



Characteristics of de novo structural changes in the human genome

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Title: Characteristics of *de novo* structural changes in the human genome

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Abstract

Small insertions and deletions (indels) and large structural variations (SVs) are major contributors to human genetic diversity and disease. However, mutation rates and characteristics of *de novo* indels and SVs in the general population have remained largely unexplored. We report 332 validated *de novo* structural changes identified in whole genomes of 250 families, including complex indels, retrotransposon insertions and interchromosomal events. These data indicate a mutation rate of 2.94 indels (1-20bp) and 0.16 SVs (>20bp) per generation. *De novo* structural changes affect on average 4.1kbp of genomic sequence and 29 coding bases per generation, which is 91 and 52 times more nucleotides than *de novo* substitutions, respectively. This contrasts with the equal genomic footprint of inherited SVs and substitutions. An excess of structural changes originated on paternal haplotypes. Additionally, we observed a non-uniform distribution of *de novo* SVs across offspring. These results reveal the importance of different mutational mechanisms to changes in human genome structure across generations.

Introduction

Genomic mutations drive human evolution and phenotypic diversity. Comparative genomics studies highlighted important small base-level and large-scale differences between human and chimpanzee genomes and noted a larger impact of segmental duplications compared to single nucleotide variations (SNVs) (Cheng et al. 2005). Whereas interspecies comparisons provide us with insight into long-range processes such as genetic drift and selection, the information derived from direct measurements of the *de novo* mutation spectrum and rates across generations is crucial for understanding mechanisms of mutation formation and inter-individual differences (Scally and Durbin 2012). While several projects have started to investigate the rates and characteristics of *de novo* SNVs (Michaelson et al. 2012; Francioli et al. 2014; Kong et al. 2012; Besenbacher et al. 2015), those of *de novo* short insertions and deletions (indels) and large structural variants (SVs) have been much less studied (Campbell and Eichler 2013).

Copy number variations (CNVs) and SVs contribute substantially to human genetic variation (Korbel et al. 2007; Sebat et al. 2004; Iafrate et al. 2004; Tuzun et al. 2005) and the phenotypic impact of CNVs may be larger than of SNVs (Conrad et al. 2010; Stranger et al. 2007; Redon et al. 2006). The impact of novel changes in genome structure is further illustrated by their role in human genetic disease (Cooper et al. 2011; Stankiewicz and Lupski 2010). Copy number variations (CNVs) are widely studied and have been implicated in a variety of neurological disorders, such as autism (Sebat et al. 2007), schizophrenia (Walsh et al. 2008) and intellectual disability (Cooper et al. 2011). Recent large-scale exome sequencing studies have uncovered *de novo* SNVs and short

indels causing various disease phenotypes, ranging from complex neurological disease to rare Mendelian disorders (Veltman and Brunner 2012).

Given the significant contribution of *de novo* mutations to human disease and evolution, studying genome-wide mutation rates and patterns is important for understanding mutation origins, locating hotspots, estimating disease risk and interpreting novel disease-associated mutations. Here, we surveyed the entire spectrum of *de novo* indels (1-20bp) and SVs (>20bp) in the human population at nucleotide-resolution using whole genome sequencing data of 250 families from the Genome of the Netherlands (GoNL) project (Boomsma et al. 2014; Francioli et al. 2014).

Results

Study design and variant detection

The Genome of the Netherlands project includes 231 parent-offspring trios, 11 quartets with monozygotic twins and 8 quartets with dizygotic twins for a total of 258 genetically distinct children. DNA material was obtained from peripheral blood mononuclear cells to avoid problems with accumulated somatic mutations routinely observed in DNA isolated from cell lines (Londin et al. 2011). The medium coverage (14.5x median sequence depth; 38.4x median physical depth) of paired-end sequencing data combined with a family-based design enabled the construction of a high-quality dataset of genomic variation (Francioli et al. 2014).

Indels (1-20bp) were called using three different tools using information from gapped reads and split-reads (**Fig. 1, Methods**). We focused exclusively on variants that were detected only in a single child by at least one tool with high confidence (**Supplemental**

Table 1). We performed experimental validation assays for all 1,169 candidate *de novo* indels in 110 children from 92 families (11 quartets with monozygotic twin pairs, 7 quartets with dizygotic twin pairs, 74 trios). We successfully re-sequenced 968 candidates in these families, of which 291 indels (203 deletions, 74 insertions and 14 complex indels) were confirmed as *de novo* events. All 31 *de novo* indels validated in monozygotic twin pairs were concordant between the two twins, showing that most of the mutations we report are germline mutations. After validation, we randomly excluded one of the twins from each monozygotic twin pair, leaving 99 children for *de novo* indel analysis. We only focused on regions where we had sufficient indel calling power by requiring at least 4 reads in the child and 10 reads in each parent. Using these thresholds a median of 77% of the genome was covered with sensitivity of 93.2% based on comparison of singletons in 11 twin pairs and 83.3% based on comparison of singletons in deep-coverage whole-exomes of 24 parents. This revealed a lower sensitivity for insertions (92.6% based on twin comparison, 75.1% based on whole-exome comparison) than for deletions (93.5% based on twin comparison, 87.4% based whole-exome comparison).

Structural variants (>20bp) were predicted by a selection of 11 tools that together use information from gapped reads, split-reads, discordant read-pairs and read depth to capture the full spectrum of SV sizes and types (**Fig. 1, Methods**). We identified a total of 601 *de novo* SV candidates in the 258 GoNL offspring based on permissive call settings and visual inspection using the Integrated Genome Viewer (IGV) (Robinson et al. 2011) (**Supplemental Table 1**). All candidates were subjected to experimental validation, resulting in a final set of 41 confirmed *de novo* SVs ranging in size from 20bp

to 327kbp (**Supplemental Figs. 1, 2**). The *de novo* SV set includes 27 deletions, 8 tandem duplications, 5 retrotransposon insertions and 1 complex interchromosomal event (that also involves a retrotransposon segment). We estimate the sensitivity of our calling for SVs sized 20-99bp and SVs larger than 100bp to be 69.4% and 85.8% that of deep coverage data, respectively. Further, nearly the complete genome, (an average of 98.8% of the haploid genome excluding assembly gaps) was covered by four or more read-pairs, a minimum threshold for calling SVs in our data (**Methods**). The sensitivity for detection of retrotransposon insertions was tested based on a previously published set of validated variants and found to be 77.6% for heterozygous retrotransposon insertions (Stewart et al. 2011). To empirically estimate the sensitivity for calling large SVs (>100 kb), we analyzed Illumina high-density SNP array data that were generated for 57 families (**Supplemental Table 2**). We detected a single *de novo* deletion (113 kb) in these data, which was already identified by whole genome sequencing.

In total, we confirmed 332 *de novo* structural changes (291 indels of size 1-20bp and 41 SVs larger than 20bp), which were used for downstream analyses (**Fig. 2A, Supplemental Table 2**). All 332 *de novo* variations are uniquely present in a single individual in the GoNL cohort. We also examined the overlap with public databases and found that 3 large SVs (>80% reciprocal overlap; Database of Genomic Variants; 1000 Genomes Phase 1) and 8 rare indels (exact match; dbSNP build 142; allele frequency < 1.5%) are overlapping, suggesting that these events might be recurring in the population (**Supplemental Table 2**).

Indel and SV mutation rates

Previous estimates of the human indel mutation rate range from 0.53 to 1.5×10^{-9} per base per generation (Campbell and Eichler 2013; Kondrashov 2003; Lynch 2010; Besenbacher et al. 2015; Ramu et al. 2013). The mutation rate for copy number variants was estimated to be 0.03 CNVs larger than 500bp (Conrad et al. 2010) and 0.012 CNVs larger than 100kbp (Itsara et al. 2010) per haploid genome. Our data indicate a mutation rate of 0.68×10^{-9} indel (1-20bp) per base per generation and 0.08 SVs (>20bp) per haploid genome (or 0.16 SVs per generation). The higher SV rates reported here in comparison to previous array CGH studies result from greater power to interrogate the full size range and spectrum of structural changes (**Fig. 2A**). For example, when considering only CNVs larger than 500bp or larger than 100kbp our data provide a rate of 0.041 and 0.0077 per haploid genome, respectively. In addition, a substantial proportion (15%) of the *de novo* SVs were retrotransposition events, allowing us to empirically estimate the rate of retrotransposition in the population to 0.023 (1/43) per generation. This is in line with estimates based on diseased subjects and on comparative genomics studies (Belancio et al. 2008; Burns and Boeke 2012).

Although the above *de novo* SV rate implies that only one in seven children bears such a mutation, we found six offspring with two and one with three *de novo* SVs (**Supplemental Table 2**). Such co-occurrence of multiple SVs is unexpected under a uniform distribution of the 41 *de novo* SVs across the 258 children ($p = 0.0074$). One individual carries two *de novo* deletions (327kbp and 1.5kbp) on maternal Chromosome 18 within a distance of 202kb of each other. This close placement of two *de novo* SVs is unlikely to be random ($p = 1.35 \times 10^{-4}$). Together, these data suggest possible differences in the effects of environmental factors or the vulnerability for acquiring *de*

de novo SVs per family (Conrad et al. 2011). We did not find evidence for a non-uniform distribution of the *de novo* indels across offspring ($p = 0.061$).

Elevated paternal mutation rates

Large-scale genome sequencing of families with disorders has shown that most *de novo* SNVs have a paternal origin, with a significant increase of *de novo* mutation burden with paternal age (Kong et al. 2012; Michaelson et al. 2012; Francioli et al. 2014; Jiang et al. 2013; Conrad et al. 2011). In addition, the majority of sporadic *de novo* CNVs and cytogenetically balanced genomic rearrangements in patients with congenital disorders are paternal in origin (Hehir-Kwa et al. 2011; Batista et al. 1994). However, it is unclear whether this bias is also present for *de novo* SVs and indels occurring in the general population. Using reads spanning neighboring phase-informative polymorphisms, we assigned a parental haplotype to 20% of the indels (39 paternal, 20 maternal) and 71% of the SVs (20 paternal, 9 maternal). We observed a significantly larger fraction (66.1%) of indels and SVs arising on paternal chromosomes than on maternal chromosomes ($p_{\text{indel}} = 0.0092$, $p_{\text{SV}} = 0.031$, **Fig. 2B**), further emphasizing the contribution of the paternal germline to human mutations. There was no significant correlation between *de novo* structural change occurrence and paternal age, possibly due to the limited number of observations.

Indel formation

We found a total of 277 simple indels with a deletion to insertion ratio of 2.74:1. This ratio is consistent with previous reports (Montgomery et al. 2013; Bhangale et al. 2005), although it is possible that this number is influenced by differences in detection power

between insertions and deletions. To investigate the mechanisms of formation of these indels, we categorized their sequence content and flanking context (**Table 1**). Most of the *de novo* indels in our data (59.9%) were found in repeat regions or resulted in local copy count changes, meaning that the long allele can be obtained by copying part or all of the short allele. More specifically, we found 28 indels in homopolymer runs (HR), 27 in tandem repeats (TR) and 111 indels resulting in a copy count change outside repeat regions (CCC). Copy-count-changing indels show a relatively balanced deletion to insertion ratio of 1.5:1. They likely arose through polymerase slippage, a process by which the leading and lagging strand become mispaired during DNA replication causing a few bases to be duplicated or deleted. Although we confirm a strong enrichment for indels in homopolymer runs (HR, $p < 2.2 \times 10^{-16}$) and tandem repeats (TR, $p < 2.2 \times 10^{-16}$) (Montgomery et al. 2013), they only represent 19.9% of our observations. This is significantly less than what we observe in polymorphic indels in our data (44.2%) and in previous reports (46.0%, Montgomery et al. 2013), possibly indicating low selective pressures on these repetitive regions (**Fig. 3A**).

The remaining 40.1% of the *de novo* indels occurred in non-repeat regions and did not lead to a copy count change (non-CCC). These likely result from imperfect double-stranded DNA break repairs by non-homologous end-joining (NHEJ) which can create indels at the repair junction. Their very high deletion to insertion ratio of 12.9:1 supports their occurrence through NHEJ (Hastings et al. 2009). This provides a mechanistic explanation for the relative depletion of short insertions in the overall size spectrum of *de novo* variation (**Fig. 2A**). We found palindromic sequences (≤ 20 bp away, ≥ 6 bp long) flanking eight of these deletions, suggesting that a secondary structure such as a

hairpin loop played a role in their formation (Hastings et al. 2009; Montgomery et al. 2013). Another five non-CCC indels presented microhomologies of at least 4bp, possibly indicating emergence through microhomology-mediated end joining (MMEJ) (McVey and Lee 2008).

In addition to the 270 simple indels, we also identified 14 complex indels (**Table 1 and Fig. 3B, Supplemental Table 3**) replacing multiple bases (2-10bp) by a different sequence (1-11bp). Although similar types of complex indels have been described previously (Levy et al. 2007), this class of variants has largely been neglected in sequencing studies and is therefore absent from variant repositories. As they represent 4.8% of the *de novo* indels in our data, we speculate that this type of polymorphism may be relatively common. Indeed, we found that 5.1% of inherited indels in the GoNL samples seem complex. One of the difficulties posed by such variation when studying polymorphisms is that they can be due to a combination of multiple separate indels or SNVs or as a single complex variant. We provide here the first *de novo* observation of such variations in humans, showing that they indeed arose as part of a single mutational event.

In contrast to simple indels, only two complex indels are located in repetitive regions, indicating that polymerase slippage is unlikely to be a major contributor to their formation. Strikingly, five of them form palindromic repeats (≥ 6 bp), a proportion significantly elevated when compared to simple insertions ($p = 0.0015$). The inserted bases for another three variants appeared to have been templated from the neighboring sequence. Such palindromic and templated complex indels have been reported in model organisms around double-stranded break repairs through synthesis-dependent

microhomology-mediated end joining (SD-MMEJ) (Yu and McVey 2010) and theta-mediated end joining (TMEJ) (Roerink et al. 2014). The formation of these indels likely follows a multi-step process involving resection of break ends, hairpin formation, microhomology-mediated annealing and DNA synthesis. **Fig. 3B** shows an example of how a *de novo* complex event we observed could have arisen through SD-MMEJ.

SV formation

To obtain insights into the origin of *de novo* SVs in the general population, we experimentally fine-mapped their breakpoints at base-pair resolution and assigned a formation mechanism (**Fig. 4A, Supplemental Table 2**) (Lam et al. 2010). The majority (N = 24, 58.5%) of the SVs larger than 20bp likely arose via non-homologous repair (NHR) as their breakpoints presented little or no homology (0-6bp, N = 19) or short inserted sequences (1-18bp, N = 5). The breakpoints junctions of eight SVs (19.5%) contained long homologous sequences (28bp to 12kb) indicating formation by homology-driven repair and these are classified as mediated by non-allelic homologous recombination (NAHR) (**Supplemental Table 2**). Three variants (7.3%) were found within a region with a variable number of tandem repeats (VNTR).

We also identified 6 *de novo* mobile element insertions (14.6% of SVs), all short interspersed elements (SINE) retrotransposon insertions of the *AluY* family (**Supplemental Fig. 2, Supplemental Table 2**). The sequences of the breakpoint junctions of the *de novo* *AluY* retrotransposon insertions all indicate the presence of target site duplication (TSD) of 3-16bp, and poly-A tails (**Supplemental Fig. 2**); both well-known signatures of retrotransposon integration (Burns and Boeke 2012).

Remarkably, in one instance of interchromosomal integration we found three breakpoint junctions leading to the joining of two small DNA fragments – one from Chromosome 3 (163bp) and another from Chromosome 19 (179bp) – into Chromosome 4 (**Fig. 4B**). We propose that this complex rearrangement has also occurred through retrotransposition, because the fragment from Chromosome 19 contains part of an *AluY* element and no DNA is lost at the original genomic positions of the inserted sequences. Furthermore, the breakpoint on Chromosome 4 likely involved a staggered cut with three overhanging nucleotides, which appear as TSDs in the final product. The fragment on Chromosome 3 is close (1.7 kbp) to the 3'UTR of the *PPARG* gene. We hypothesize that the fragment could represent a retrocopy of an RNA product from this region, e.g. an elongated version of the *PPARG* mRNA or another transcript.

We compared the proportion of *de novo* SVs derived from each of four mechanisms with inherited SVs from the GoNL project. This revealed a larger proportion of mobile element insertions (MEI, 40.8%, $p = 0.029$) for inherited SVs and a lower proportion of NHR (30.3%, $p = 0.0072$), while similar proportions of VNTR (10.5%) and NAHR (18.4%) mediated variants were found. In addition, we compared the proportion of each SV mechanism with those reported previously (Mills et al. 2011; Pang et al. 2010, 2013; Kidd et al. 2010) (**Supplemental Table 4**) and found substantial differences between studies, which probably reflect methodological differences (Pang et al. 2013).

Functional impact of *de novo* structural changes

Although none of the *de novo* indels overlapped with protein-coding exons, in total 6 large *de novo* SVs (3.7kbp – 327kbp) affect coding regions, resulting in exonic duplications of *BANK1* (1 exon), *PROC*, *GCNT3*, *GTF2A2* and *BNIP2* (complete

genes), and deletions in *LYN* (1 exon), *PTPRM* (6 exons) and *UBR5* (8 exons) (**Fig. 5, Supplemental Table 2**). Four SVs potentially disrupt gene function by changing reading frames, introducing premature stop codons or truncating the protein. Examination of these genes in the exome sequencing database from the Exome Aggregation Consortium (ExAC, <http://exac.broadinstitute.org>) revealed that all of them contain heterozygous loss-of-function mutations in the population. This indicates that heterozygous changes in these genes possibly have no early developmental consequences. Mutations in two of the affected genes - *BANK1* and *PROC* - are associated with systemic lupus erythematosus (Kozyrev et al. 2008) and thrombophilia (Romeo et al. 1987), respectively. However, *PROC* and *BANK1* duplications – as observed in our study – have not been reported to be associated with a clinical phenotype and the offspring carrying these *de novo* SVs appeared healthy at the time of sampling (aged 39 and 32).

Next, we compared the genomic footprints of *de novo* SVs and indels with SNVs (**Supplemental Methods**). Consistent with recent studies involving families with disorders (Kong et al. 2012; Michaelson et al. 2012; Jiang et al. 2013; Gilissen et al. 2014), an average of 45 *de novo* SNVs per child were detected in the GoNL Project (Francioli et al. 2014). While the cumulative burden of *de novo* indels was only 7.1bp per child, we found that despite their lower frequency *de novo* SVs affected on average 4,084 genomic bases (**Fig. 6A**). This relatively large impact of SVs was also found in coding regions where an average of 28.6 coding bases per generation were affected by *de novo* SVs, while only 0.55 coding bases per generation were mutated by *de novo* SNVs (**Fig. 6B**). The larger number of affected bases for SVs relative to SNVs is largely

due to their difference in size. We observed that per offspring 18 times more genes are hit by *de novo* SNVs (0.55) versus SVs (0.03) (**Fig. 6C**). However, only 5% of *de novo* SNVs is potentially disruptive (stop gained, stop lost, splice-site change), whereas 50% (4/8) of the *de novo* SVs possibly have a major impact on gene structure and function (**Fig. 5**).

Finally, we investigated differences in the genomic footprint of *de novo* and inherited SVs and SNVs identified in the GoNL data. We found that on average large *de novo* SVs (>20bp) affect 90.6 times more genomic bases, 52.0 times more coding bases and 60.1 to 114.7 times more bases marked by histone modifications than *de novo* SNVs (**Fig. 6D**). In contrast, inherited SVs affected on average only 1.6 times more bases when compared to inherited SNVs. Altogether, these data demonstrate the overall impact of *de novo* SVs on the genome when compared to *de novo* SNVs and indels.

Discussion

The human genome continuously evolves as a result of mutation and selection. Because of the relatively low rate of SV and indel formation, large numbers of parent-offspring families are required to capture the full spectrum of *de novo* changes that alter genome structure every generation (Campbell and Eichler 2013). Moreover, the detection and genotyping of these variants remain challenging given their diversity in both size and type (Alkan et al. 2011). Although limited by the short size of reads and the relatively low coverage depth used in this study, we have provided a representative picture of the landscape of *de novo* SVs and indels in the human genome based on whole-genome sequencing of 250 families by leveraging multiple calling approaches.

Our work demonstrates that both *de novo* indels and SVs originate primarily in the paternal germline, complementing recent findings on *de novo* SNVs (Kong et al. 2012; Michaelson et al. 2012; Francioli et al. 2014). We provide empirical estimates for the rate of *de novo* SVs and indels across the complete size spectrum, including relative frequencies of different variant sizes and types. These rates define a baseline for the general population and will help guide the interpretation of *de novo* indels and SVs in the diagnosis of individual patients (Stankiewicz and Lupski 2010). Roughly 15% of patients with intellectual disability or congenital abnormalities harbor an apparently causative CNV, most of which occur *de novo* (Hochstenbach et al. 2011). Estimating pathogenicity of these CNVs is based on their overlap with known disease CNVs, protein coding genes and control databases, but should also consider the background rate of large CNVs as described here. Specifically, we find that changes in gene structure - i.e. deletion or tandem duplication of entire exons - occur at a rate of 1 in 43 offspring in the general population.

In spite of their low frequency, large *de novo* SVs have a substantial impact on the genome. Due to their larger size, the average genomic footprint of *de novo* SVs is much greater than that of *de novo* SNVs and they are much more likely to hit a coding region. Indeed, 14.6% of the *de novo* SVs we observed affected exons, whereas only about 1.3% of the *de novo* SNVs did. The considerable influence of *de novo* SVs is however primarily driven by a limited number of *de novo* SVs altering multiple kilobases of genomic sequence in a single generation. These rare but large variants may be quickly removed from the population by purifying selection, particularly when they hit genes or

other important genomic elements (**Fig. 5**) (Mills et al. 2011; Conrad et al. 2010). This may explain why inherited SVs and SNVs affect a similar number of bases.

Previous studies have convincingly shown that large and dramatic genome changes introduced by large structural mutations can be associated with a multitude of pathological conditions (Stankiewicz and Lupski 2010). In this study we demonstrate that a broad range of *de novo* indels and structural variations is also characteristic for individuals obtained from a general human population.

Methods

Whole genome sequencing and alignment

Genomic DNA from nucleated blood cells was obtained from 250 Dutch families (231 trios, 8 quartets with dizygotic twins and 11 quartets with monozygotic twins), which were selected without phenotypic ascertainment. Library construction and whole-genome sequencing was performed using the Illumina HiSeq 2000 platform (500 bp insert size, 90bp paired-end reads).

Reads were aligned to the GRCh37/hg19 human genome reference using BWA 0.5.9-r164 (Li and Durbin 2009). We expect that alignment to GRCh38 would not significantly alter our findings, given that *de novo* variation is dependent on differences between parental and offspring genomes. Aligned data were processed following the Genome Analysis Toolkit (GATK) best practices v2 (DePristo et al. 2011): duplicate reads were marked using Picard tools (<http://picard.sourceforge.net>), reads were realigned around indels using GATK IndelRealigner and base quality scores were recalibrated using GATK BaseRecalibrator. Additional details regarding the study design, sequencing and alignment can be found in (Francioli et al. 2014).

Detection of *de novo* variants

Indels were called using GATK UnifiedGenotyper (DePristo et al. 2011) and Pindel (Ye et al. 2009) and all calls were further genotyped with GATK HaplotypeCaller (**Supplemental Methods**). We used GATK PhaseByTransmission (PBT) to call *de novo* variants from the GATK UnifiedGenotyper and HaplotypeCaller calls using a mutation prior of 10^{-4} per base per generation. We kept calls with (a) no evidence of the non-reference allele in the parents, (b) no non-reference allele called in any other GoNL

sample, (c) at least 2 reads supporting the non-reference allele in the child, (d) a PBT posterior of at least Q20. Pindel calls with non-reference reads in the child only, at least 2 reads supporting the non-reference allele in the child and no significant strand bias were kept as *de novo* candidates. All putative *de novo* indels from either method were experimentally validated in 92 of the families (including 7 quartets with dizygotic twin pairs).

De novo SVs were called and filtered independently by 11 algorithms based on the following approaches: gapped/split read mapping (Pindel (Ye et al. 2009), GATK UnifiedGenotyper (DePristo et al. 2011), GATK HaplotypeCaller), analysis of discordant pairs (BreakDancer (Chen et al. 2009), 1-2-3-SV (<http://tools.genomes.nl/123sv.html>) (Kloosterman et al. 2011), Genome STRiP (Handsaker et al. 2011), MATE-CLEVER (Marschall et al. 2013)), read depth analysis (CNVnator (Abyzov et al. 2011), DWAC-seq (<http://tools.genomes.nl/dwac-seq.html>), FACADE (Coe et al. 2010)). In addition, Mobster was used to call *de novo* mobile element insertions (MEIs) (Thung et al. 2014). For each algorithm, variant calls confined to kid(s) of a single family, but not detected in any other GoNL samples were selected and visually evaluated with IGV (Robinson et al. 2011) to discard false positives due to alignment artifacts. We then created a union of all remaining calls by merging variants detected by multiple methods in the same child based on SV type and overlapping coordinates. We retained the most precise breakpoints for each variant based on the calling algorithm (in order: split-read, discordant read-pairs, read-depth). Local *de novo* assembly (SOAPdenovo (Luo et al. 2012)) was used for breakpoint fine-mapping for SVs greater than 100bp. A detailed

description of the tools, settings, filtering and variant calls, including sensitivity analysis is provided in the **Supplemental Methods**.

Experimental validation

Oligonucleotide primers for amplification of a genomic segment containing the variant (for mutations smaller than 100bp) or variant breakpoints (for larger SVs) were designed using Primer3 software (**Supplementary Table 2**). PCR products were resequenced with Sanger, IonTorrent or MiSeq (2x250 bp) technologies. Genotyping of the resequenced variants is described in the **Supplemental Methods**.

Parental origin

We used genotypes from phased haplotypes (Francioli et al. 2014) to interrogate the parental origin of *de novo* indels and SVs. For indels, we identified read-pairs containing both the *de novo* allele and a phase-informative SNP allele.

Parental haplotypes for SVs were determined from allele ratios at overlapping SNPs. Assignment to the paternal or maternal haplotype was made if: a) one or more homozygous alleles in the offspring are located inside a *de novo* deletion and could only be inherited from one parent; b) one or more polymorphic SNPs in offspring are located inside a *de novo* duplication and have a 2:1 (or 1:2) ratio with the reference allele and can be assigned unambiguously to either the paternal or maternal haplotype; c) a SNP in the offspring was located within a discordant read pairs supporting the *de novo* SV and could be assigned to either the paternal or the maternal genome.

Paternal and familial biases

We tested for enrichment of *de novo* mutations on the paternal haplotypes using a one-tailed binomial test and found that both indels ($p = 0.0092$) and SVs ($p = 0.031$) were indeed enriched. Additionally, we fit a linear model to the number of *de novo* indels in the 99 independent offspring and the father's age at conception correcting for coverage but did not find a significant association ($p = 0.24$).

We used a multinomial model with equal probability for each child to receive a *de novo* variant to test for uniform distribution of variants across children (goodness-of-fit p-value obtained using 100,000 Monte Carlo replicates).

In one sample, we observed two SVs occurring on maternal Chromosome 18 at a distance of 201kbp. We computed the probability of observing 2 independent deletions so closely located by direct enumeration. Let E_1 and E_2 be the smaller and larger deletion events, respectively, having respective lengths of L_1 and L_2 bases. Neglecting edge effects at the ends of chromosomes, the number of ways E_1 could be placed in the genome is $(G - L_2 + 1) - (L_1 + L_2 - 1)$, where G is the nominal genome size. The first term represents the possible placements of E_1 , the second the number of placements that would result in the collapse of both events. If D is the observed distance in bp between the two events, then the number of the total placements that are significant is $2D$, since E_1 could be on either side of E_2 implying a “two-sided” test. The ratio of these two counts represents the tailed P-value. Given $G \approx 3 \times 10^9$ and the observed values $L_1 = 1,552$, $L_2 = 326,954$, and $D = 201,790$, we find a P-value of 1.35×10^{-4} .

Computation of mutation rates

To compute the indel rate, we used validated *de novo* indels in 99 children from 92 families, including 11 quartets with monozygotic (MZ) twins, 7 quartets with dizygotic (DZ) twins and 74 trios. We only used one child from each of the MZ twin pairs and considered the 14 children from the 7 DZ twin pairs as independent for this analysis. Using permutations, we ruled out any correlation between siblings from a DZ pair ($p = 0.59$). The rate was computed as the sum of *de novo* indels divided by the sum of accessible bases in the 99 children.

The SV rate was computed over 258 children from all 250 families. Only one child was considered for each of the monozygotic twin pairs and siblings from dizygotic twin pairs were considered as genetically independent with respect to *de novo* SVs. The rate was calculated by dividing the number of *de novo* SVs ($N = 41$) by the 258 children times 2 transmitted haplotypes. We also report the rate for *de novo* MEIs ($N = 6$, including one interchromosomal event which involved an *AluY* element) computed in a similar fashion.

Indel and SV formation mechanisms

Indels were annotated using the classification proposed by Montgomery *et al.* (Montgomery *et al.* 2013), except for Predicted Hotspots (PR) that we did not use since they were not readily available and complex indels that are new in our data.

Analysis of mutation formation mechanisms of SVs was performed using BreakSeq software v. 1.3 (Lam *et al.* 2010). See the **Supplemental Methods** for a full description of indel and SV classification.

Data access

Sequence data have been deposited at the European Genome-phenome Archive (EGA), which is hosted by the European Bioinformatics Institute (EBI), and are available via <https://www.ebi.ac.uk/ega/studies/EGAS00001000644>.

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Author Contributions

WPK, LCF, VG and KY planned and directed the research. CW, CD, GO, PES, DB and PdB supervised the GoNL data generation. MS supervised read mapping. JHK, AS, TM, FH, BPC, AA, EL, DTT, MM, REH, VG, KY, LCF and VK performed SV and indel calling. IR, EC, PA, WPK and LK performed validation assays and analysis. EDS, CW, AU and DB provided DNA samples for validation. MR, LCF and VG performed phasing of indels and SVs. MW, TM and AS provided input for statistical testing. MMcV provided input on indel formation mechanisms. WPK, LCF, KY and VG wrote the manuscript. FH, CW, TM, AS, JHK, EC, MCW, CMD, DB, AA, EE and PIWB commented on the manuscript.

Figure legends

Figure 1. Overview of study design. A total of 250 parent-offspring families were sequenced at 14.5x coverage. *De novo* indel and structural variant (SV) calling was performed using 11 algorithms combining gapped reads, split reads, discordant read-pairs and read depth approaches to cover the entire mutation size spectrum. All candidate indels (1,169 in 99 children) and SVs (601 in 258 children) were subjected to experimental validation leading to 291 validated *de novo* indels and 41 *de novo* SVs.

Figure 2. Frequency of *de novo* indels and SVs. (A) Size-frequency distribution of 332 validated *de novo* indels and SVs identified in this study. In addition, the frequency of *de novo* SNVs is shown (Francioli et al. 2014). The asterisk denotes a size bin containing one *de novo* tandem duplication and six *de novo* retrotransposon insertions. (B) Barplot indicating the numbers of *de novo* indels and SVs on paternal and maternal haplotypes.

Figure 3. Overview of *de novo* and inherited indel classes and their formation mechanisms. (A) Proportion of *de novo* and inherited indels by class. Inherited indels exhibit a 2.3 fold enrichment in indels located in homopolymer runs (HR) and tandem repeats (TR) when compared to *de novo* indels, suggesting lower selective pressures in these regions. (B) Outline of a plausible 7-step process that could account for the formation of a complex *de novo* indel by SD-MMEJ.

Figure 4. Mechanisms contributing to the formation of *de novo* SVs. (A) Overview of four SV formation mechanisms, including examples and observed counts for each of

these. L=left flank; R=right flank; J=junction. **(B)** Schematic structure of a complex *de novo* interchromosomal SV involving an insertion of DNA from Chromosomes 3 and 19 into Chromosome 4. TSD: target site duplication.

Figure 5. Effect of *de novo* SVs on protein coding genes. **(A)** Deletion of 6 exons of *PTPRM* resulting in an in-frame shortened gene. **(B)** Deletion of 1 exon of *LYN* causing an out-of-frame effect at the transcript level. **(C)** Deletion of 5 exons of *UBR5* causing an out-of-frame effect at the transcript level. **(D)** Duplication of 1 exon of *BANK1*, possibly resulting in a premature stop. **(E)** Duplication of the entire *PROC1* gene. **(F)** Duplication of 3 entire genes (*GCNT3*, *GTF2A2*, *BNIP2*). Duplications are shown in green and deletions in red. A, ancestral allele; D, derived allele.

Figure 6. Functional impact of *de novo* indels and SVs. **(A)** Average number of genomic bases affected by *de novo* SNVs, indels and SVs per child. **(B)** Average number of coding bases affected by *de novo* SNVs, indels and SVs per child. **(C)** Average number of genes affected by *de novo* SNVs, indels and SVs per child. The relative frequencies of the effects of the variations on the gene are indicated. **(D)** Comparison of the footprint of *de novo* (blue bars) and inherited (brown bars) large SVs (>20bp) relative to the footprint of SNVs. The footprint was computed genome-wide, in protein-coding regions and genomic regions marked by H3K4Me1, H3K4Me3 and H3K27ac based on data from the ENCODE project (The ENCODE Project Consortium, 2007). The y-axis shows the ratio of the average number of affected bases per offspring relative to SNVs.

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Supplemental Materials

Supplemental Figures 1 and 2.

Supplemental Tables 1-5.

Supplemental Methods.

Table 1. Indel classes and mechanisms

Class	Example ¹	Observations	Possible Mechanisms	Sequence Features
Homopolymer Run	Ref. CTGAGGAAGAG <u>TTTTTTT</u> TACA	21 insertions	Polymerase slippage	Repeat context
	De Novo CTGAGGAAGAG- <u>TTTTTTT</u> TACA	7 deletions		
Tandem Repeats	Ref. CTACCCAGGC <u>AGAGAGAG</u> AAA	8 insertions	Polymerase slippage	Repeat context
	De Novo CTACCCAGGC- <u>---</u> AGAGAAA	19 deletions		
Copy Count Changing	Ref. CAGAAGG- <u>---</u> TAGCTAGTCAG	37 insertions	Polymerase slippage	Local copy count change
	De Novo CAGAAGG <u>TAGCTAGCT</u> AGTCAG	74 deletions		
Non Copy Count Changing	Ref. CTAAAGGGCAGTCTTGCAAAAG	8 insertions	NHEJ ²	Blunt or microhomology at breakpoints
	De Novo CTAAAGGGCAG--TTGCAAAAG	90 deletions		
	Ref. AGTCAAAAACCA <u>AA</u> GTTTTGAA	8 deletions	NHEJ ² / hairpin loop	Palindrome (≥6bp) in surrounding context (≤20bp)
	De Novo AGTCAAAAACCA- <u>---</u> TTTTGAA			
	Ref. GGGGAGAA <u>TTGAGACT</u> TGATCA	5 deletions	NHEJ ² / MMEJ ³ / replication slippage	Microhomology ≥4bp at breakpoints
	De Novo GGGGAGAA- <u>-----</u> TTGATCA			
Complex	Ref. ACTCACAAAAAAATTTTTTTTCC	2 variants	Polymerase slippage	Repeat context
	De Novo ACTCACAAAAA- <u>TTTTTTTT</u> TCC			
	Ref. CACATGGGCTTCC- <u>---</u> TGTC	8 variants	SD-MMEJ ⁴ TMEJ ⁵	Palindromic or templated insertion
	De Novo CACATGGGCT <u>GGAGCCCA</u> TGTC			
	Ref. CCAAAGTGCTGGGATTACAGGC	4 variants	Unknown	None
	De Novo CCAAAGTGCTC-GATTACAGGC			

¹All examples are chosen from observed validated *de novo* indels and their positions are given with respect to the start of the variant on the human reference genome build 37. In the alleles column, “A” denotes the ancestral allele and “D” the derived allele. Differences between the ancestral and derived alleles are highlighted in bold. Repeats and palindromes are underlined with straight and wavy lines respectively.

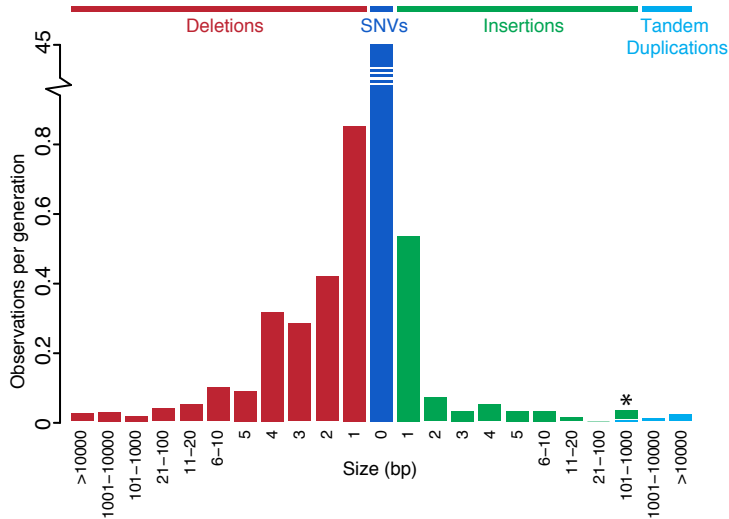
²NHEJ: Non-homologous end joining

³MMEJ: Microhomology-mediated end joining

⁴SD-MMEJ: Synthesis-dependent microhomology-mediated end joining

⁵TMEJ: Theta-mediated end joining

A



B

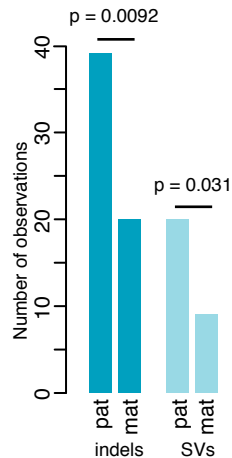
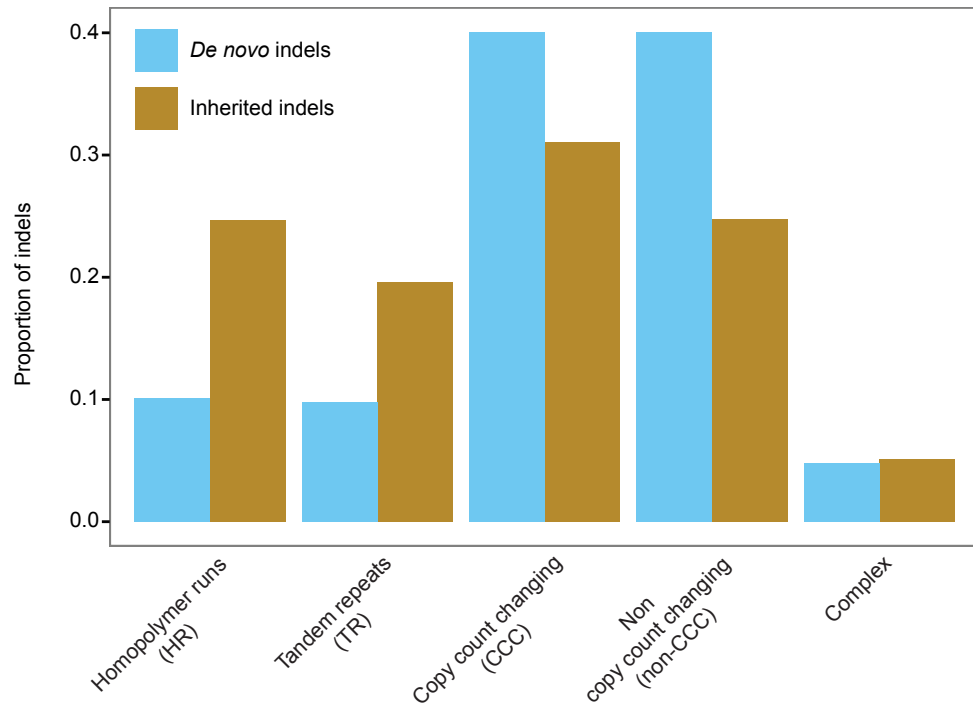


Figure 2

A**B****1. double-strand break at CG/TA**

5' CAAATGTGCTTCATTTCAAACGAGC TATTTTACCCACCTCTCTTCA 3'
 3' GTTACACGAAGTAAAGTTTGCTCG ATAAAATGGGTGGAGAGAAGT 5'

**2. 5' to 3' resection**

5' CAAATGTGCTTCATTTCAAACGAGC A 3'
 3' G ATAAAATGGGTGGAGAGAAGT 5'

**3. snapback to form hairpin**

5' CAAATGTGCT TCATT A 3'
 3' G CGA GCAAC ATAAAATGGGTGGAGAGAAGT 5'

**4. limited synthesis (polQ?)**

5' CAAATGTGCT TCATT A 3'
 3' GTTACACGA GCAAC ATAAAATGGGTGGAGAGAAGT 5'

**5. unwinding of hairpin**

5' CAAATGTGCTTCATTTCAAACGAGC ACATT A 3'
 3' G ATAAAATGGGTGGAGAGAAGT 5'

**6. anneal at ATTT/TAAA microhomology**

5' CAAATGTGCTTCATTTCAAACGAGC ACATT A 3'
 3' G TAAAATGGGTGGAGAGAAGT 5'

**7. tail clipping, fill-in synthesis and ligation**

5' CAAATGTGCTTCATTTCAAACGAGC ACATT TATTTTACCCACCTCTCTTCA 3'
 3' GTTACACGAAGTAAAGTTTGCTCG GTAAAATGGGTGGAGAGAAGT 5'

Red = deletion

Blue = new synthesis

Green = insertion

Figure 3

A

Class	Example	Observed counts
Non-homologous repair	deletion Ref. L J R <i>De novo</i> Left TTTTTCATAAATTTAGGGTAGCCTAAGTGT Right TAGCGCGATCTCAGTTCAC TGCAAGCTCCA Junction TTTTTCATAAATTTATCATGCAAGCTCCA	18 deletions 6 tandem duplications
Non-allelic homologous recombination	deletion Ref. L J R <i>De novo</i> Left GCAGCGACGAGCAGGTG.....GGGGCCCCGGGGTCGCTGC Right GGAGGCCGTGAGCAGGTG.....GGGGCCCCGGGGCTCCGGG Junction GCAGCGACGAGCAGGTG(>200bp)GGGGCCCCGGGGCTCCGGG	8 deletions
Variable number of tandem repeats	deletion Ref. L J R <i>De novo</i> Left CCTCTCACTTATAACCCAAAACACACACACACGACACACACAC Right ACACACGACACACACACACACACACACACACACACACCCTT Junction CCTCTCACTTATAACCCAAAACACACACACACACACACACCCTT	1 deletions 2 tandem duplications
Mobile element insertions	AluYb8 insertion Ref. <i>De novo</i> aluYb8 GTCCTTTAACTTCTTTATGTA TSD poly-A tail TSD	6 insertions

B

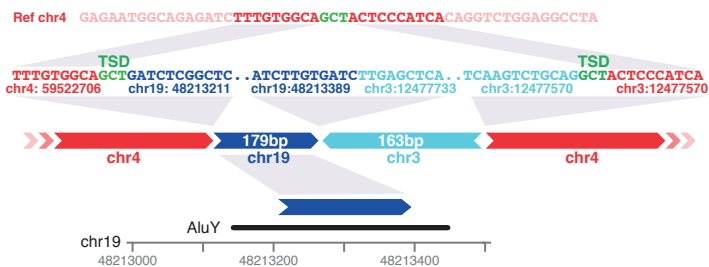


Figure 4

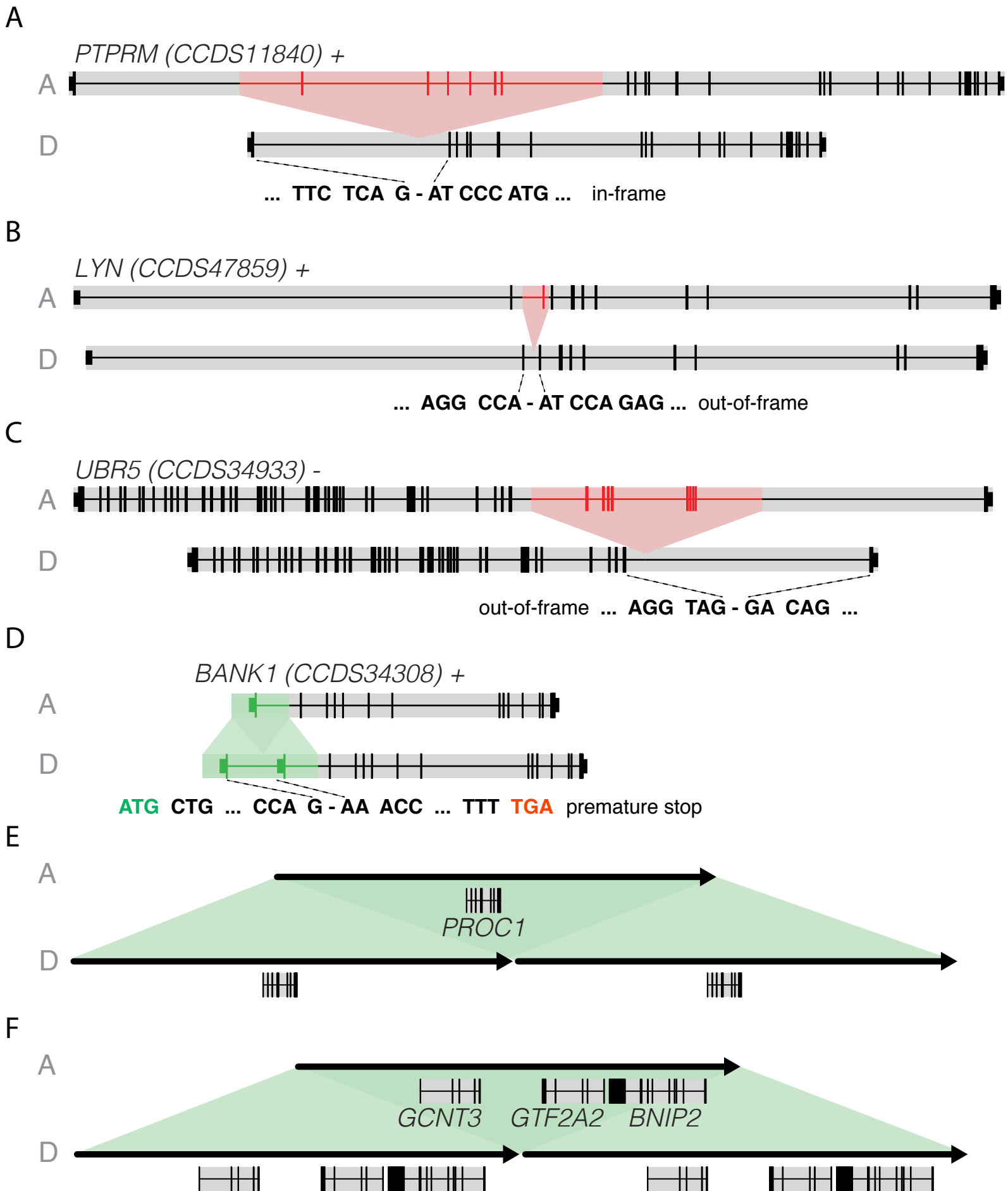


Figure 5

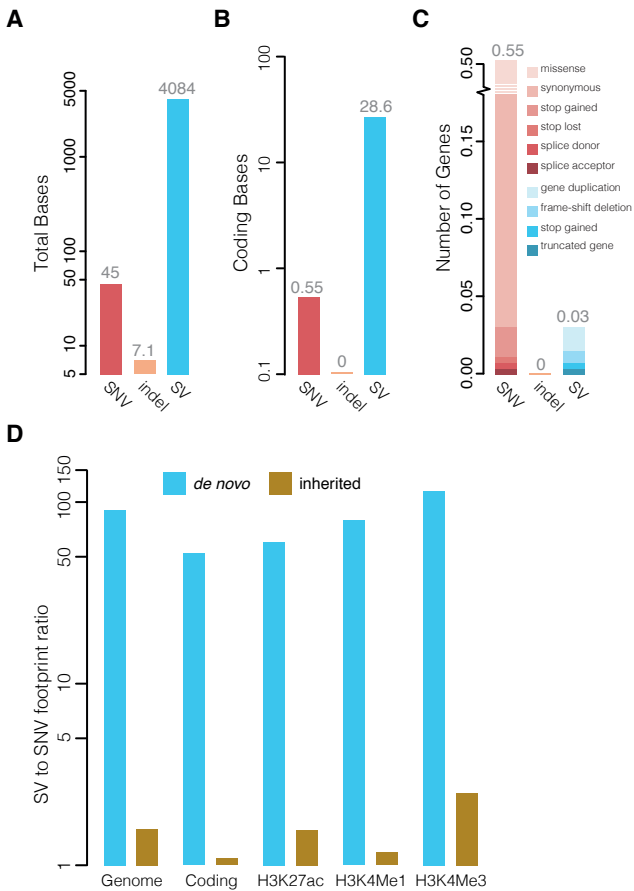


Figure 6