one mapped read	Percentage of targeted positions with a sequence coverage $\geq 8X$
HUE52	<i>O. c. algirus</i>	17,506,287	0.17	40	0.998	0.974
PAN2	<i>O. c. algirus</i>	16,022,802	0.16	33	0.999	0.963
PED8	<i>O. c. algirus</i>	14,159,013	0.18	34	0.998	0.964
PED16	<i>O. c. algirus</i>	13,204,738	0.20	34	0.998	0.969
PFR11	<i>O. c. algirus</i>	13,263,605	0.17	30	0.998	0.956
PFR15	<i>O. c. algirus</i>	16,326,838	0.17	37	0.998	0.972
LLE10	<i>O. c. cuniculus</i>	18,203,833	0.18	44	0.999	0.977
LLE11	<i>O. c. cuniculus</i>	8,344,822	0.18	20	0.996	0.895
ZRG2	<i>O. c. cuniculus</i>	11,125,191	0.17	26	0.998	0.934
ZRG3	<i>O. c. cuniculus</i>	18,488,930	0.15	35	0.986	0.859
ZRG7	<i>O. c. cuniculus</i>	14,836,863	0.17	35	0.998	0.967
ZRG13	<i>O. c. cuniculus</i>	18,062,081	0.17	42	0.999	0.978
LT2012	<i>Lepus timidus</i>	7,520,483	0.20	19	0.945	0.832*

<sup>a</sup>After duplicate removal.

\*Sequence coverage higher than 4X.