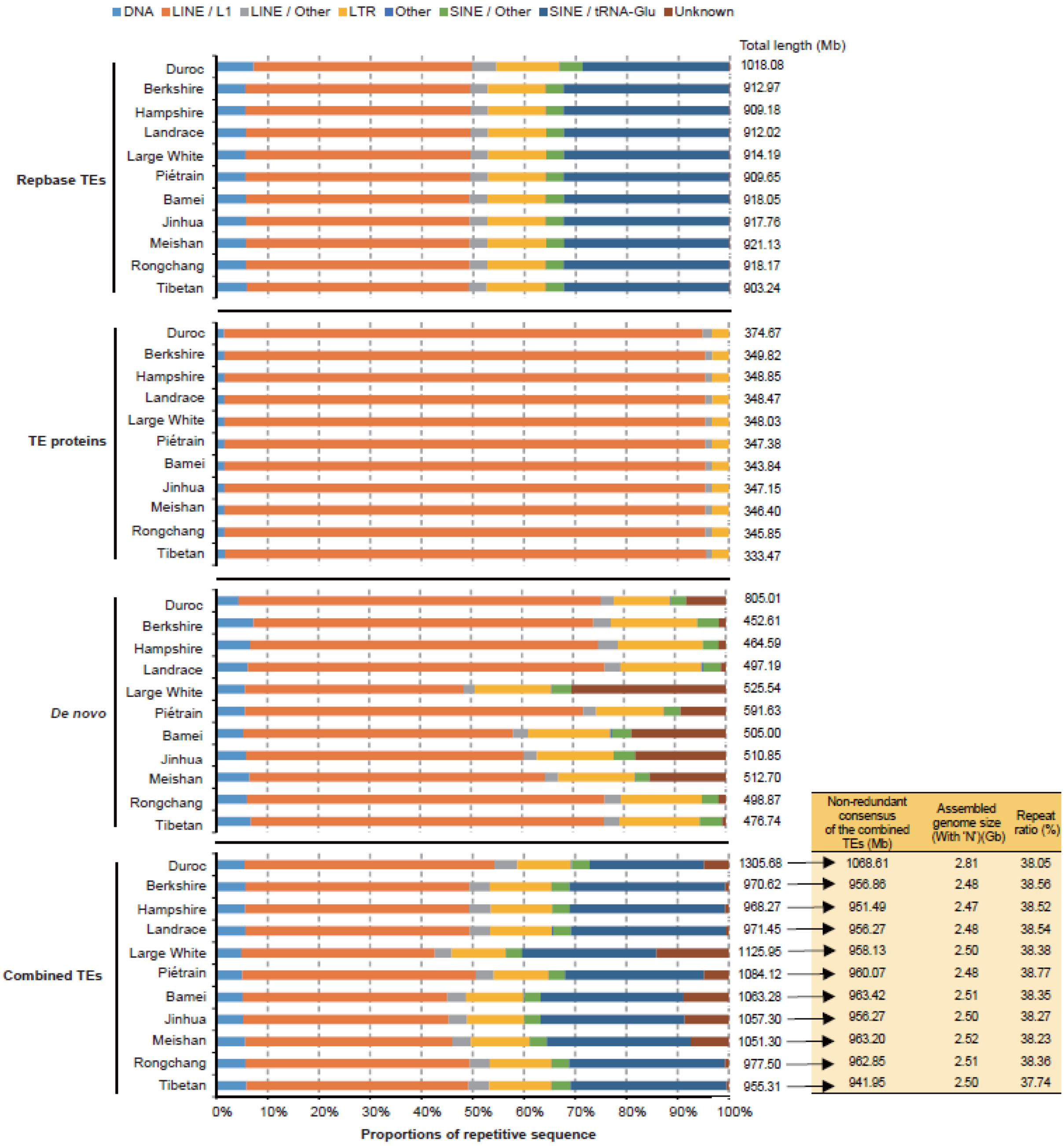

Non-redundant consensus of the combined TEs (Mb)	Assembled genome size (With 'N')(Gb)	Repeat ratio (%)
1068.61	2.81	38.05
956.86	2.48	38.56
951.49	2.47	38.52
956.27	2.48	38.54
958.13	2.50	38.38
960.07	2.48	38.77
963.42	2.51	38.35
956.27	2.50	38.27
963.20	2.52	38.23
962.85	2.51	38.36
941.95	2.50	37.74

Supplemental Fig. S5. Statistics of repeats in pig genomes. Repbase TEs: results of RepeatMasker analysis using Repbase. TE proteins: results of RepeatProteinMask analysis using Repbase. *De novo:* results of RepeatModeler analysis using the library predicted by the *de novo* method. Combined TEs: the combined results for all repeat prediction/classification methods employed (i.e. Repbase TEs, TE proteins, and the *de novo* methods). Other: repeats classified by RepeatMasker, which are not included in other groups; Unknown: predicted repeats that cannot be classified by RepeatMasker. LINE, long interspersed nuclear elements; LTR, long terminal repeat; SINE, short interspersed nuclear elements. The repeat ratio (%) was calculated by the total length of non-redundant consensus of combined TEs against the size of the assembled genomes (With 'N, unidentified nucleotides).