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Genomics Data

Data in Brief

Genome-wide copy number profiling of mouse neural stem cells during differentiation

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ABSTRACT

There is growing evidence that gene amplifications were present in neural stem and progenitor cells during differentiation. We used array-CGH to discover copy number changes including gene amplifications and deletions during differentiation of mouse neural stem cells using TGF-ß and FCS for differentiation induction. Array data were deposited in GEO (Gene Expression Omnibus, NCBI) under accession number GSE35523. Here, we describe in detail the cell culture features and our TaqMan qPCR-experiments to validate the array-CGH analysis. Interpretation of array-CGH experiments regarding gene amplifications in mouse and further detailed analysis of amplified chromosome regions associated with these experiments were published by Fischer and colleagues in Oncotarget (Fischer et al., 2015). We provide additional information on deleted chromosome regions during differentiation and give an impressive overview on copy number changes during differentiation induction at a time line.

Specifications	
Organism/cell line/tissue	*Mus musculus*
Sex	n.d.
Sequencer or array type	NimbleGen 720K mouse whole genome tiling arrays.
Data format	Raw data: PAIR file, analyzed data: txt file
Experimental factors	SFME cells vs normal mouse genomic DNA, SFME cells grown as spheres and after differentiation induction using TGF-ß or FCS
Experimental features	SFME cells were grown as spheres for undifferentiated state. Differentiation was induced by withdrawal of EGF and addition of TGF-ß or FCS. Array-CGH experiments were done with undifferentiated cells, 24 h-TGF-ß differentiation induced cells and 12 h-FCS differentiation induced cells.
Consent	n/a
Sample source location	SFME cells (CRL-9392™) from ATCC

1. Direct link to deposited data

Deposited data can be found here: http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE35523.

2. Experimental design, materials and methods

2.1. Cell culture and differentiation

SFME cells cultured in the absence of fibronectin formed spheres and served as non-differentiated controls. SFME cells were seeded on fibronectin-coated cultureware and allowed to grow for 18 h prior to differentiation induction with TGF-β or FCS. SFME cells were differentiation induced using above supplemented ATCC DMEM:F12 Medium containing TGF-β (10 ng/ml) for 8 h, 12 h and 24 h or DMEM:F12 supplemented with FCS for 8 h, 12 h and 24 h.

Cells were harvested and cell pellet was frozen before proceeding to DNA extraction as described previously (Fischer et al., 2014 genomics data) [1].

2.2. Array-CGH data analysis

Array data were deposited in GEO under accession number GSE35523.

Signal intensity data were extracted from scanned images of each array using Roche NimbleGen NimbleScan v2.6 software. After spatial correction, the Cy3 and Cy5 signal intensities were normalized using qspline normalization. Following normalization a $10\times$ window–averaging step is applied. For amplification and deletion detection we used the dynamic segMNT algorithm that identifies segments by minimizing the squared error relative to the segment means. To detect representative alterations and to minimize the identification of random alterations, we extracted

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Table 1
Overview of deleted chromosome regions.
Start and end points of deleted chromosome regions are according to NCBI37/mm9. Size is displayed in kb.

Sphere					24 h TGF-ß					12 h FCS				
	Start	End	log$_2$	Size		Start	End	log$_2$	Size		Start	End	log$_2$	Size
					chr1	3019999	9259999	−0.11308	6240					
					chr1	10419999	12539999	−0.16881	2120					
					chr1	21459999	33339999	−0.12453	11,880					
					chr1	47059999	51179999	−0.20953	4120					
					chr1	67859999	68979999	−0.20877	1120					
					chr1	95859999	106179999	−0.11556	10,320					
					chr1	108899999	120099999	−0.13136	11,200					
chr1	110459999	112459999	−0.15437	2000										
chr1	125099999	125779999	−0.1133	680										
					chr1	141739999	151499999	−0.12807	9760					
chr1	157499999	166019999	−0.11672	8520						chr1	157699999	164339999	−0.11251	6640
										chr1	179699999	180099999	−0.17032	400
					chr2	39299999	49379999	−0.11759	10,080					
					chr2	80899999	83139999	−0.16313	2240					
chr2	85619999	89979999	−0.1151	4360	chr2	85539999	89979999	−0.19832	4440					
chr2	94819999	101179999	−0.10144	6360	chr2	94419999	101179999	−0.14893	6760					
chr2	140259999	140739999	−0.10916	480										
chr2	174619999	176979999	−0.10819	2360	chr2	174539999	176979999	−0.10409	2440					
					chr3	3179999	7819999	−0.16459	4640					
chr3	10779999	15219999	−0.10217	4440	chr3	10699999	14179999	−0.21013	3480					
chr3	15259999	15819999	−0.25966	560	chr3	15339999	18379999	−0.18784	3040	chr3	15459999	15779999	−0.2969	320
					chr3	23219999	26019999	−0.12403	2800					
					chr3	41659999	48699999	−0.20394	7040					
chr3	47419999	48019999	−0.20803	600	chr3	48739999	50819999	−0.10307	2080					
					chr3	66659999	67219999	−0.14445	560					
					chr3	69859999	71299999	−0.14	1440					
chr3	71339999	73539999	−0.1502	2200	chr3	71339999	72859999	−0.24188	1520					
					chr3	72899999	75019999	−0.12964	2120					
					chr3	76179999	78579999	−0.10363	2400					
chr3	80059999	81099999	−0.14237	1040	chr3	80659999	81059999	−0.20763	400					
chr3	93699999	94059999	−0.18368	360	chr3	93699999	94059999	−0.16031	360					
					chr3	110219999	115099999	−0.16927	4880					
					chr3	116859999	120779999	−0.1109	3920					
chr3	123499999	125779999	−0.2668	2280	chr3	123399999	125779999	−0.35956	2440	chr3	123059999	127819999	−0.16916	4760
chr3	125819999	127739999	−0.16144	1920	chr3	125819999	128939999	−0.16294	3120					
					chr3	131419999	132379999	−0.13963	960					
					chr3	140139999	140899999	−0.18969	760					
					chr3	149859999	151299999	−0.18356	1440					
					chr3	154499999	159578619	−0.10621	5079					
					chr4	12379999	32099999	−0.13785	19,720					
					chr4	35779999	39859999	−0.20166	4080					
					chr4	64579999	75579999	−0.11545	11,000					
chr4	75659999	80779999	−0.2069	5120	chr4	75619999	80779999	−0.2917	5160	chr4	75579999	78339999	−0.19677	2760
					chr4	89259999	94339999	−0.13013	5080					
					chr5	5939999	7859999	−0.15729	1920					
					chr5	11859999	19539999	−0.12821	7680					
					chr5	54859999	61859999	−0.20136	7000					
					chr5	67699999	72699999	−0.13854	5000					
					chr5	78299999	91059999	−0.10839	12,760	chr5	81459999	81739999	−0.14919	280
										chr5	146259999	146579999	−0.10129	320
chr6	41499999	47339999	−0.10686	5840	chr6	41539999	47099999	−0.16256	5560					
					chr6	55739999	66419999	−0.10699	10,680					
					chr6	73379999	81459999	−0.11413	8080					
					chr6	103779999	112019999	−0.1065	8240					
chr6	138299999	140059999	−0.14334	1760	chr6	138379999	140059999	−0.22473	1680					
					chr7	56899999	70659999	−0.10699	13,760					
					chr7	75539999	79379999	−0.11891	3840					
					chr7	91779999	103339999	−0.10018	11,560					
chr7	10699999	12139999	−0.24888	1440										
chr7	110659999	111699999	−0.23809	1040	chr7	110619999	111379999	−0.20134	760					
					chr8	4579999	9659999	−0.11752	5080					
chr8	99539999	106019999	−0.10809	6480										
					chr8	29979999	34539999	−0.13338	4560					
					chr8	49459999	55619999	−0.16084	6160					
					chr8	98739999	106419999	−0.17182	7680					
					chr9	3139999	7299999	−0.10507	4160					
					chr9	10419999	12939999	−0.15382	2520					
					chr9	16739999	20259999	−0.10813	3520					
					chr9	33219999	34019999	−0.11795	800					
chr9	35659999	35939999	−0.21324	280	chr9	35659999	36299999	−0.16454	640	chr9	35659999	36059999	−0.16676	400
chr9	37699999	38899999	−0.10023	1200	chr9	37419999	39979999	−0.10149	2560					
										chr9	71699999	72019999	−0.1087	320