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Corrigendum: Discovery and genotyping of structural variation from long-read haploid genome sequence data

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Due to a formula error, Table 2 in the above article displayed incorrect values of the observed structural variants. The authors would like to correct these values and the text referring to them (page 680), which should read as follows:

> Of all 461,480 insertions and deletions detected as SVs or indels, only 1.8% of events occurred within a GENCODE or RefSeq coding exon, noncoding exon, or untranslated region (UTR) (Table 2). An additional 4.3% of events occurred in predicted noncoding regulatory regions, including DNase hypersensitivity sites, promoters (H3K27ac), and enhancers (H3K4me3), while 37.0% of events occurred in introns (Harrow et al. 2012).

The authors apologize for any inconvenience. Table 2 and its associated text have been updated online to reflect the corrected values.

Table 2. Summary of SVs and indels in the theoretical diploid CHM1/CHM13 by putative functional effect

	Structural variants			Indels				
Effect type[a]	Deletion	Insertion	All	Deletion	Insertion	All	Total	Proportion of all events
Coding exon (not multiple of three)	45	11	56	91	86	177	233	0.0005
Coding exon (multiple of three)	57	84	141	223	214	437	578	0.0013
UTR	49	67	116	2340	2084	4424	4540	0.0098
Noncoding exon	116	121	237	1505	1390	2895	3132	0.0068
Noncoding regulatory[b]	542	869	1411	9203	9345	18,548	19,959	0.0432
Intronic	4447	7288	11,735	85,522	73,613	159,135	170,870	0.3703
Functional	5256	8440	13,696	98,884	86,732	185,616	199,312	0.4319
Not functional	6235	10,061	16,296	128,866	117,006	245,872	262,168	0.5681
Proportion functional	0.4574	0.4562	0.4567	0.4342	0.4257	0.4302	0.4319	0.4319
Total	11,491	18,501	29,992	227,750	203,738	431,488	461,480	1.0000

[a]Annotations of coding exons, 3′ and 5′ UTRs, noncoding exons, and introns are based on RefSeq and GENCODE comprehensive annotations.
[b]Regulatory regions were annotated as previously described by Gordon et al. (2016).

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