

Supplemental Table S6. Evaluation of the completeness of assembled pig genomes using 248 core eukaryotic genes (CEGs, v.2.5) mapping approach.

Species	Breed	Complete				Partial			
		No. of mapped proteins	Completeness (%)	Total	Paralogy index (%)	No. of mapped proteins	Completeness (%)	Total	Paralogy index (%)
Pig	Berkshire	225	90.73	309	26.22	235	94.76	397	40.43
	Bamei	218	87.90	294	26.61	232	93.55	388	41.38
	Hampshire	227	91.53	313	26.43	238	95.97	398	41.18
	Jinhua	223	89.92	305	27.35	235	94.76	397	42.13
	Landrace	222	89.52	310	28.38	235	94.76	397	40.43
	Large white	227	91.53	311	26.87	236	95.16	400	41.53
	Meishan	232	93.55	309	23.71	239	96.37	384	36.82
	Piétrain	224	90.32	313	28.12	237	95.56	396	40.51
	Rongchang	230	92.74	317	27.83	240	96.77	401	41.25
	Tibetan wild boar	222	89.52	311	28.83	236	95.16	412	44.92
	Reference genome	204	82.26	305	32.35	227	91.53	402	44.49
	Cow	229	92.34	346	30.13	237	95.56	429	43.46
Sheep	224	90.32	339	31.70	236	95.16	435	44.49	

“Complete” indicates that proteins from 248 core eukaryotic genes (CEGs, v.2.5)⁴⁴ were covered by the genome assembly with an alignment length longer than 70%. “Partial” indicates that CEG proteins were covered by the assembly with a coverage rate that exceeded a pre-computed minimum alignment score. “Number of mapped proteins” indicates number of 248 ultra-conserved CEGs present in genome. “Completeness (%)” indicates percentage of 248 ultra-conserved CEGs present. “Total” indicates the total number of CEGs present including putative orthologs. “Paralogy index (%)” indicates the proportion of mapped CEGs that have more than one ortholog.