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Supplemental Data

**Multicentric Carpotarsal Osteolysis is Caused
by Mutations Clustering in the Amino-Terminal
Transcriptional Activation Domain of *MAFB***

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Table S1. Summary Statistics for Mapping and Coverage

	SKDP 1.3	SKDP 15.3	SKDP 20.4	SKDP 28.3	SKDP 8.3	Mean values
Total bases	1731677499	2279192082	2378161980	1484849487	1957529739	1966282157
Total mapped bases	1715783807	2263250635	2358325193	1470261623	1906540732	1942832398
Bases on target exons (+/-200bp)	1506970573	1999233622	2078292179	1255222192	1630376221	1694018957
Bases on target exons	1049421463	1388403439	1430071373	892412954	1143024536	1180666753
% bases on target exons (+/- 200bp)	87.8	88.3	88.1	85.4	85.5	87.0
% bases on target exons	61.2	61.3	60.6	60.7	60.0	60.8
Target exon median base coverage	31.9	45.0	46.4	29.2	36.4	37.8
Target exon mean base coverage	43.7	58.8	60.5	37.0	48.3	50.0
Target exon bases with coverage >1	98.7	98.5	98.4	98.3	98.5	98.5
Target exon bases with coverage >5	92.4	94.0	94.3	91.9	93.6	93.2
Target exon bases with coverage >10	82.1	87.4	88.0	81.6	85.4	84.9
Target exon bases with coverage >15	71.8	80.0	81.0	70.6	76.3	75.9

Table S2. Detailed Base Calling Information

Note: these results refer to SNPs/indels that have passed quality and coverage filtering as described.

Class	Type	SKDP 1.3		SKDP 15.3		SKDP 20.4		SKDP 28.3		SKDP 8.3	
		ALL	Novel	ALL	Novel	ALL	Novel	ALL	Novel	ALL	Novel
snp	Downstream	29	0	37	0	54	2	20	0	37	0
	Intergenic	80	0	67	1	84	0	87	3	60	1
	Intronic	8495	96	10121	93	10766	71	7033	104	8408	114
	ncRNA	591	8	655	5	672	4	498	8	568	4
	Nonsynonymous	5191	119	5617	108	5651	105	5163	139	5195	106
	Splicing (5bp)	373	7	414	5	421	5	371	10	385	12
	Stop-gain	34	2	46	5	44	1	50	4	44	4
	Stop-loss	7	0	11	0	10	0	8	0	8	0
	Synonymous	6744	71	6875	62	6973	58	6366	108	6495	58
	Unknown	0	0	0	0	0	0	0	0	1	0
	Upstream	77	0	93	1	105	0	70	2	89	1
	Upstream; downstream	8	0	14	0	8	0	6	0	8	0

	3' UTR	506	6	582	2	632	6	455	5	491	3
	5' UTR	363	8	391	8	390	3	311	2	315	4
	5' UTR; 3' UTR	0	0	0	0	0	0	0	0	1	0
indel	Downstream	1	0	4	0	4	0	1	0	4	0
	Intergenic	2	0	1	0	3	0	2	0	1	0
	Intronic	595	91	720	108	762	108	428	66	619	100
	ncRNA	31	7	32	6	44	11	30	6	38	11
	Splicing (5 bp)	28	5	29	4	33	6	21	4	29	7
	Stop-gain	3	1	2	1	2	1	2	1	3	1
	Stop-loss	0	0	0	0	1	0	0	0	1	0
	Upstream	6	1	5	0	11	1	5	0	6	1
	Upstream; downstream	1	0	1	0	2	0	0	0	2	1
	3' UTR	28	5	39	6	39	7	37	6	29	2
5' UTR	14	0	21	2	16	0	15	1	15	0	