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we found that the snp that associates with ear type is also most significantly associated with body mass in the same direction (additional file 10 : figure s3). although these effects were measured in the same tissue, they do not appear to be caused by the same causal mutation or otherwise in linkage disequilibrium. the snp that associates with body mass has very low coverage in the sequence capture sequencing data, and is therefore represented by a single snp in the whole genome sequence data. however, the snp that associates with ear type has some representation in both data types, but the allele frequencies are significantly different in the sequence capture data (fisher's exact test p

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here we performed targeted sequencing of the pax8 gene in 30 of the same dogs, which showed the most extreme ear type phenotypes in our dataset. the three samples with the most extreme drop ears had the following pax8 genotypes: 'a/t', 'c/a' and 't/t', suggesting the 'a' allele is associated with the drop ear type. similarly, the two samples with the most extreme prick ears had the following pax8 genotypes: 'g/t' and 't/t', suggesting the 't' allele is associated with the prick ear type. the remaining sample with the most extreme prick ear had the pax8 genotype 't/t', suggesting that this genotype is either associated with the prick ear type or is not associated with any specific ear type phenotype in this individual. the pax8 gene was therefore associated with two distinct traits in our data: ear morphology and body mass, suggesting that this gene is involved in the regulation of both traits. we also found that pax8 is located within the top 1% of genes most strongly associated with body mass (table 3). these data therefore indicate that the snp associated with ear type is on the long haplotype that is also associated with body mass (rs9346728). by contrast, the snp associated with body mass is on a separate haplotype that shows little overlap with that associated with ear type and has likely been influenced by selection acting independently of the selection driving the formation of the breeds with non-drop ears. we therefore searched for additional features that might indicate

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a role for this region in the phenotypes considered in this study. the two haplotype blocks that associate with ear type and body mass are conserved across the genomes of canids (chimpanzee, dog, wolf, jackal, coyote, and bush dog) in the region of cfa10 ( ). we also compared the sequences in this region in several other dog breeds, namely pug, chinese shar pei, shih tzu, tibetan mastiff, giant schnauzer, australian cattle dog, old english sheepdog, miniature pinscher, and japanese spitz. this suggests that this region is under selection in dog breeds with non-drop ears and is not shared with any other breed with drop ears (additional file 6 : figure s5). 5ec8ef588b

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