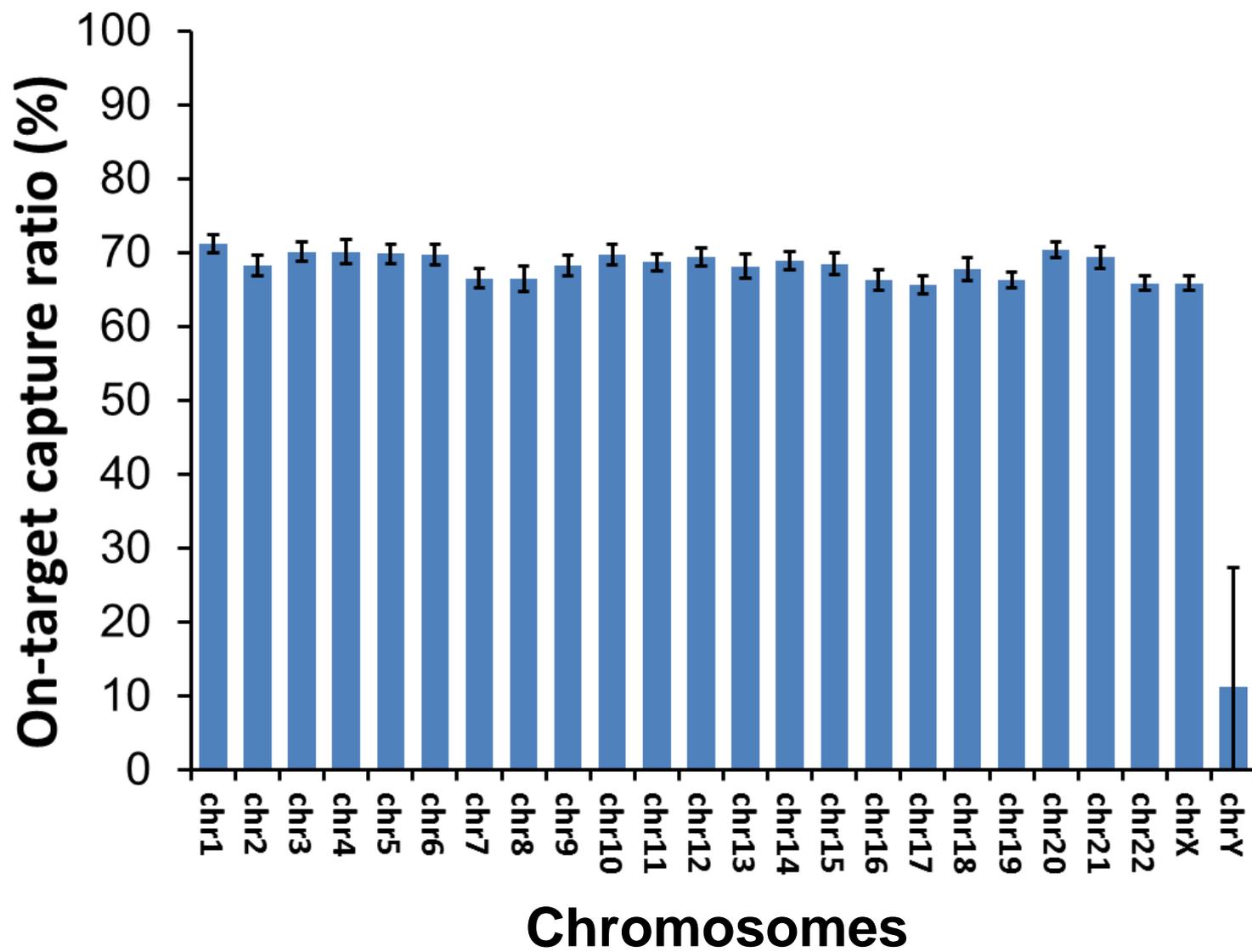
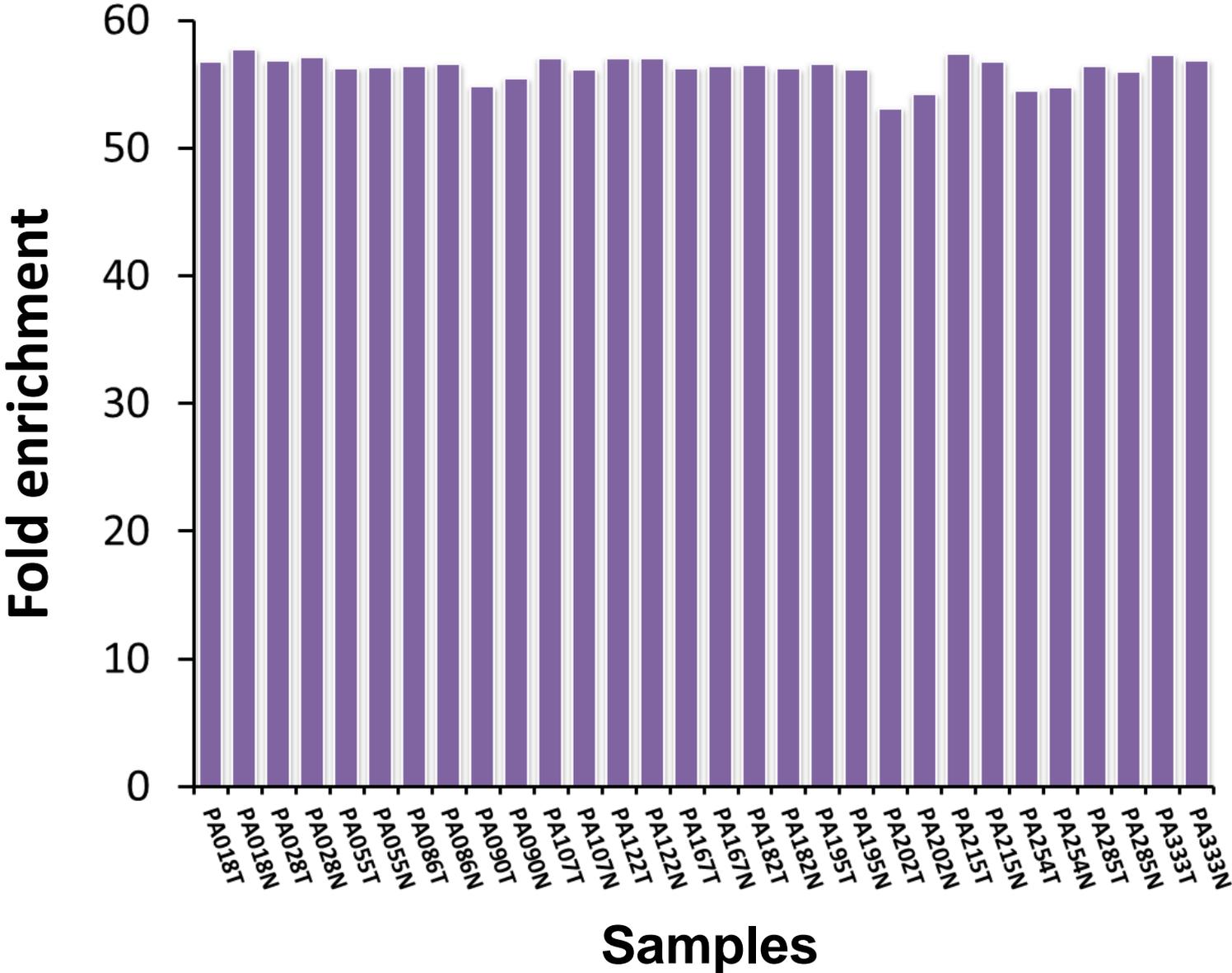


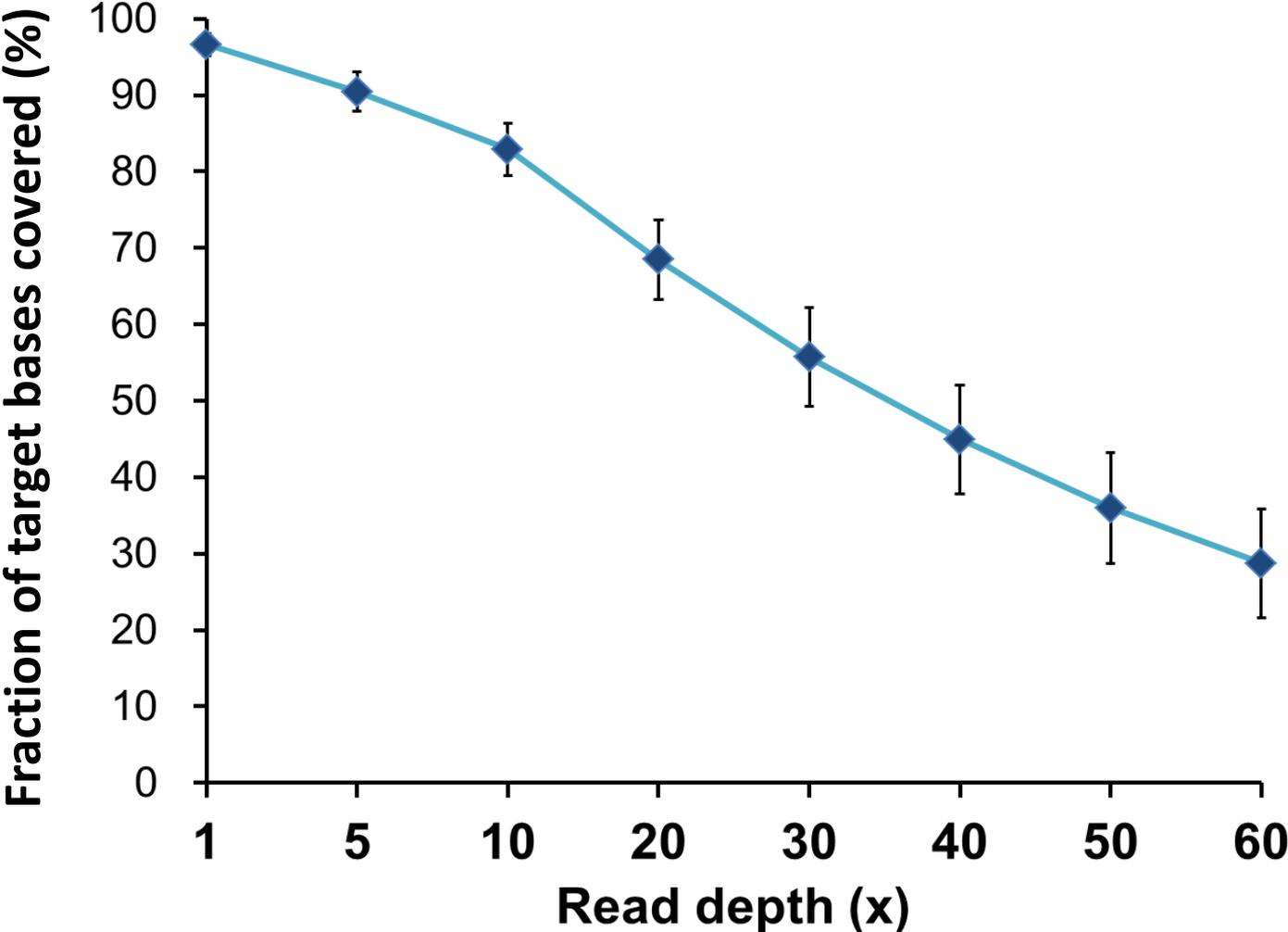
Supplemental Figure S1



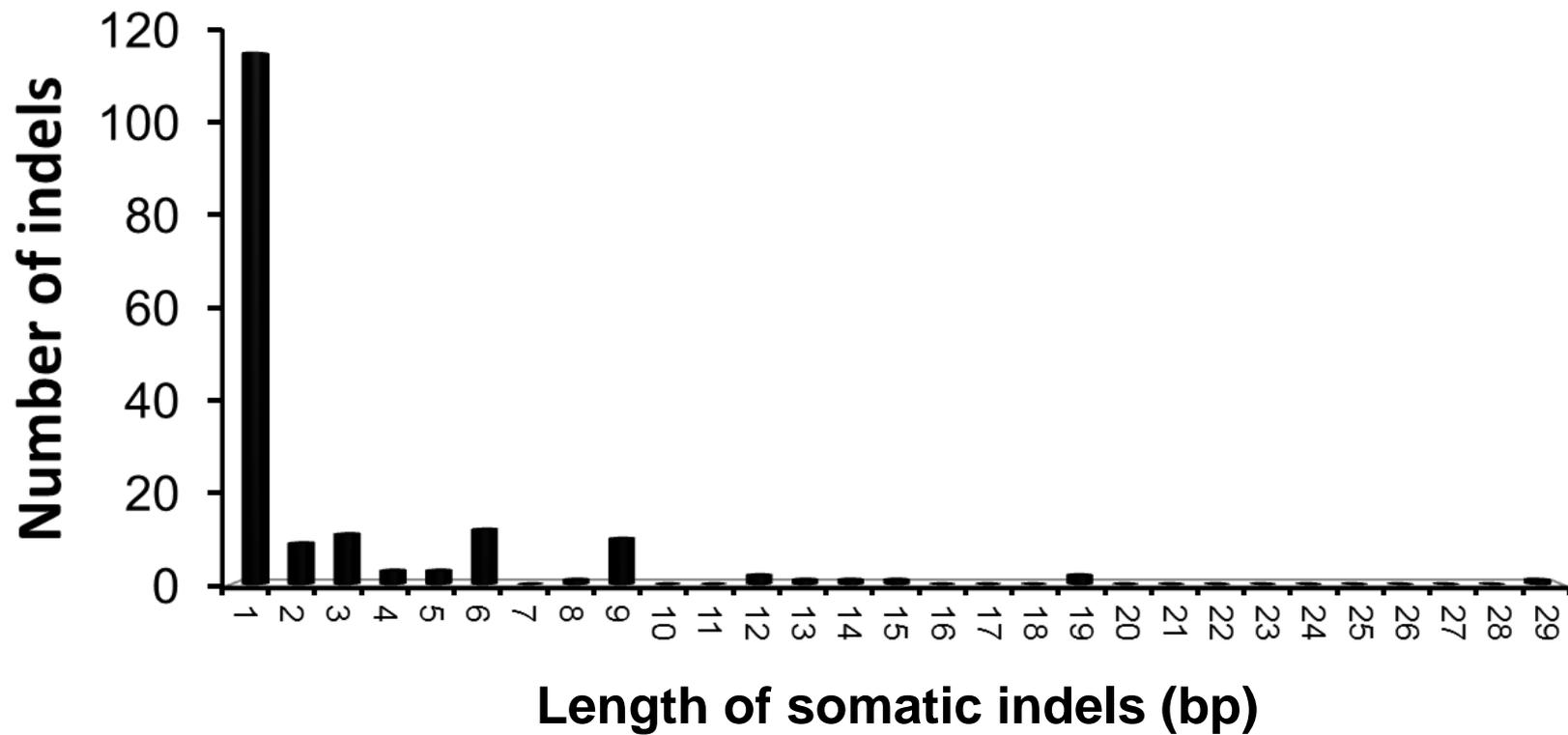
Supplemental Figure S2



Supplemental Figure S3



Supplemental Figure S4

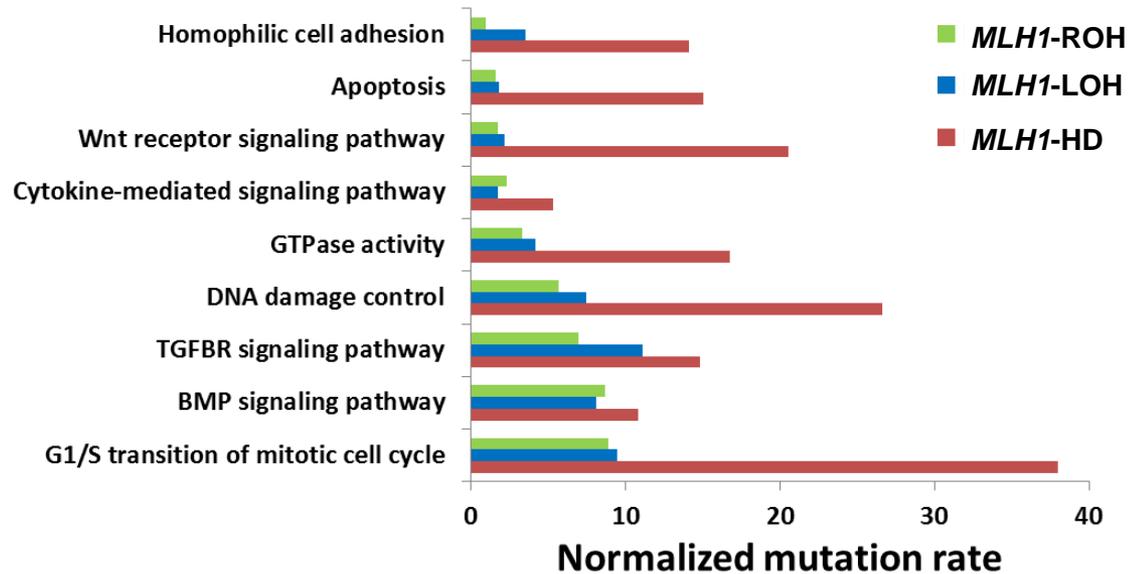


Supplemental Figure S6

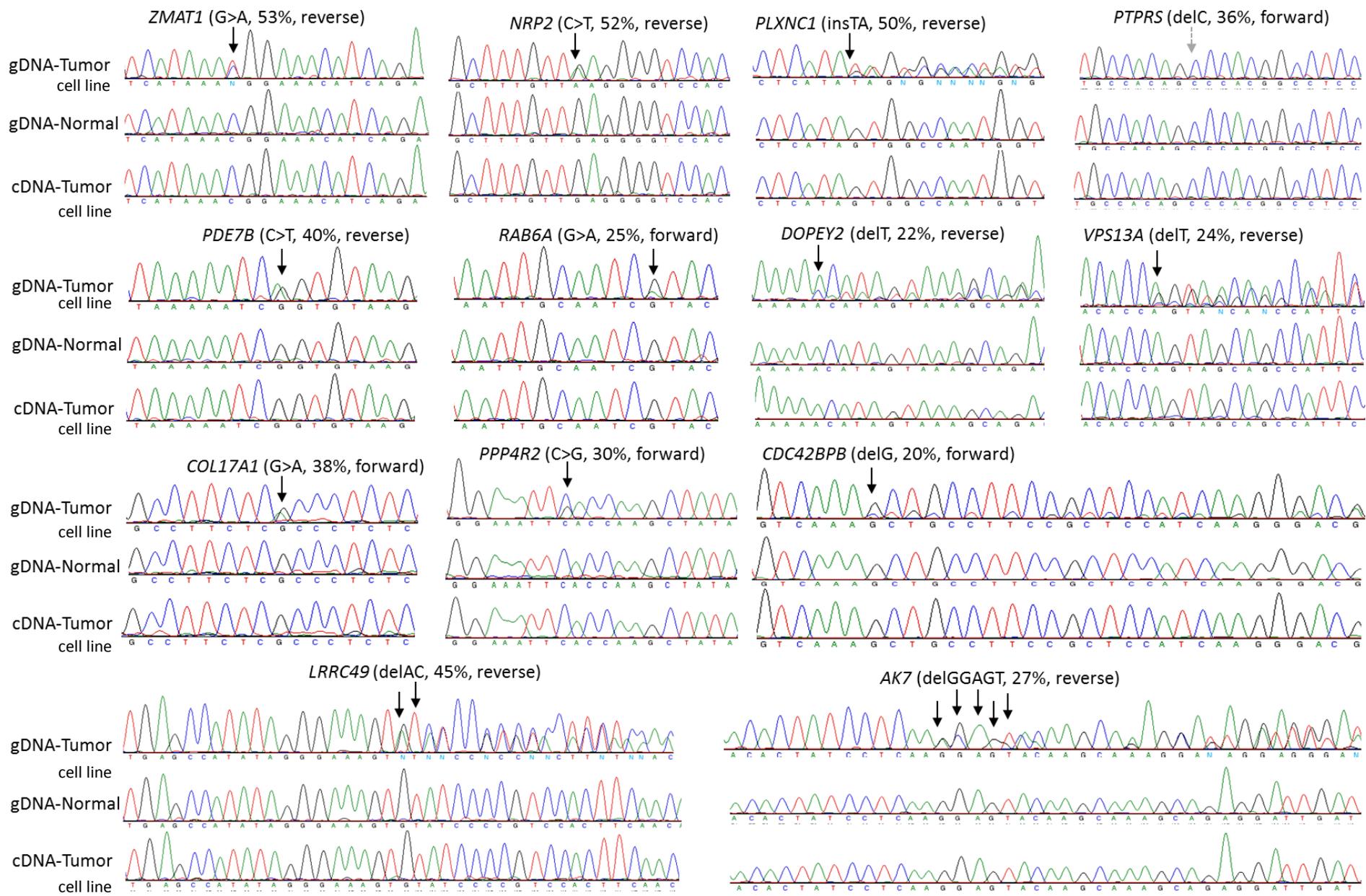
A

Rank	Pathway	Number of genes on targeted regions	Length of coding regions (Mb)	Number of genes mutated in all tumor cell lines	Tumor identified mutations in ≥ 1 of the genes	Number of mutations Identified in all tumor cell lines	Normalized mutation rate	Representative altered genes
1	G1/S transition of mitotic cell cycle	42	0.08	4	73%	13	11.0	<i>CDKN2A, CDK4, CUL3, CUL5</i>
2	BMP signaling pathway	42	0.09	4	67%	12	8.7	<i>BMP7, ACVR2A, SMAD4, CHRDL1</i>
3	TGFBR signaling pathway	82	0.20	7	93%	26	8.6	<i>SMAD4, TGFB1, FOS, JUN, TP53, BCL9L</i>
4	DNA damage control	112	0.30	13	87%	34	7.5	<i>TP53, CDKN2A, BRCA2, ATM, APC</i>
5	GTPase activity	199	0.30	6	100%	20	4.5	<i>KRAS, ARF1, EHD3, GFM2, MFN1, RAB6A</i>
6	Wnt receptor signaling pathway	166	0.34	14	53%	16	3.1	<i>APC, CYLD, FGF9, LRP1, MACF1, PTEN</i>
7	Apoptosis	847	1.93	50	100%	74	2.6	<i>TP53, CDKN2A, CARD10, GLI2, IGF2R</i>
8	Homophilic cell adhesion	139	0.42	15	40%	16	2.5	<i>FAT2, PCDH10, PCDHA1, PIK3CB, CDH6</i>
9	Cytokine-mediated signaling pathway	255	0.56	5	100%	20	2.4	<i>DUOX1, IL1B, IL6, KRAS, LRP8</i>

B



Supplemental Figure S7



Supplemental Figure S8



This study

56 genes

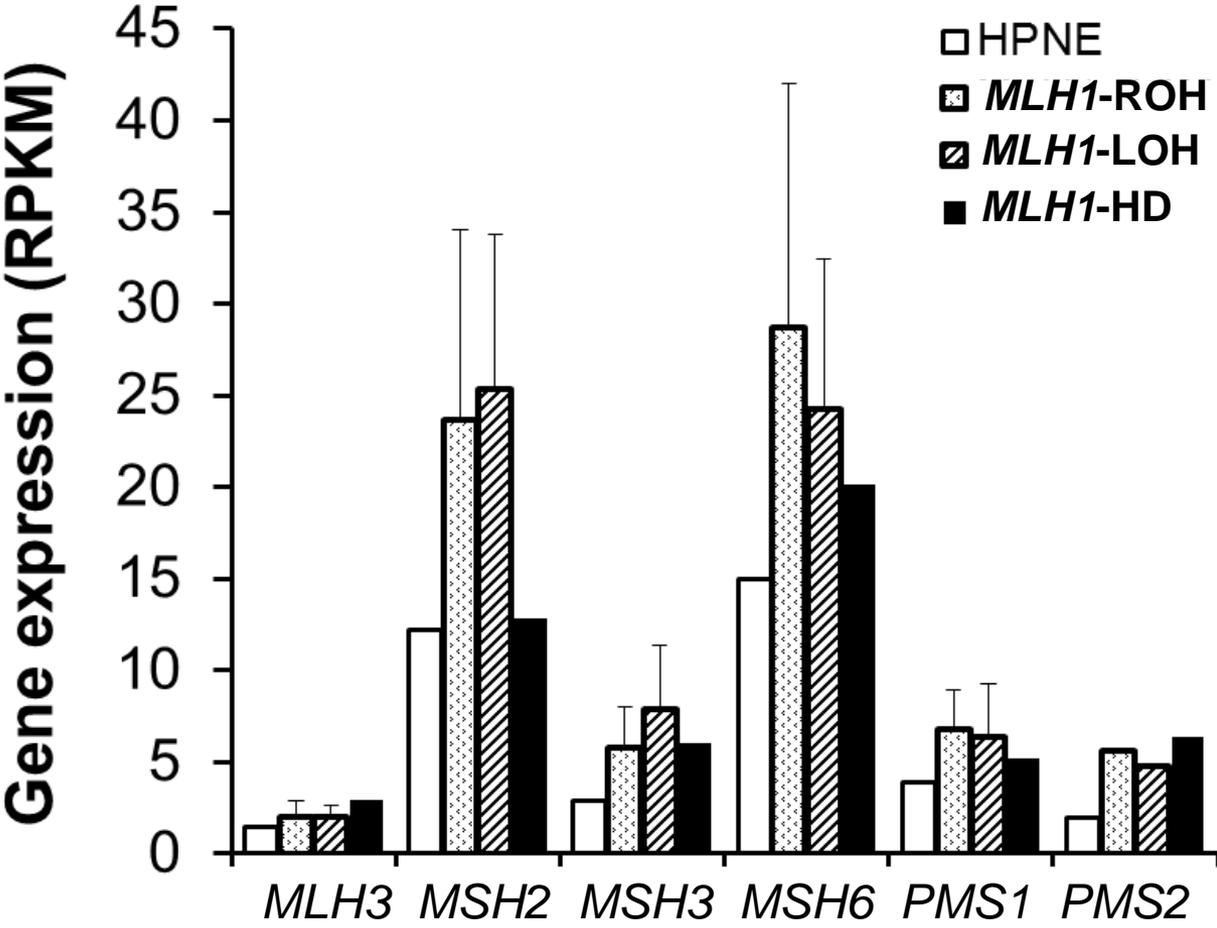
With ≥ 2 deleterious mutations in ≥ 2 cell lines (total 15 tumor cell lines)

Jones, et al. 2008

86 genes

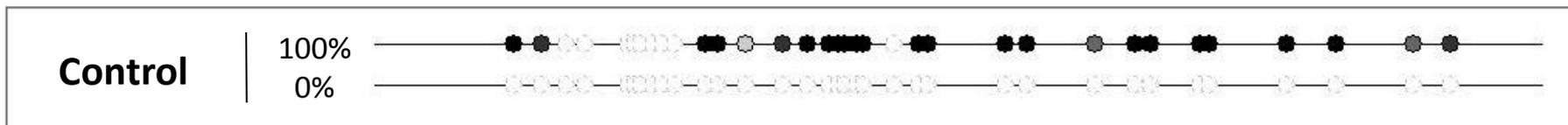
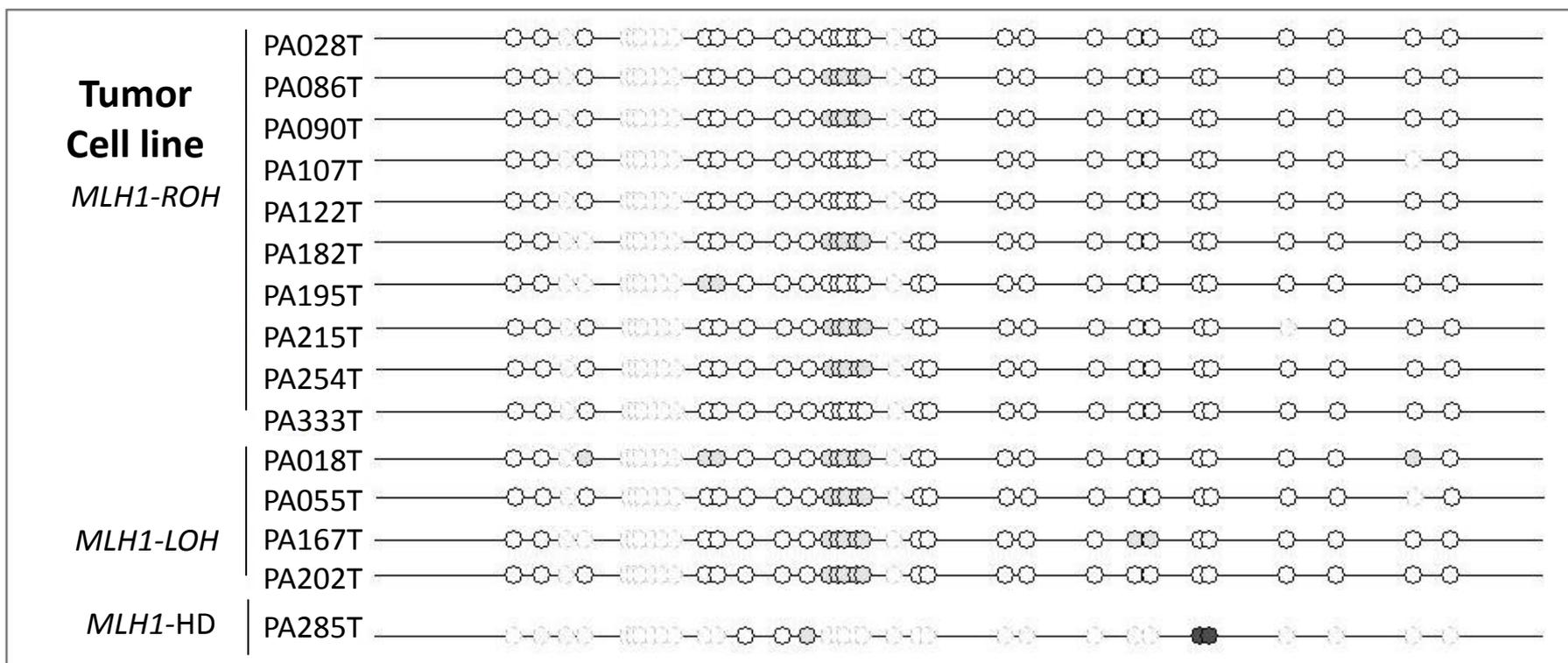
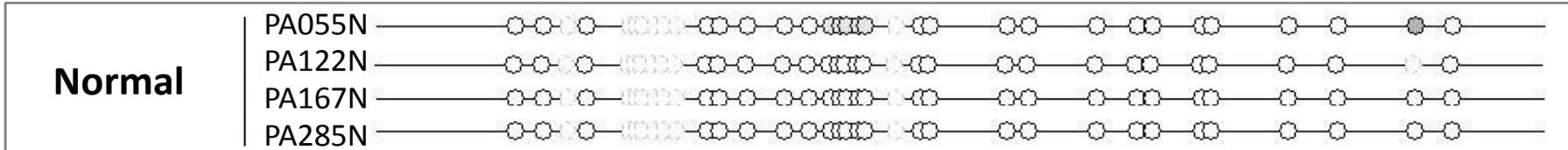
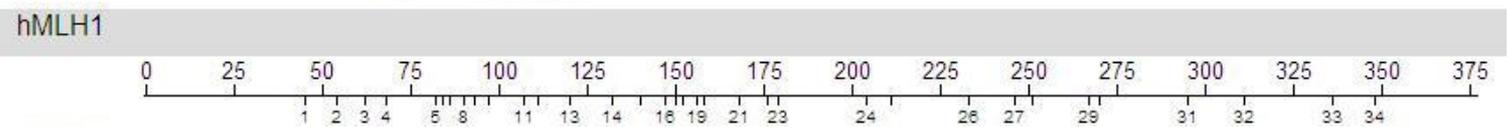
With ≥ 2 deleterious mutations in ≥ 2 tumors (total 25 tumor cell lines and 89 xenografts)

Supplemental Figure S9

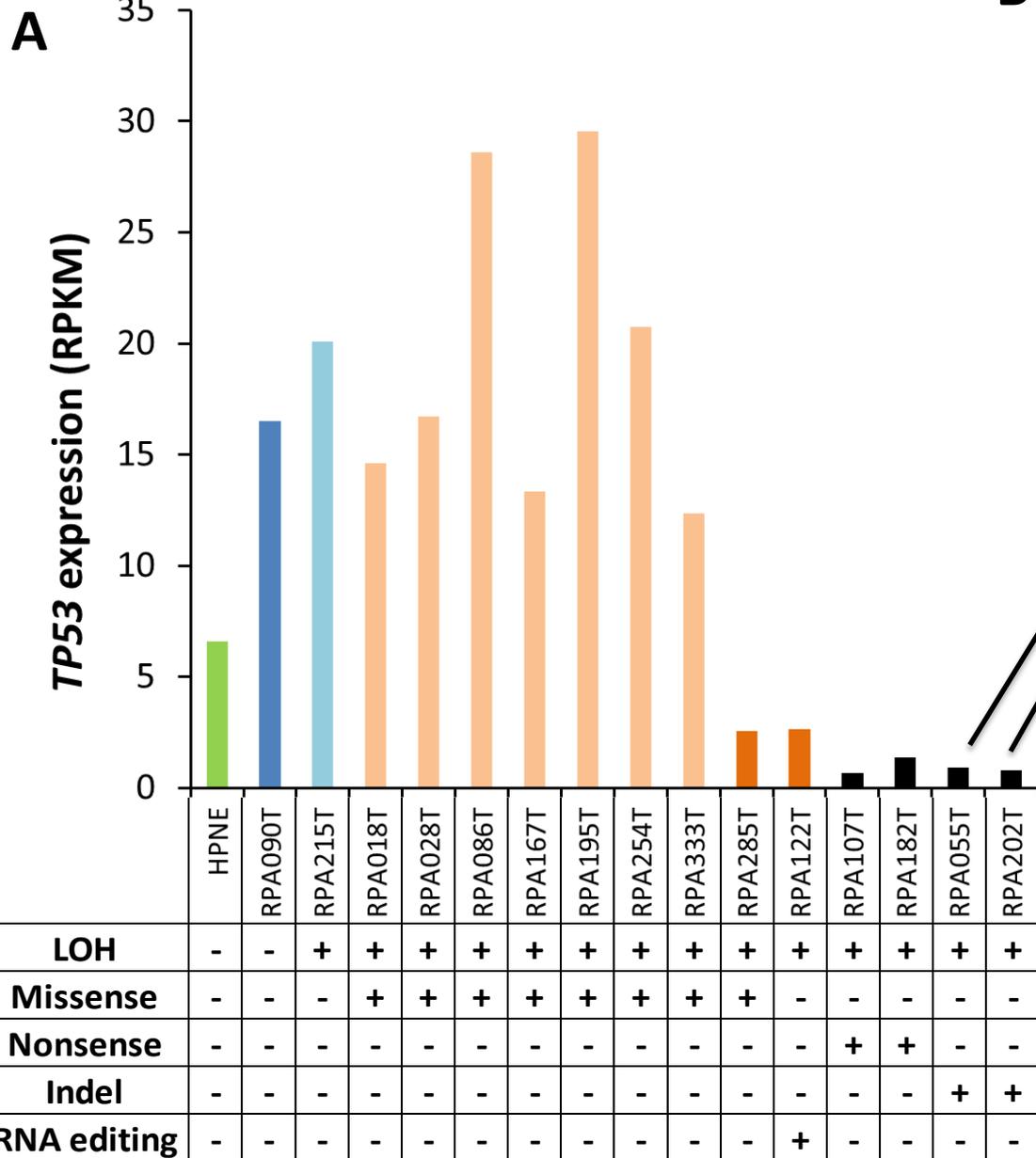


Supplemental Figure S10

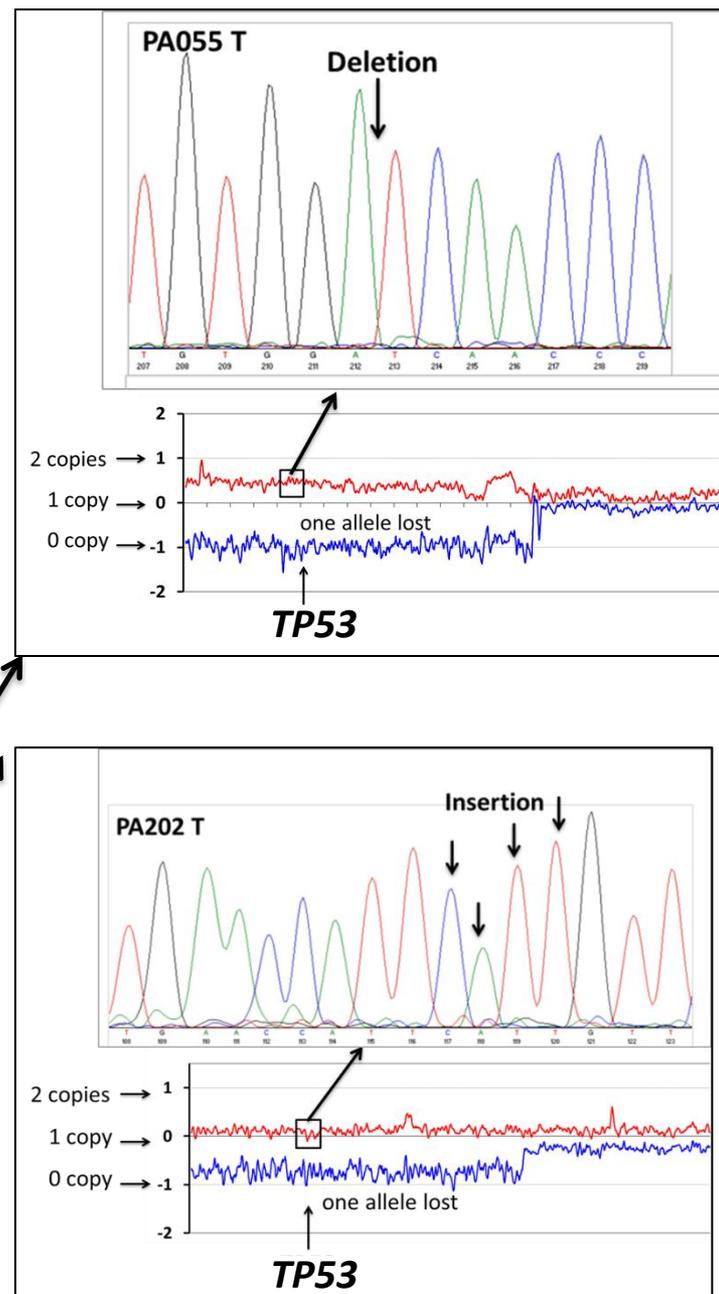
0% 100% Not analyzed:



Supplemental Figure S11



B

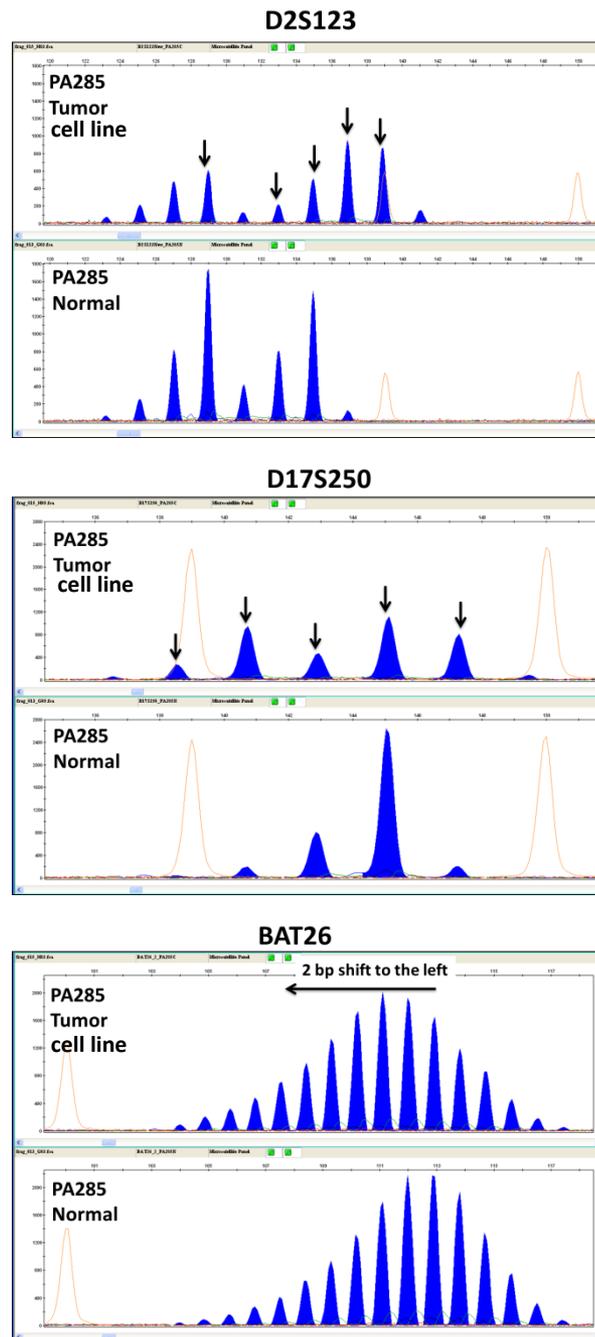


Supplemental Figure S12

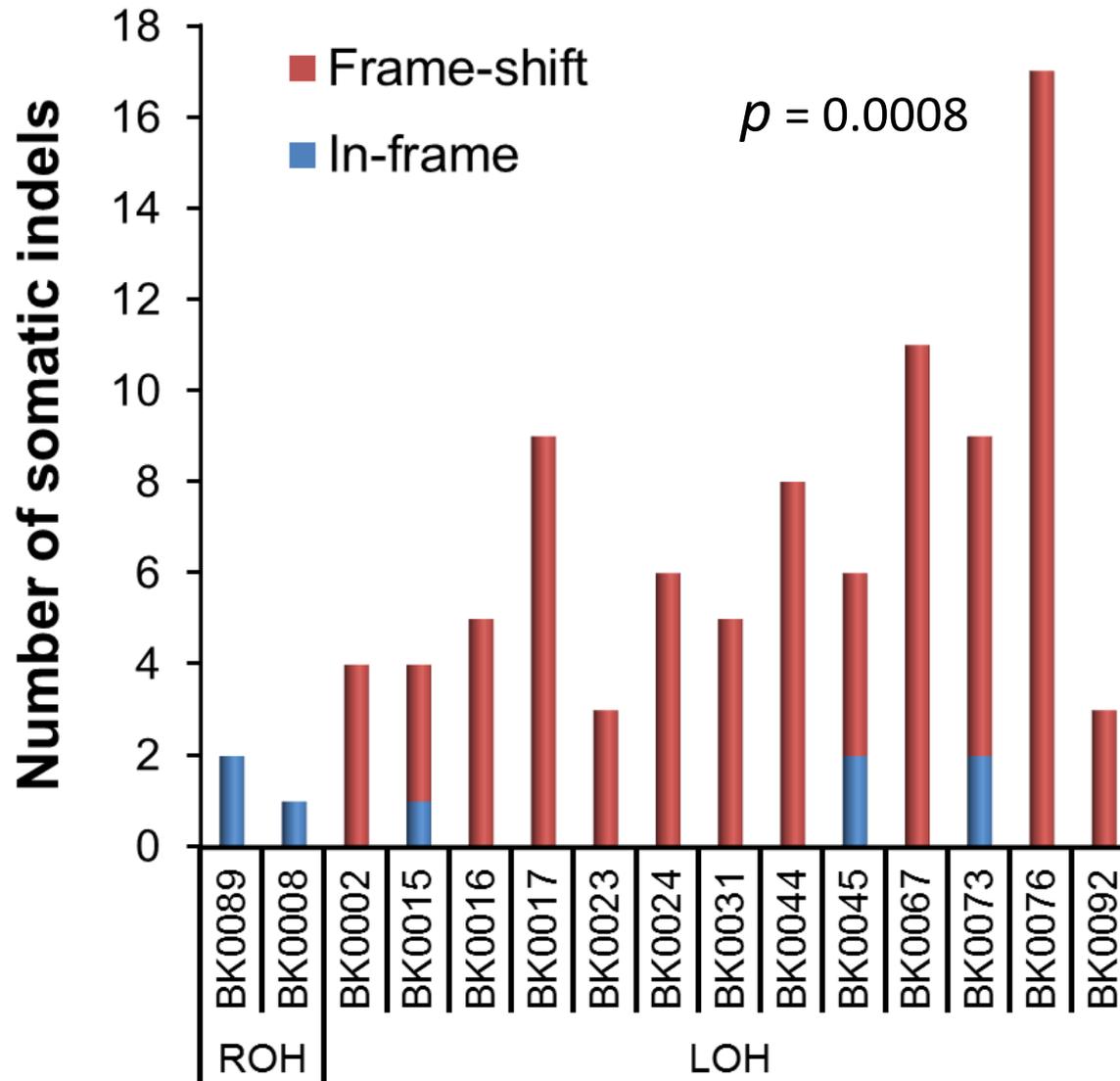
A

	<i>MLH1</i> ROH										<i>MLH1</i> LOH				<i>MLH1</i> HD
	PA028T	PA086T	PA090T	PA107T	PA122T	PA182T	PA195T	PA215T	PA254T	PA333T	PA018T	PA167T	PA202T	PA055T	PA285T
BAT25	-	-	-	-	-	-	-	-	-	-	-	-	1L	-	1R
BAT26	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2L
D2S123	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+
D25S346	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
D17S250	-	-	-	-	-	-	-	-	-	-	-	-	-	-	+
NR21	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
NR27	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1L
MSI status	MSS										MSS				MSI-H

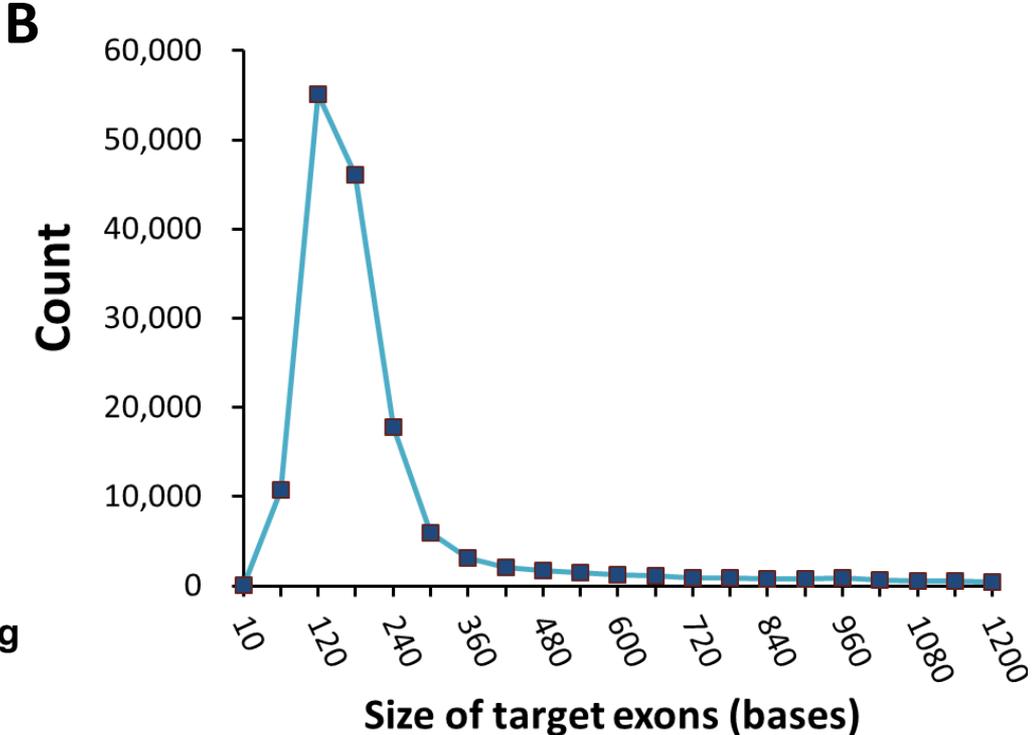
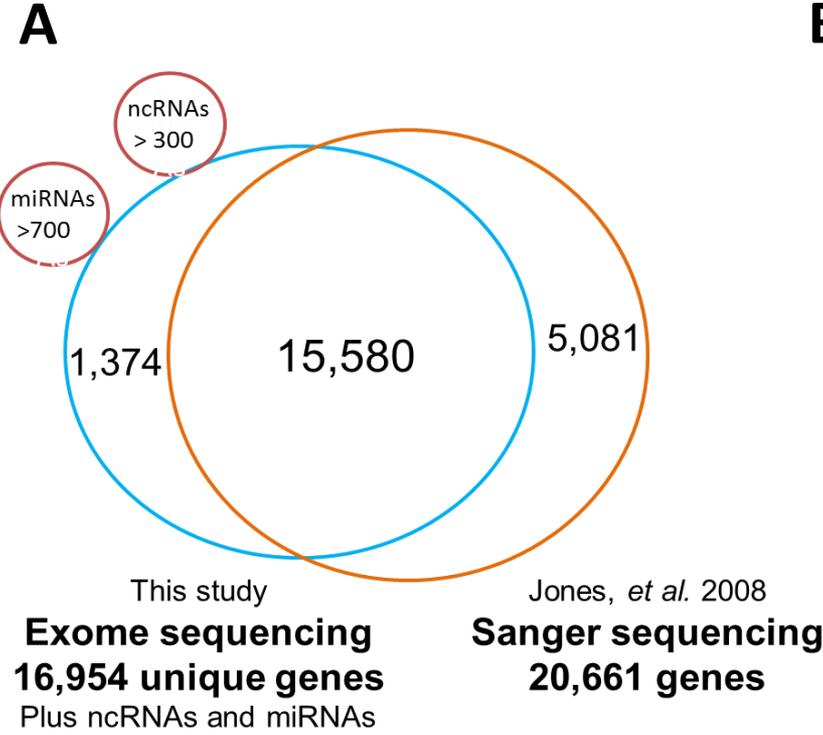
B



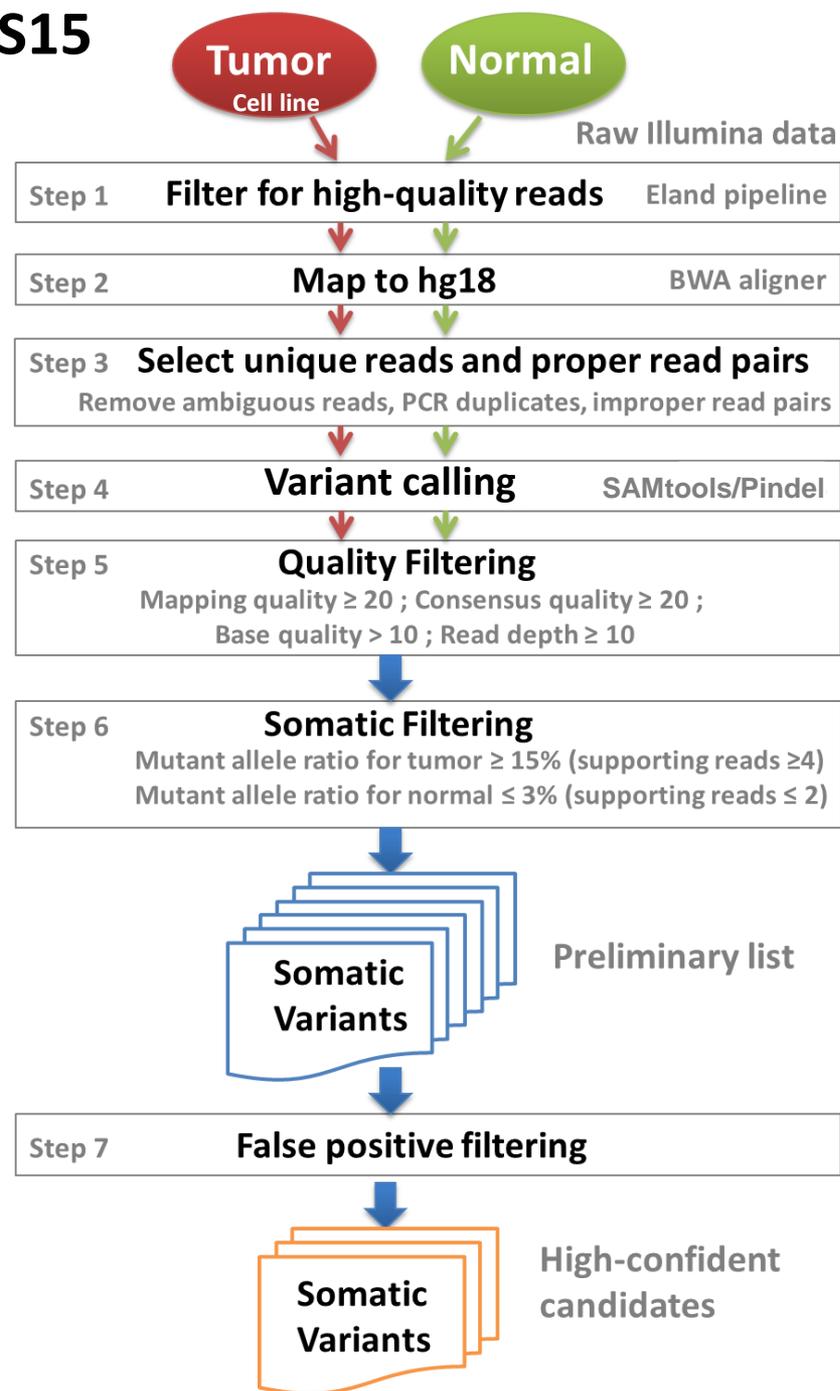
Supplemental Figure S13



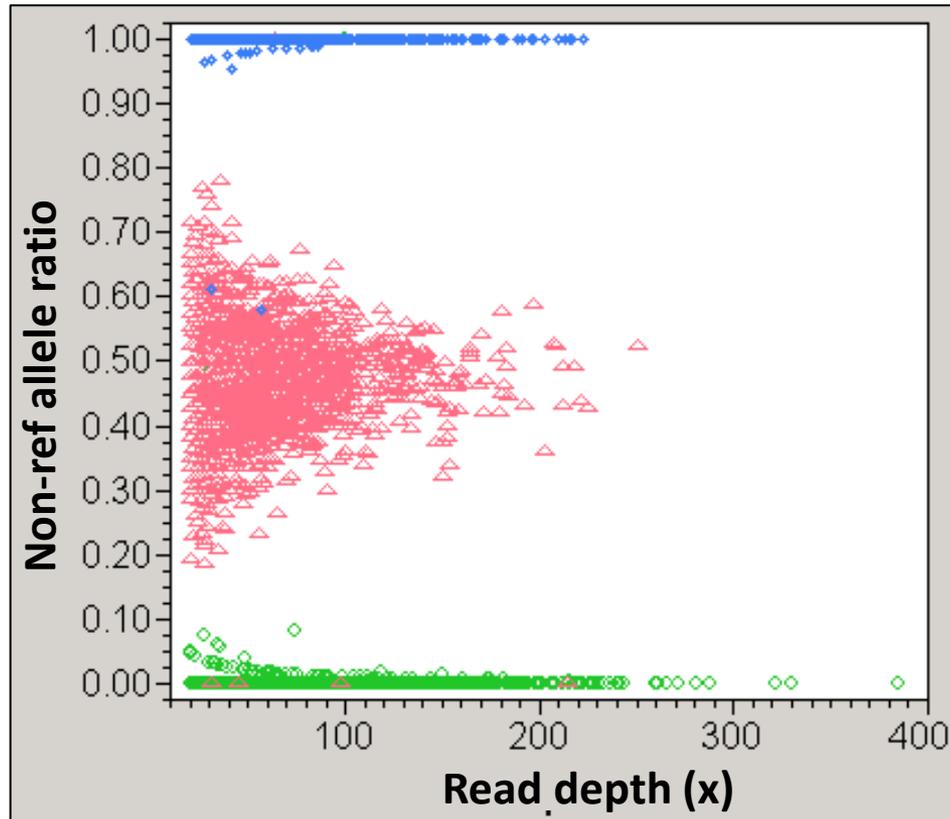
Supplementary Figure S14



Supplementary Figure S15



Supplementary Figure S16



	AA (green)	AB (red)	BB (blue)
≥ 0.80	1	1	1246
0.20-0.80	2	1647	2
≤ 0.20	4779	6	0

← Genotypes
SNP array

↑
non-reference allele ratio
Exome-Seq

7699/7711=99.84%