Table S2 Gene Ontology (GO) terms and KEGG pathways enriched ($P < 0.05$) based on annotated genes within ROH islands for the chestnut Noriker sample

Category	**Term**	**p-value**	**Genes**	**Fold Enrichment**	**Bonferroni adjusted p-value**
Biological process	GO:0048704~embryonic skeletal system morphogenesis	<0.001	*HOXB3*, *HOXB1*, *PCGF2*, *HOXB2*, *HOXB7*, *HOXB8*, *HOXB5*, *HOXB6*	47.73	0.000
	GO:0009952~anterior/posterior pattern specification	<0.001	*HOXB3*, *HOXB1*, *PCGF2*, *HOXB2*, *HOXB7*, *HOXB8*, *HOXB5*, *HOXB6*	22.09	0.000
	GO:0021570~rhombomere 4 development	0.011	*HOXB1*, *HOXB2*	184.97	0.917
	GO:0010482~regulation of epidermal cell division	0.016	*KDF1*, *SFN*	123.31	0.976
	GO:0043410~positive regulation of MAPK cascade	0.025	*CDK10*, *BANK1*, *NGFR*	12.06	0.997
	of GO:0045606~positive regulation epidermal cell differentiation	0.032	*KDF1*, *SFN*	61.66	0.999
	GO:0021612~facial nerve structural organization	0.042	*HOXB1*, *HOXB2*	46.24	0.999
	GO:0003334~keratinocyte development	0.042	*KDF1*, *SFN*	46.24	0.999
Cellular component	GO:0005776~autophagosome	0.013	*OSBPL7*, *CALCOCO2*, *PIP4K2B*	16.71	0.670
Molecular function	GO:0003700~transcription factor activity, sequence-specific DNA binding	0.002	*ZNF304*, *KAT7*, *HOXB2*, *HOXB7*, *HOXB8*, *HOXB6*, *ZFAT*, *TCF25*	4.32	0.139
	GO:0043565~sequence-specific DNA binding	0.037	*HOXB1*, *HOXB2*, *HOXB7*, *HOXB6*, *HOXB13*	3.89	0.931
KEGG pathway	ecb03010:Ribosome	0.049	*MRPL10*, *RPL23*, *RPL13*	7.98	0.864