Heterozygous Mutations of \textit{FREM1} Are Associated with an Increased Risk of Isolated Metopic Craniosynostosis in Humans and Mice

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Abstract

The premature fusion of the paired frontal bones results in metopic craniosynostosis (MC) and gives rise to the clinical phenotype of trigonocephaly. Deletions of chromosome 9p22.3 are well described as a cause of MC with variably penetrant midface hypoplasia. In order to identify the gene responsible for the trigonocephaly component of the 9p22.3 syndrome, a cohort of 109 patients were assessed by high-resolution arrays and MLPA for copy number variations (CNVs) involving 9p22. Five CNVs involving \textit{FREM1}, all of which were de novo variants, were identified by array-based analyses. The remaining 104 patients with MC were then subjected to targeted \textit{FREM1} gene re-sequencing, which identified 3 further mutant alleles, one of which was de novo. Consistent with a pathogenic role, mouse \textit{Frem1} mRNA and protein expression was demonstrated in the metopic suture as well as in the pericranium and dura mater. Micro-computed tomography based analyses of the mouse posterior frontal (PF) suture, the human metopic suture equivalent, revealed advanced fusion in all mice homozygous for either of two different \textit{Frem1} mutant alleles, while heterozygotes exhibited variably penetrant PF suture anomalies. Gene dosage-related penetrance of midfacial hypoplasia was also evident in the \textit{Frem1} mutants. These data suggest that CNVs and mutations involving \textit{FREM1} can be identified in a significant percentage of people with MC with or without midface hypoplasia. Furthermore, we present \textit{Frem1} mutant mice as the first bona fide mouse model of human metopic craniosynostosis and a new model for midfacial hypoplasia.

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Introduction

During development the calvarial bones are separated by regions of non-calcified intrasutural mesenchyme which permit skull deformation during birth and accommodate brain growth during childhood. Craniofacial malformations caused by the premature fusion of cranial sutures are common presenting features in clinical genetics practice with an overall incidence of approximately 1 in 2500 live births. Non-syndromic forms of craniosynostosis predominate, but there are more than 90 described syndromic craniosynostoses which are conventionally classified by their pattern of suture involvement and dysmorphic features [1]. Syndromic craniosynostoses have been shown to arise from at least 6 different mechanisms; activation of receptor kinase signaling pathways (FGFR1-3, TGFBR1-2, EFNB1), inactivation of transcription factors (TWIST1, MSX2), alterations to, or interactions with, extracellular matrix

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Author Summary

Although twin and family studies have shown that genes play a critical role in the timing of fusion of skull bones, the identification of specific genes that may be involved has remained somewhat elusive except in the case of the dominantly inherited craniosynostosis syndromes. Metopic craniosynostosis (MC), the early fusion of the forehead (frontal) bones, accounts for 5%–15% of all craniosynostosis cases. This premature fusion of the frontal bones results in a characteristically altered skull shape, termed trigonocephaly, that usually requires surgical correction. Remarkably, the cause of the majority of cases of MC remains unknown (idiopathic). Here, we report genetic variants involving chromosome 9 which involve and interrupt the structure of the FREL1 gene in a large cohort of patients presenting with unisutural metopic craniosynostosis. Micro-computed tomographic (microCT) imaging and quantitative analysis of skull shape reveal both premature fusion of the PF suture (metopic equivalent) and also changes in frontal bone shape supportive of a role for FREL1 in regulation of the metopic suture. Taken together with FREL1 gene and protein expression findings, these data indicate that mutations in FREL1 can give rise to metopic craniosynostosis.
14.20 and 16.34 Mb [hg18] which involved only 9 genes. This region extends from NFIB intron 2 to the intergenic region between C9orf93 and BNC2 also deleting FREM1. All CNVs were confirmed by MLPA and were shown to be de novo.

The common 0.65 Mb region of deletion overlap identified in the four samples contains 4 genes NFIB, ZDHHC21, CER1 and FREM1. Importantly two patients were identified to have CNVs whose boundaries disrupt the coding region of the FREM1 gene. These CNV data are consistent with a model in which haploinsufficiency of FREM1 is associated with MC. These findings prompted us to investigate whether DNA sequence analysis of FREM1 might identify additional pathogenic mutations.

Prior to re-sequencing of the 35 coding exons of FREM1 (see below), the 105 additional patients with MC were pre-screened for point mutations in CER1 and deletions of FREM1. One further patient (patient 5) was confirmed to have a whole FREM1 gene deletion as a result of a cytogenetically visible 9p22.3 deletion. No mutations were identified in CER1, consistent with previous reports [13].

Missense mutations in FREM1 in patients with MC

104 patients with a clinical diagnosis of MC were screened for DNA sequence mutations in FREM1. Two previously unreported nucleotide substitutions were identified in three patients (Table 1; Figure 1c). The first of these mutations, NM_144966.4:c.4499A>T [NP_659403.4: p.(Glu1500Val)] in exon 25, was observed in two unrelated patients (patient 6 and patient 7). p.Glu1500Val was also present in patient 6 as a de novo event (Figure 1b) consistent with both his parents being clinically normal. The Grantham score for this substitution is substantial at 121 and the mutation is predicted not to be tolerated by SIFT, and possibly damaging by Polyphen2 [HumVar] with a score of 0.309 [17–19]. The PhyloP score for nucleotide conservation for chr9:g.14766145 is 2.55 suggesting it is under negative selection [20]. This mutation was not detected in 142 control chromosomes of Caucasian origin and 110 ethnically matched control chromosomes consistent with it not being a population polymorphism.

The second individual had no abnormal craniofacial findings. The second mutation, NM_144966.4:c.1493G>A [NP_659403.4:p.(Arg498Gln)], in exon 9, was observed in a single patient (Patient 8). Although the Grantham score is only 43, this amino acid is highly conserved with 20 vertebrate species having an
arginine at this position. The PhyloP score for nucleotide conservation for chr9:g.14832559 is 2.79. It is predicted as not being tolerated by SIFT, and probably damaging by Polyphen2 [HumVar] with a score of 0.996. The proband was born to a 35 year old G1 P0 mother and 32 year old father at full term by Caesarian section. He had isolated MC corrected at six months of age. There was no family history of craniofacial dysmorphism. A fetal ultrasound at 20 weeks was reported as normal. The birth weight was 3.42 kg (75–90th centile), length 50.8 cm (50–75th centile). Craniosynostosis was suspected at birth and confirmed by a cranial CT scan at five months of age. The proband is currently four years of age with normal development. The mutation was proven to be paternally inherited but was absent in 138 control chromosomes excluding a population polymorphism.

A third potential FREM1 mutation NM_144966.4:c.854A>G (NP_659403.4:p.(Tyr285Cys)), in exon 6, was identified in a proband in a Brazilian family however this mutation did not segregate with the disease and was detected in 1 of 142 control chromosomes of Caucasian origin and 5 of 120 ethnically matched control chromosomes. These results are consistent with this variant being a novel population polymorphism.

Frem1 is expressed in the developing frontal and nasal sutures in mice

To ascertain a potential role for Frem1 in the formation of the metopic suture we examined the expression of the gene prior to fusion of the suture in wildtype mice. In situ hybridization of mouse embryos from mid to late gestation (E14.5–E16.5) delineated expression of Frem1 between the developing frontal bones in the region fated to form the posterior-frontal suture (Figure 2). Antibody staining at P0 highlighted fibrillar pericranial expression of Frem1 overlying the developing frontal bones as well as staining in the dura mater underlying these bones. Low levels of diffuse Frem1 staining were also noted in the osteogenic precursors between the frontal bones, further suggesting a role for the protein in the development of the posterior frontal suture.

Table 1. Molecular and clinical patient information.

<table>
<thead>
<tr>
<th>FREM1 mutation</th>
<th>Inheritance</th>
<th>General Clinical features</th>
<th>Additional clinical features</th>
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<td><strong>Patients with mutations affecting FREM1</strong></td>
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<td>FREM1 mutation</td>
<td>Inheritance</td>
<td>General Clinical features</td>
<td>Additional clinical features</td>
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<td>renal abnormalities: –</td>
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<td>Hypotonia: +</td>
<td>Cardiac malformations: PS/I</td>
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<td>De novo</td>
<td>Height: -1 SD</td>
<td>Other: –</td>
</tr>
<tr>
<td>De novo De novo De novo De novo</td>
<td>Maternally inherited</td>
<td>Head circumference: unknown</td>
<td>Hypoglycemic neonatal seizures: –</td>
</tr>
</tbody>
</table>

*More detailed clinical descriptions can be found in Swinkels et al. (ref11); del, deletion; dup, duplication; ex, exon; SD, standard deviation; PS/I. Pulmonary stenosis/incompetence; PPS, peripheral pulmonary stenosis; VSD. Ventriculo-septal defect; +, present; -, absent; NA, not available.

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Frem1 mice show craniofacial abnormalities consistent with MC

Semi-landmark-based geometric morphometrics is a powerful means of distinguishing localized differences in form between two groups. We therefore used this approach to obtain further evidence as to whether Frem1 mutations can cause MC. The skulls of bat mutant mice were imaged by mCT and analyzed using semi-landmark-based geometric morphometrics over the anterofrontal aspects of the skull (coronal suture to nasal tip). Results of principal component analysis of the postero-frontal aspects of the cranium revealed that the first two principal components (PC1 and 2) account for more than 45% of the variation in the dataset (data not shown). PC1 is usually correlated with the size of the individuals. In geometric morphometrics, size of the specimen is determined by the centroid size, which is the square root of the summed distances between the centroid (arithmetic mean of landmarks) and each landmark of the specimen. Regression of the first two PCs against centroid size showed that size was not correlated with either of the principal components (F testpc1: 1.8 on 1 and 18 DF, p-value: 0.1964; F testpc2: 0.9419 on 1 and 18 DF, p-value: 0.3447). In contrast, regression of the first two PCs against the homogenes, heterozygotes, and wildtype showed a significant correlation with the genotype of the individuals (for PC1: \( R^2 = 0.3943 \) F statistic: 5.533 on 2 and 17 DF, p-value: 0.0141; for PC2: \( R^2 = 0.3604 \) F statistic: 4.789 on 2 and 17 DF, p-value: 0.02241) (Figure 3b).

Overlay of the mean positions of each semi-landmark between homogygotes and wildtype skulls showed that the homogygote upper midfaces were raised along the proximal aspect of the metopic suture (black arrowheads, Figure 3c) and were significantly wider at the level of the coronal suture (compare colored arrows, Figure 3c). Notably, the increased width in the homogygotes is more prominent posteriorly. Furthermore, the lateral aspects of the homogygote skulls decline more sharply than controls (colored arrows Figure 3c and white arrowheads in Figure 3d). Heterozygotes also show a decline at the lateral aspects although this was less pronounced than in homogygotes.

Also of significance, one of the homozygotes from this initial set of imaged skulls showed marked deviation of the midface. To investigate this further, we scanned an additional 25 male heads from mutant and wildtype mice ranging in age from 28 days to 240 days, including 13 homozygotes and 7 heterozygotes. Visual inspection of 3D rendered images of each skull revealed varying degrees of midfacial asymmetry and/or midface hypoplasia in a significant proportion of Frem1 homozygotes (7/16 total; 45% - when also including those used in the shape analyses; Figure 4) and to a lesser degree the Frem1 heterozygotes (2/21 total; 9.5%). For the homozygotes, leftward deviation was more frequent than rightward deviation (5 left vs 1 right; 1 general hypoplasia). In summary, morphometric analysis of skulls from bat homozygous and heterozygous mice identified craniofacial malformations consistent with the craniofacial features, in particular MC and midfacial asymmetry/hypoplasia, seen in the 9p22 deletion syndrome, with the penetrance of the phenotypes in mice correlated to mutant gene dosage.

Different Frem1 mutant alleles show advanced fusion of the posterior frontal suture in mice

To investigate the basis for the altered frontal cranial shape, three-dimensional rendered images generated from scans of Frem1\( ^{bat} \) homozygote, heterozygote and wildtype skulls were sectioned virtually in the coronal plane at the equivalent position on the posterior frontal suture. Examination of the suture in control C57BL/6J mice revealed a generally patent suture with only intermittent contact between the frontal bones either endocranially or ectocranially. In contrast, age, sex and background matched Frem1\( ^{bat} \) homozygote animals all exhibited complete fusion of the PF suture (Figure 5). Notably, 42% of heterozygous animals showed variable suture anomalies including complete fusion (1/14; 7%), obvious sutural asymmetry (3/14; 21%) and advanced endocranial suture fusion (2/14; 14%). Importantly, the findings in the Frem1\( ^{bat} \)
mice were validated by the analysis of a litter of mice carrying a second Frem1 mutation, the Frem1\textsuperscript{Qbrick} null allele; the single homozygote mouse showed complete fusion of the PF suture, while two of the three heterozygotes analyzed showed similar suture anomalies to those seen in Frem1\textsuperscript{bat} heterozygotes (Figure 5).

To investigate whether either of the two remaining genes within the refined critical interval might also contribute to the craniofacial phenotype of the 9p22 deletion syndrome, we first analyzed a small number of Zdhhc21\textsuperscript{dep/dep} homozygotes. Comparison of these mice to the analyzed Frem1 mice (37d vs 28-30d), demonstrated that none had PF suture fusion or sutural anomalies (data not shown). Assessment of the cranioskeletal phenotype of late stage homozygous Nfib\textsuperscript{-/-} fetuses with age matched C57BL/6J control embryos showed that the Nfib\textsuperscript{-/-} fetuses exhibited reduced overall size and relatively delayed cranial bone growth (data not shown), but without evidence of premature suture fusion.

Discussion

In this study we report that FREM1 is a dominantly-acting metopic craniosynostosis gene based upon findings of: i) patients with trigonocephaly with CNVs which disrupt or delete the coding sequence of the gene; ii) missense mutations in FREM1 in patients with isolated MC; iii) expression of mouse Frem1 gene and protein in the posterior frontal suture (metopic suture equivalent); iv) advanced fusion of the PF suture, altered frontal bone curvature and midfacial malformations in two independent mouse lines carrying distinct Frem1 loss-of-function mutations, and: v) absence of an overt cranial suture phenotype in mice deficient in either of the two remaining genes (Zdhhc21 and Nfib) that reside within the 9p22 critical interval.

FREM1 is composed of several functional domains, including a conserved signal sequence, a CALXb calcium-binding loop typically found in Na\textsuperscript{+}-Ca\textsuperscript{2+} exchange proteins, 12 chondroitin sulfate proteoglycan (CSPG) elements, and a C-terminal lectin Type C domain [21]. FREM1 is a basement membrane protein which forms a ternary complex with the FRAS1 and FREM2 proteins, although the topology and stoichiometry of the subunits is not certain. FREM1 orthologs are highly conserved throughout evolution and the 12 CSPG repeats are highly homologous with each other. Both point mutations observed in the MC cohort affect residues within the CSPG repeats whose physico-chemical
properties are also strongly conserved in evolutionary history. Prediction of the consequences of these mutations, based on similarity to the structurally related NG2 protein, suggest they affect surface residues of FREM1, potentially disturbing the interactions with other proteins. CSPG repeats of the NG2 proteoglycan have been shown to interact with basic fibroblast growth factor [22]. It is intriguing to speculate that FREM1 could also bind FGFs and that the craniosynostosis associated with a mutation in these repeats arises through altered FGFR activation as a result of increased intrasutural FGF availability or its affinity for their receptors. A similar mechanism has recently been shown for the Eks mouse which carries a gain-of-function mutation in Fgf9 [14].

Recently, Alazami et al. (2009) demonstrated expression of Frem1 in the developing midface by whole mount in situ hybridization in normal embryonic day 11.5 mice, consistent with the midfacial phenotypes seen in both BNAR and FREM1-trigonocephaly [15]. We have now demonstrated that expression of Frem1 mRNA is also present in the developing interfrontal suture. These findings are also validated by immunohistochemical detection of Frem1 protein within the sutural mesenchyme as well as in the dura mater and pericranium prior to the initiation of the posterior frontal suture at postnatal day 7. We speculate that expression of FREM1 within the intrasutural mesenchyme would be consistent with a role in modulating Fgf or other growth factor availability.

An important role for Frem1 in regulating suture patency is supported by our mCT investigations of Frem1bat and Frem1Qbrick mice. Previous studies have established that the posterior frontal suture in C57BL/6J mice begins to fuse after postnatal day 25 and morphologically completes fusion around day 45. This timing is consistent with the findings in our postnatal day 28-30 wildtype mice.
mice, which show only sparse contact between the frontal bones. In contrast, virtual cross-sectional analysis of Frem1\textsuperscript{bat} and Frem1\textsuperscript{Qbrick} homozygotes revealed almost complete fusion of the posterior frontal suture, both ectocranially and endocranially (Figure 5). Importantly, heterozygotes of each mutation also showed variable posterior frontal sutural anomalies ranging from complete fusion to atypical sutural asymmetry to a normal appearing suture. Furthermore geometric morphometric analysis of heterozygote and homozygote Frem1\textsuperscript{bat} skulls and wildtype genetic background controls revealed that Frem1 mutant mice show altered frontal bone curvature, in particular at the level of the posterior frontal suture. Although more evident in the homozygote skulls, the medial aspects over the posterior frontal suture appear raised relative to the lateral aspects which decline more sharply than in controls (see Figure 3a and 3b). The variably penetrant posterior frontal sutural anomalies in Frem1 heterozygotes and the lack of overt cranial and/or sutural defects in homozygous Zdhhc21 and Nfib mutants supports a causative role for Frem1 haploinsufficiency in the 9p22.3-trigonocephaly in humans. Further to this, the analyses of the mouse craniofacial skeleton also revealed that homozygous Frem1\textsuperscript{bat} mice, and to a lesser extent heterozygous mice, generally have a shorter upper midface, including nasal bone and premaxilla (midfacial hypoplasia/asymmetry) and slightly wider nasal bones (Figure 4). These findings are consistent with the earlier reported expression of Frem1 in the developing facial prominences and the role of recessive Frem1 mutations in BNAR syndrome [15]. Notably, midfacial hypoplasia is one of the major clinical features of 9p22.3-trigonocephaly and was noted in at least six of the eight probands reported here (Table 1).

The Frem1 mutational classes identified in humans include structural variants that interrupt the gene, CNVs of the entire Frem1 locus and point mutations of the Frem1 coding sequence. The observed mutational heterogeneity is reminiscent of other dominantly-acting mutations of ECM multimeric proteins such as collagen type 1 \( \alpha 1 \), collagen type 1 \( \alpha 2 \) [23] and fibrillin [24] where multi-exon deletions and missense mutations both result in the same disease phenotype. It is interesting to note however, that the Frem1 mutations identified in this study are heterozygous (dominantly acting) with the morphological consequences largely restricted to the craniofacial complex (metopic suture and midface) compared with the multi-organ involvement in the autosomal recessive disorder, BNAR. The phenomenon of dominant and recessive mutations in the same gene is well described and associated with a range of molecular etiologies. Classically, recessive mutations may produce a spectrum of disorder severity based on allele dosage, as has been described in familial hypercholesterolemia [25]. Alternatively autosomal dominant gain of function mutations may be associated with a different spectrum of disease compared with loss of function mutations. This is exemplified by heterozygous gain of function mutations in RET which are associated with thyroid carcinoma and multiple endocrine neoplasia types 2A and 2B versus homozygous loss of function mutations in Hirschsprung disease [26]. Finally, dominant and recessive mutations may involve different stages of protein biosynthesis or functional domains, as described for mutations in the insulin gene in which dominant neonatal diabetes arises from mutations associated with misfolding of proinsulin whereas recessive mutations reduce insulin biosynthesis [27]. The difference in range and severity of organ involvement is consistent with MC arising as a result of haploinsufficiency for Frem1. BNAR and Frem1-trigonocephaly could therefore be considered to form a spectrum of disorders within the same genetic pathway distinguished by dominant and recessive inheritance.

Phenotypic variability and incomplete penetrance are typical findings in the TWIST1 and FGFR-associated craniosynostoses and are therefore not unexpected findings in this MC patient cohort. The p.Glu1500Val mutation was present in de novo form in one affected individual. In a second family this mutation was inherited from the proband’s mother who has facial features of hypertelorism (>3SD) and upslanting palpebral fissures. The mutation was also present in three siblings, one of whom (the proband) had trigonocephaly and microcephaly (<3SD), a sister who had piosis and hypertelorism, and a third sibling who has relative hypertelorism but no significant findings. Similarly, the p.Arg198Gln mutation was inherited from a clinically unaffected father.

In line with the variable clinical presentations, Frem1\textsuperscript{bat} mice have been previously reported as showing a number of variably penetrant features including renal agenesis (~20%), limb (digit) anomalies (<5%) and unilateral or bilateral cryptophthalmos [21]. However, mouse lines carrying other mutant Frem1 alleles (that arose on different inbred backgrounds) typically do not present with renal phenotypes and show variable penetrance of other features as well [28,29]. The variable expression and penetrance of skull deformations in the inbred Frem1\textsuperscript{bat} line is consistent with
these observations. The influence of genetic background on the presentation of the Frem1 mutant phenotype and that of the broader family of blebs mouse mutants which carry mutations in the other Fras1/Frem genes has been confirmed by placing the same mutations on different backgrounds (I. Smyth, personal communication). We therefore speculate that the variable penetrance and expressivity of the human Frem1 mutations is due to a combination of factors, including genetic modifiers and epigenetic modulators. Such penetrance and expressivity must therefore be considered when counseling patients in regard to recurrence risk. This group of clinical findings suggest that the phenotypic consequences of Frem1 mutations in humans and mice include but are not limited to MC.

In summary, we provide evidence that Frem1 mutations are associated with trigonocephaly. Taken together, our data support the study into unisutural synostosis biology. Furthermore, we present mice include but are not limited to MC.

**Materials and Methods**

**Ethics statement**

All animals were handled in strict accordance with good animal practice as defined by the relevant national and/or local animal welfare bodies, and all animal work was approved by the University of Washington Research Ethics Committee.

**Patients**

109 patients with non-syndromic MC were ascertained from five participating centers of the International Craniosynostosis Consortium (http://genetics.ucdavis.edu/icc.cfm) (University of California, Davis, USA n = 34; Seattle Children’s Hospital, Seattle, USA, n = 33; Universidade de São Paulo, São Paulo, Brazil, n = 24; Australian Craniofacial Unit, Adelaide, Australia, n = 14; and RUNMC, Nijmegen, The Netherlands n = 4). DNA was isolated or purified using a QiAamp DNA mini kit (QiAgen, the Netherlands) following standard procedures. Parental samples were collected when available, and informed consent was obtained in all cases following local institutional human research ethics guidelines. Mutation pre-screening of the regions of the FGFR and TWIST1 genes associated with syndromic craniosynostosis was performed by bi-directional DNA sequence analysis; including FGFR1 exon 7, FGFR2 exons 3, 5, 8, 10, 11 and 14-17, FGFR3 exons 7 and 10 and TWIST1 [30,31].

**Fine mapping of CNVs using chromosome 9 microarray analyses**

Chromosome 9 specific oligonucleotide microarray analyses were performed using a 385K array following the manufacturer’s instructions (Roche NimbleGen). The acquired images were analyzed using NimbleScan V2.4 extraction software (Roche NimbleGen). Data were visualized in SignalMap V1.9 software to determine the boundaries of the CNVs (Roche NimbleGen).

**Multiplex ligation-dependent probe amplification (MLPA) of Frem1**

An in-house MLPA kit was developed to screen for CNVs at 9p22.3. A set of uniquely-sized MLPA probes hybridizing to exon 2 of CER1, exons 2, 9, 16, 23, 31 of Frem1 and to intron 8 of TTC39B were developed. These MLPA probes were combined with four unlinked standard control probes. All probes were designed following the protocol of MRC-Holland and the sequences are provided in Table S3 (http://www.mlpa.com/index.htm). Hybridization, ligation and amplification of the MLPA probes were performed as described previously [32]. Amplification products were identified and quantified by capillary electrophoresis on an ABI3730 or 3100 Genetic Analyzer, using GeneMapper software (Applied Biosystems).

**Sequence analysis of CER1 and Frem1**

All coding regions and adjacent splice sites of CER1 (NM_005454) and Frem1 (NM_144966) were amplified and sequenced (PCR primers and conditions available on request). PCR products were cycle sequenced (ABI 3730 or 3100) and analyzed for mutations using the Vector NTI v11 software together with visual inspection. Potential mutations were tested for de novo occurrence through mutation analysis of parental DNA where available. Sequence variants are described following the HGVS nomenclature guidelines.

**Mouse strains**

Mice carrying the ENU-generated Frem1bat mutation maintained on a C57Bl/6J background were used for this study. The bat allele is the result of a single nucleotide change that affects the normal mRNA splicing of exon 25 of the mouse Frem1 gene, leading to a frameshift and premature truncation of the protein. The mutant allele is thought to be hypomorphic rather than a null allele [21]. Standard mating protocols were used to generate heterozygote and homozygote animals that were each identified by PCR-based genotyping [21]. Mice were sexed based on genital morphology at weaning. A single litter of mice carrying a Frem1 null allele (Frem1-/-) was also made available for analysis, including three heterozygous animals, one surviving homozygote and three littermate C57BL/6J controls. These mice were generated by a traditional gene targeting approach [28] and also maintained on a pure C57BL/6J background. A small number of mice from mutant lines representing both of the remaining genes that reside within the refined critical interval, DhhHC21 and Nfib, were also obtained. The ZDisc21 line [33] carries a three base pair deletion (single amino acid deletion) that results in protein mislocalization and loss of enzyme activity and is associated with delayed hair shaft differentiation. The remaining mutant carries a null allele of Nfib, generated through traditional gene targeting [34]. Nfib heterozygotes are apparently healthy and show no overt phenotype, while Nfib homozygotes die just prior to birth. A limited number of late stage homozygous Nfib/- fetuses were available. Both lines were provided on a C57BL/6J background.

**Micro-computed tomography (mCT) and skull shape analysis**

For the purpose of assessing suture patency and comparing cranial shape, a total of 21 specimens were subjected to mCT using a SkyScan model 1076 in-vivo microtomograph (SkyScan, Belgium). All specimens were scanned at the Small Animal Tomographic Analysis (SANTA) Facility at the University of Washington, using and following optimized protocols (0.018 mm voxel resolution, 65 kV, 150 uA, 1.0 mm Al filter) previously reported [35,36]. Out of the 21 specimens, three were homozygotes, four were wild-type and the remainder were Frem1bat heterozygotes. A further seven 4 week-old Frem1bat knockout mice (three heterozygotes, one homozygote, and three C57Bl/6J controls) were also scanned. Raw scan data were reconstructed using NRecon software (SkyScan, Belgium) and rendered using the
volume exploration software, Drishti V2.0 (http://anu.edu.au/Vizlab/drishti/). Virtual cuts in the coronal plane were then made at the same planar level in each rendered skull to assess the patency of the posterior frontal suture. To ensure direct comparability, all scan, reconstruction and rendering parameters were kept identical for all skulls.

3D mesh models of each skull created using the CTan software (Skyscan, Belgium) and then were imported into Rapidform (Inus Technology) in which the mandibles and other unwanted elements were segmented out. Cleaned meshes were then imported into the 3D landmark software developed by the Institute for Data Analysis and Visualization (IDAV Landmark). A flexible patch was applied to the region between the rostrum and the coronal suture in the dorsal view. Each patch had 9 control points anchored to biologically homologous structures to ensure the consistency of the patch placement (Figure 3a inset). Finally, the patch was converted into a 15 x 21 deformable grid, and the 3D coordinates of 315 grid points were exported. Due to some mesh inconsistencies, the Landmark software could place 309 of 315 grid point in all skulls, and these were used in all subsequent analyses. 3D renderings of the skulls indicated a high level of deformation in one of the initial homozygous specimens. Although biologically highly relevant, this specimen was excluded from the shape analyses to preclude any undue influence of this outlier.

Generalized procrustes analysis (GPA) was used to quantify and visualize the localized shape differences among the groups as implemented in the R “shapes” package [37]. The bones were ordinated in shape-space using principal components analysis. Each principal component summarizes a unique portion of the shape variation that is not explained by any of the preceding components. Typically, the morphospace is centered on the mean (or consensus) shape configuration of the GPA, so that each point in the morphospace can be visualized as deviation from the mean shape. Principal components also can be used as shape variables on which statistical tests can be applied.

Subsequent to the detailed shape analyses, a further twenty five Frem1het males (thirteen homozygotes, seven heterozygotes, and five controls) ranging from postnatal day 28 through to postnatal day 240 were scanned and 3D rendering models generated using Drishti V2.0 (http://sf.anu.edu.au/Vizlab/drishti/). Five 37 day old zdhhc21+/−/− mice were also obtained for imaging. In addition, three embryonic day 18.5 Nfib+/− mice were analysed. All skulls were visually inspected and any gross malformations recorded.

Analysis of Frem1 expression

Frem1 transcripts were detected using specific riboprobes to the 3’ UTR of the gene as described previously [21]. A rabbit polyclonal Frem1 antiseras was raised against Frem1 C-terminal domain 11 and partial domain 12 (aa 1500–1637) expressed and purified as a His-tagged recombinant protein [38]. Immunohistochemistry was performed on 10 micrometer frozen sections of P0 mouse heads using antibodies to Frem1 (above) and entactin (Abcam) detected using Alexa conjugated secondary antibodies (Molecular Probes). Images were captured on a Leica SP5 confocal microscope.

Supporting Information

Table S1 Syndromes with metopic synostosis/trigonocephaly. (DOC)
Table S2 Craniofacial measurements. (DOC)
Table S3 MLPA probes used for CNV screening of FREM1. (DOC)

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References

10. Schedule of experiments: TR MFB JAV TCC IS SAB MLC LELMV. Performed the experiments: LELMV AMM IMJ KS FW. Analyzed the data: TR MFB TCC IS HbB. Contributed reagents/materials/analysis tools: FJ DB MRB MLC SAB CM PJA KMS DK.
11. Crowther S, Amin DE, Justice MJ, Beutler B, et al. (2004) The extracellular domain 11 and partial domain 12 (aa 1500–1637) expressed and purified as a His-tagged recombinant protein [38]. Immunohistochemistry was performed on 10 micrometer frozen sections of P0 mouse heads using antibodies to Frem1 (above) and entactin (Abcam) detected using Alexa conjugated secondary antibodies (Molecular Probes). Images were captured on a Leica SP5 confocal microscope.

Author Contributions

Conceived and designed the experiments: TR MFB JAV TCC IS SAB MLC LELMV. Performed the experiments: LELMV AMM IMJ KS FW JLG. Analyzed the data: TR MFB TCC IS HbB. Contributed reagents/materials/analysis tools: FJ DB MRB MLC SAB CM PJA KMS DK. Wrote the paper: TR LELMV MFB TCC IS.