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Data Article

Dataset of TWIST1-regulated genes in the cranial mesoderm and a transcriptome comparison of cranial mesoderm and cranial neural crest

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ABSTRACT

This article contains data related to the research article entitled "Transcriptional targets of TWIST1 in the cranial mesoderm regulate cell-matrix interactions and mesenchyme maintenance" by Bildsoe et al. (2016) [1]. The data presented here are derived from: (1) a microarray-based comparison of sorted cranial mesoderm (CM) and cranial neural crest (CNC) cells from E9.5 mouse embryos; (2) comparisons of transcription profiles of head tissues from mouse embryos with a CM-specific loss-of-function of *Twist1* and control mouse embryos collected at E8.5 and E9.5; (3)

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ChIP-seq
Embryo
Cranial mesenchyme
Craniofacial

ChIP-seq using a TWIST1-specific monoclonal antibody with chromatin extracts from TWIST1-expressing MDCK cells, a model for a TWIST1-dependent mesenchymal state.

Specifications Table

Subject area	Biology
More specific subject area	Developmental Biology
Type of data	Tables
How data was acquired	Illumina Mouse WG-6 v2 arrays; Chromatin-immunoprecipitation and next generation sequencing
Data format	Analyzed
Experimental factors	Samples for microarray analysis were collected from either FACS sorted GFP-positive embryonic head tissues, or whole embryo heads. Chromatin for ChIP-seq was collected from MDCK cells over-expressing human *TWIST1.*
Experimental features	Transcriptome comparison between sorted E9.5 cranial mesoderm (CM) and neural crest cells. *Twist1* conditional knockout and control tissues (E8.5 & E9.5). TWIST1 genomic binding sites in MDCK cells.
Data source location	Children's Medical Research Institute, Sydney Medical School, University of Sydney, Australia
Data accessibility	The microarray and ChIP-sequencing data within this article are accessible in GEO under accession number GEO: GSE80663. http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE80663

Value of the data

- The data set provides an important reference for all studies investigating *Twist1* function in the context of development and cancer.
- By comparing the transcriptome of the cranial mesoderm and cranial neural crest, the data set provide a useful tool for studying the complex process of craniofacial development.
- The data set potentially contributes to the identification of genes that control the mesenchymal cell state in development and cancer.

1. Data

Dissociated craniofacial tissues that were FACS-sorted by GFP expression reporting either *Mesp1*-Cre or *Wnt1*-Cre activity were compared using microarrays (Supplementary Tables 1 and 2). Dissected embryo heads of control (*Twist1*$^{flox/+}$), heterozygote (Twist1$^{del/+}$), mesoderm heterozgote (*Twist1*$^{flox/+}$; *Mesp1*$^{Cre/+}$) and conditional knockout (*Twist1*$^{flox/del}$; *Mesp1*$^{Cre/+}$) (Supplementary Tables 3 and 4) genotypes were compared using microarrays. Chromatin immunoprecipitation using an anti-TWIST1 antibody was performed on MDCK cells that express human *TWIST1* (Supplementary Table 5).

2. Experimental design, materials and methods

2.1. Isolation and analysis of CM and CNC populations

Embryo were collected at E9.5 from *Mesp1*-Cre x Z/EG (for CM) and *Wnt1*-Cre x Z/EG (for CNC) [2–4]. Heads were dissected below the first branchial arch, dissociated and prepared for cell sorting as