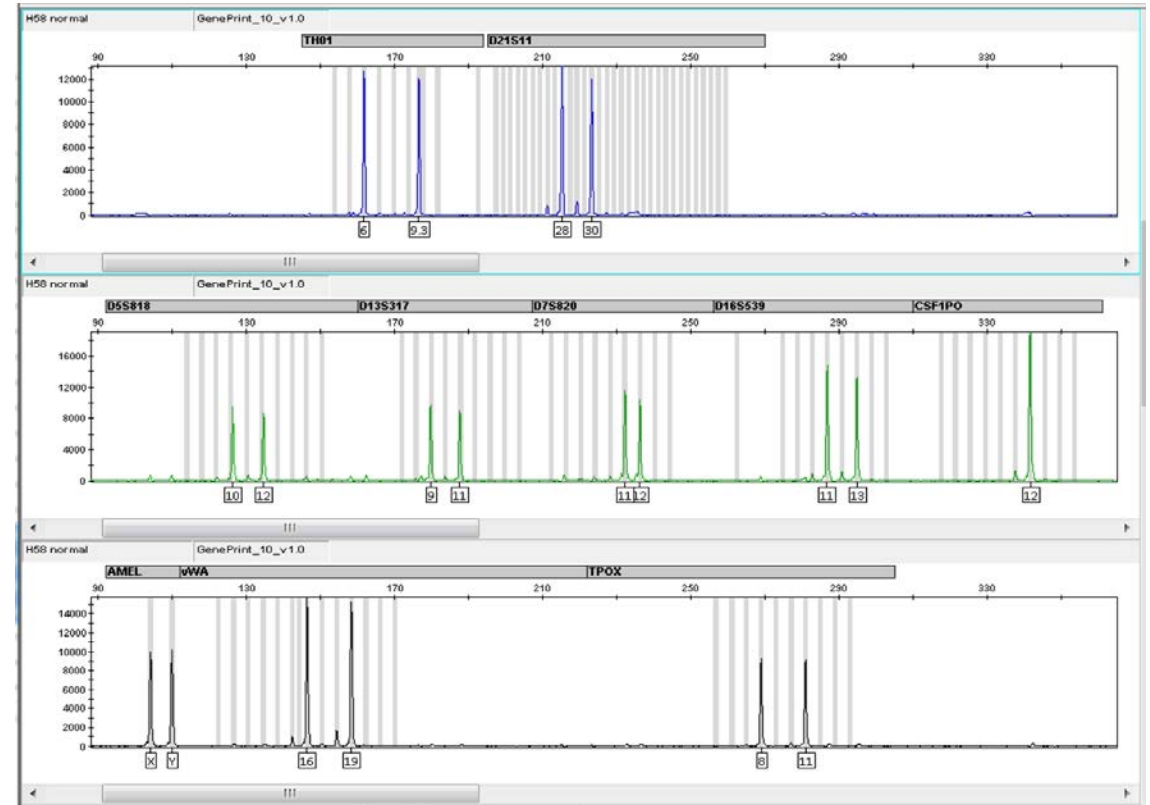
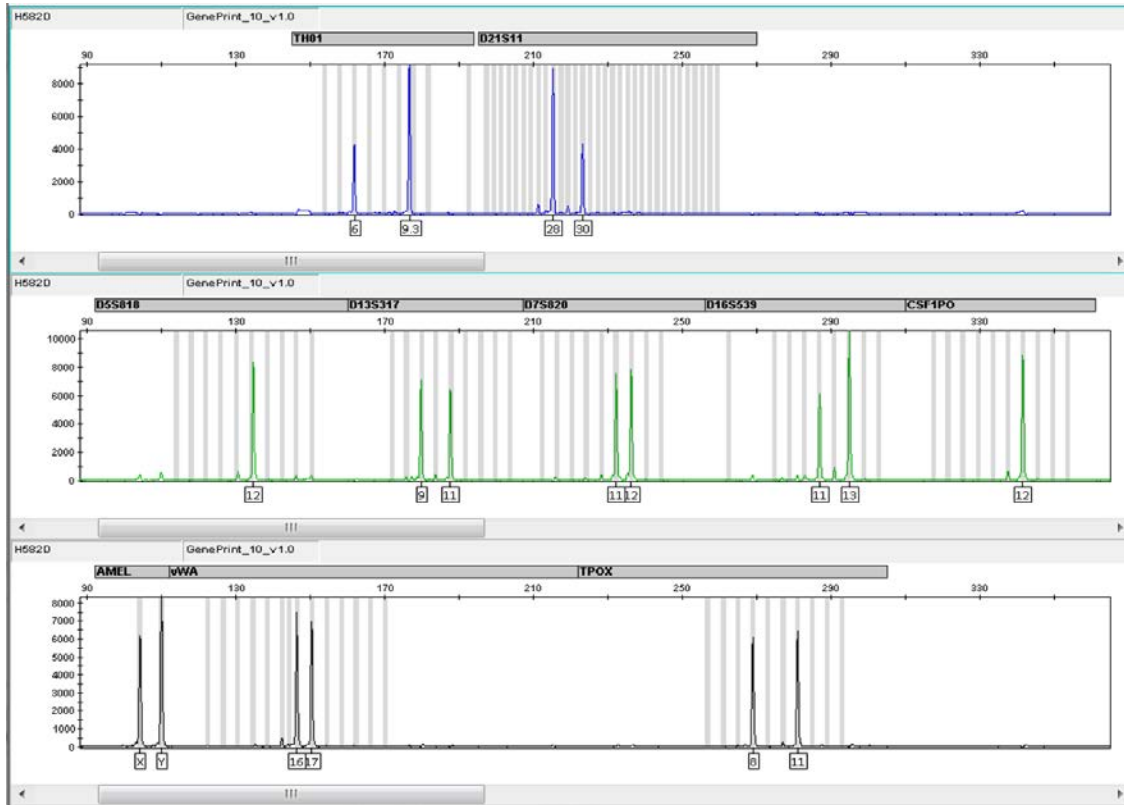
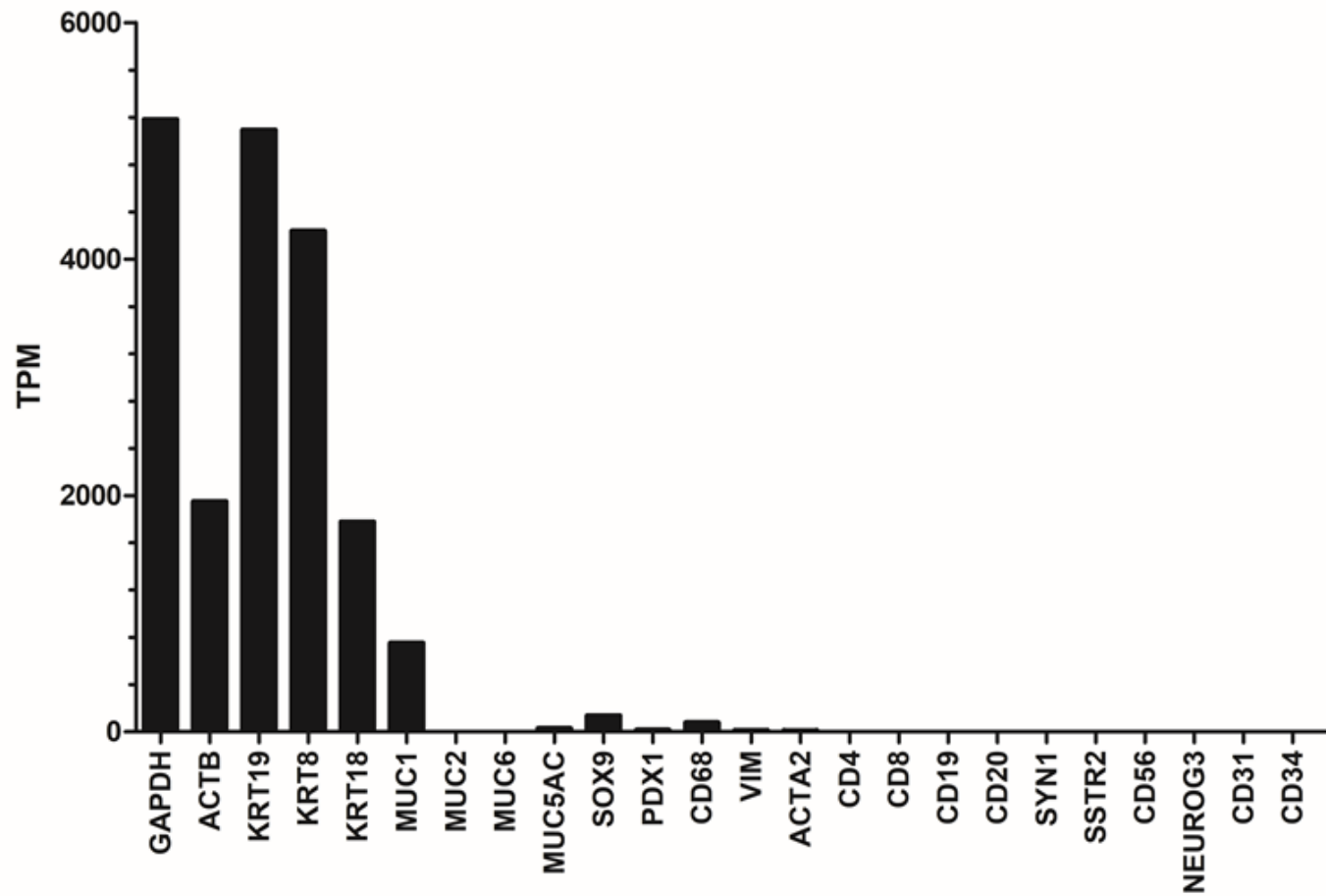


H58	
AMEL	X,Y
CSF1PO	12
D13S317	9,11
D16S539	11,13
D21S11	28,30
D5S818	12
D7S820	11,12
TH01	6,9.3
TPOX	8,11
vWA	16,17

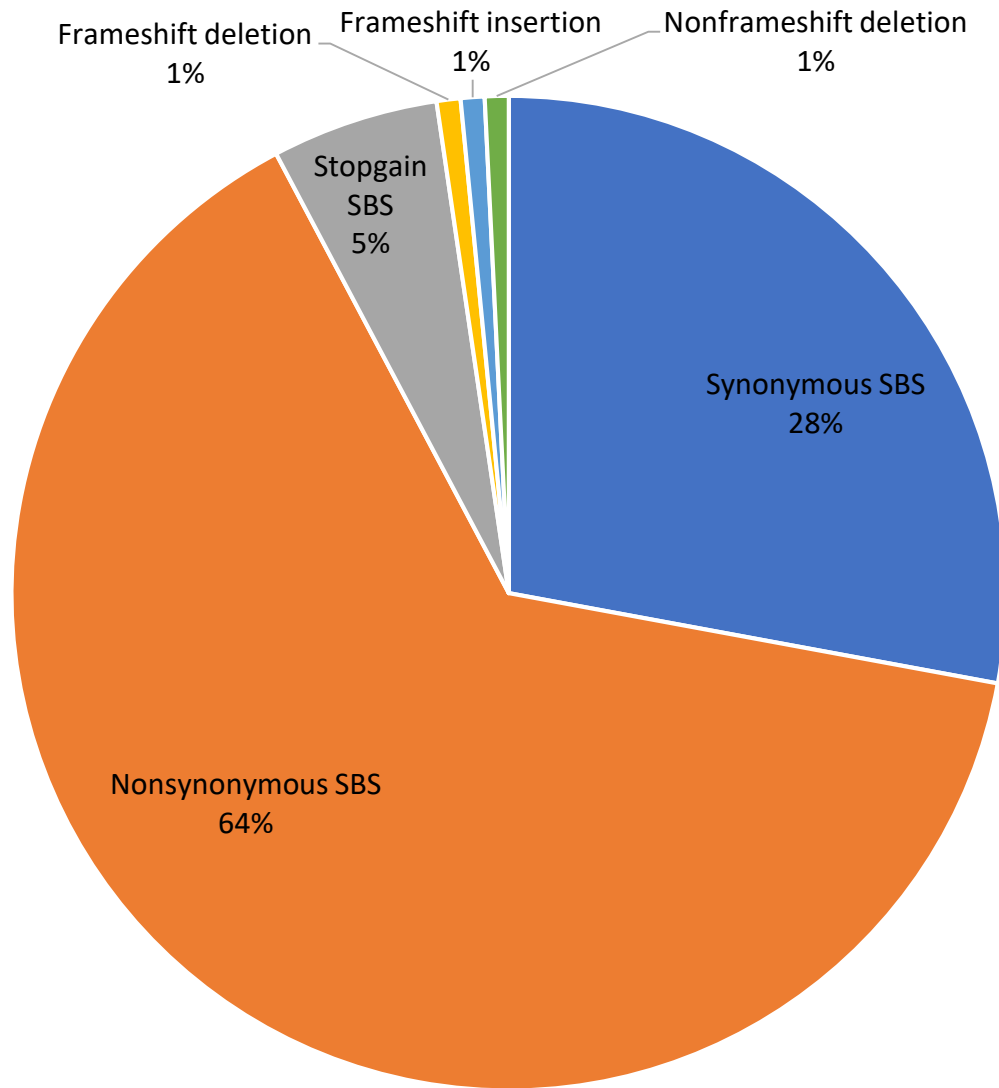
H58 Normal	
AMEL	X,Y
CSF1PO	12
D13S317	9,11
D16S539	11,13
D21S11	28,30
D5S818	10,12
D7S820	11,12
TH01	6,9.3
TPOX	8,11
vWA	16,19



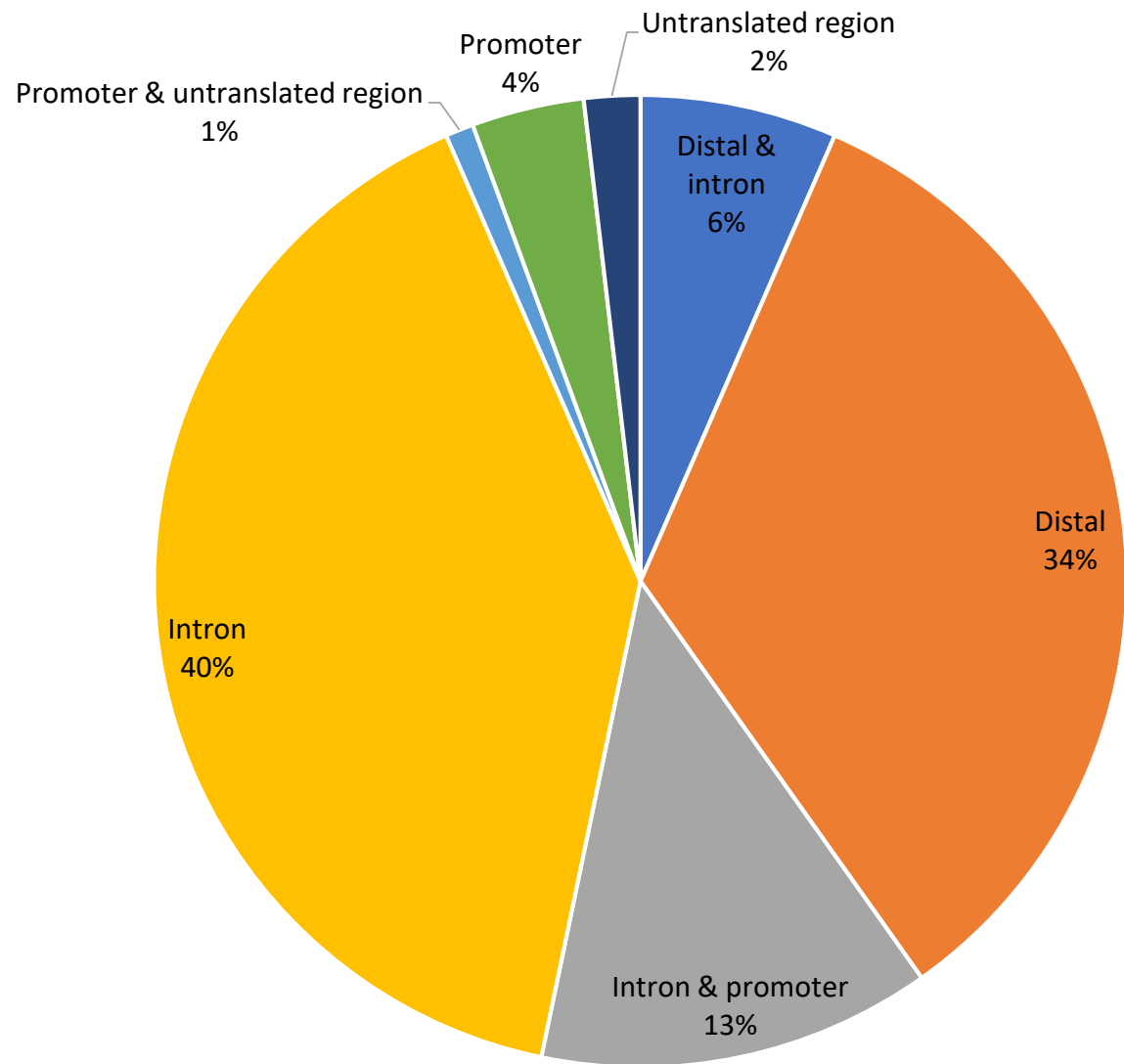
Supplementary Figure 1. STR analysis of H58 and matched normal tissue. Short tandem repeat (STR) fingerprinting analysis was performed using the Promega GenePrint 10 assay on the H58 cell line (left) and normal tissue from the same surgical resection (right), confirming a common origin of both specimens.



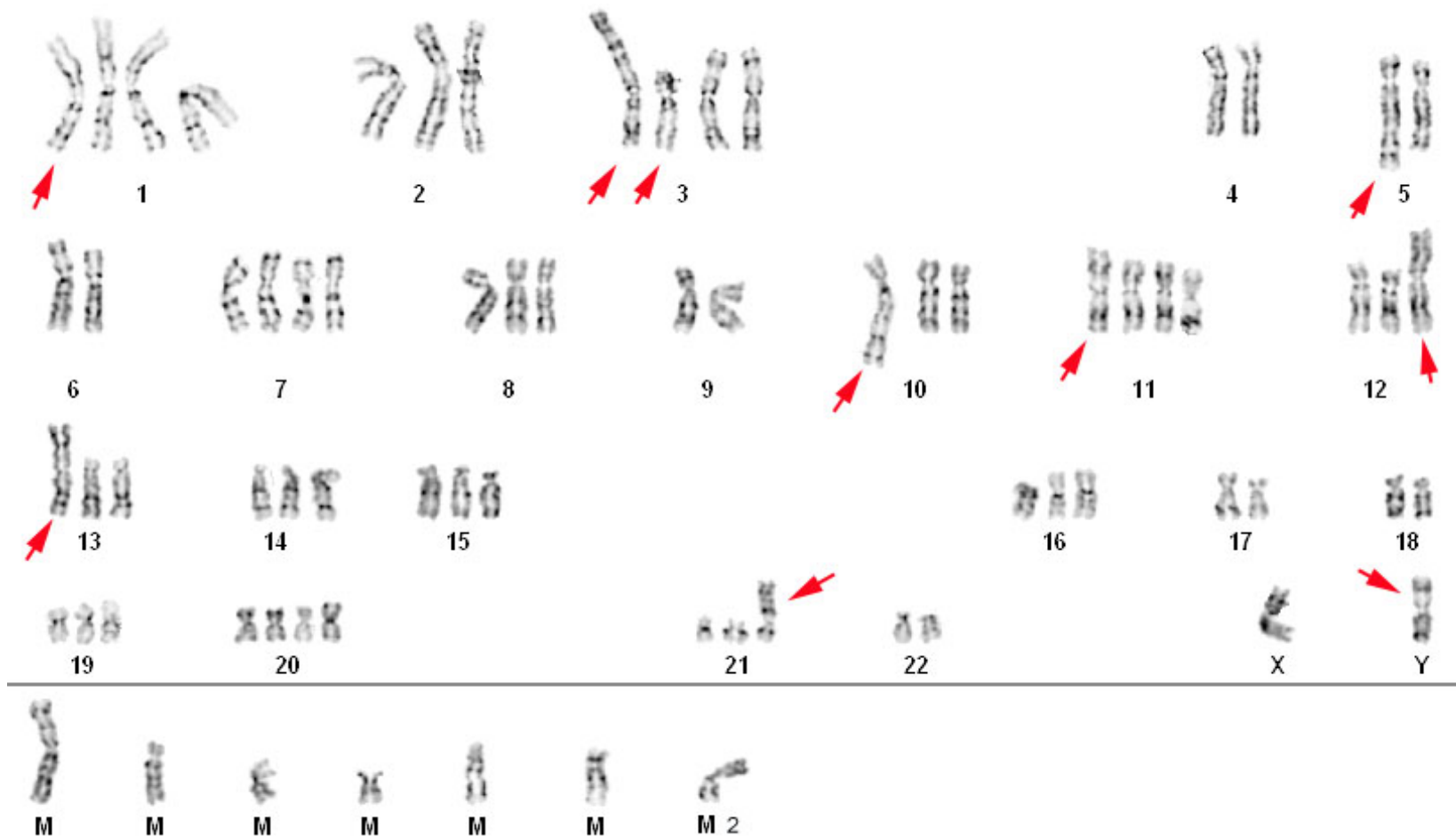
Supplementary Figure 2. Expression of lineage specific markers in RNA Seq data. Expression of lineage specific markers as tags per million (TPM) from RNA-Seq of H58 in three-dimensional culture. GAPDH and ACTB shown for reference.



Supplementary Figure 3. Coding mutations identified by whole genome sequencing. Distribution of coding mutations present in H58 by functional type.

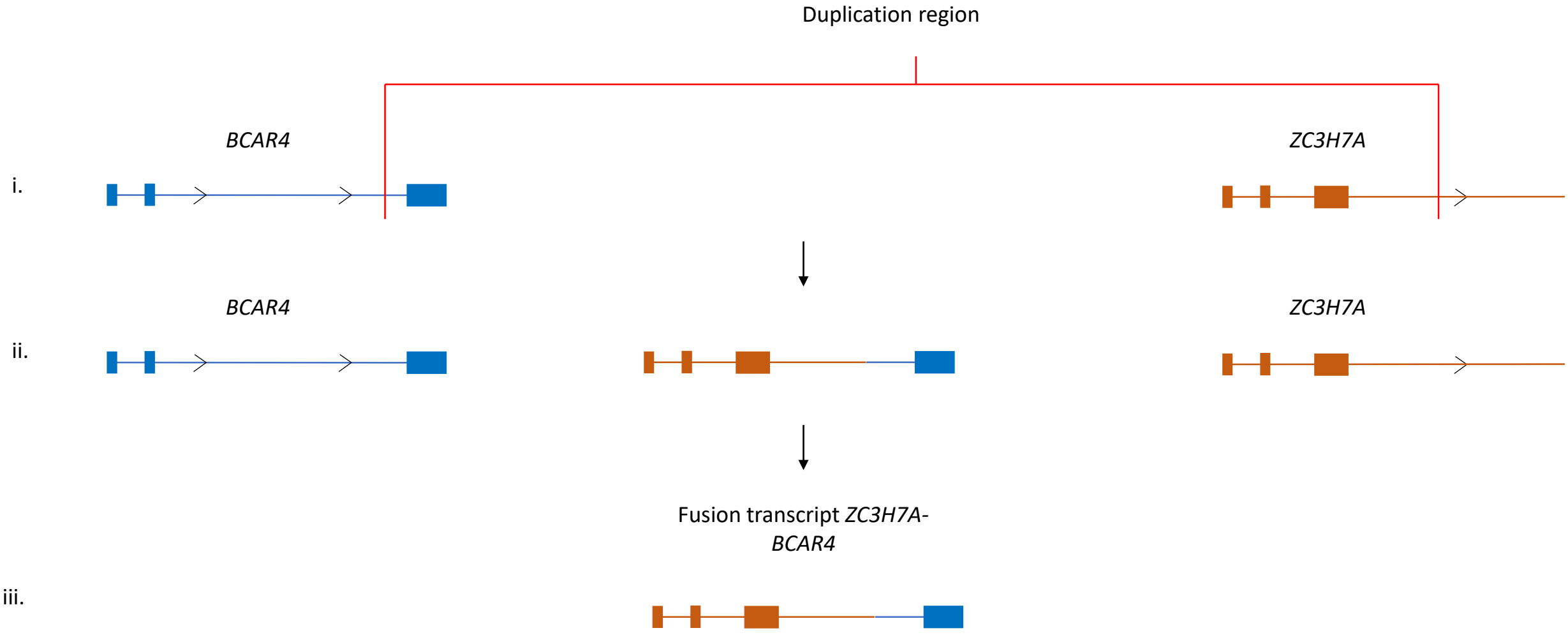


Supplementary Figure 4. Noncoding mutations identified by whole genome sequencing. Distribution of noncoding mutations present in H58 by functional type.

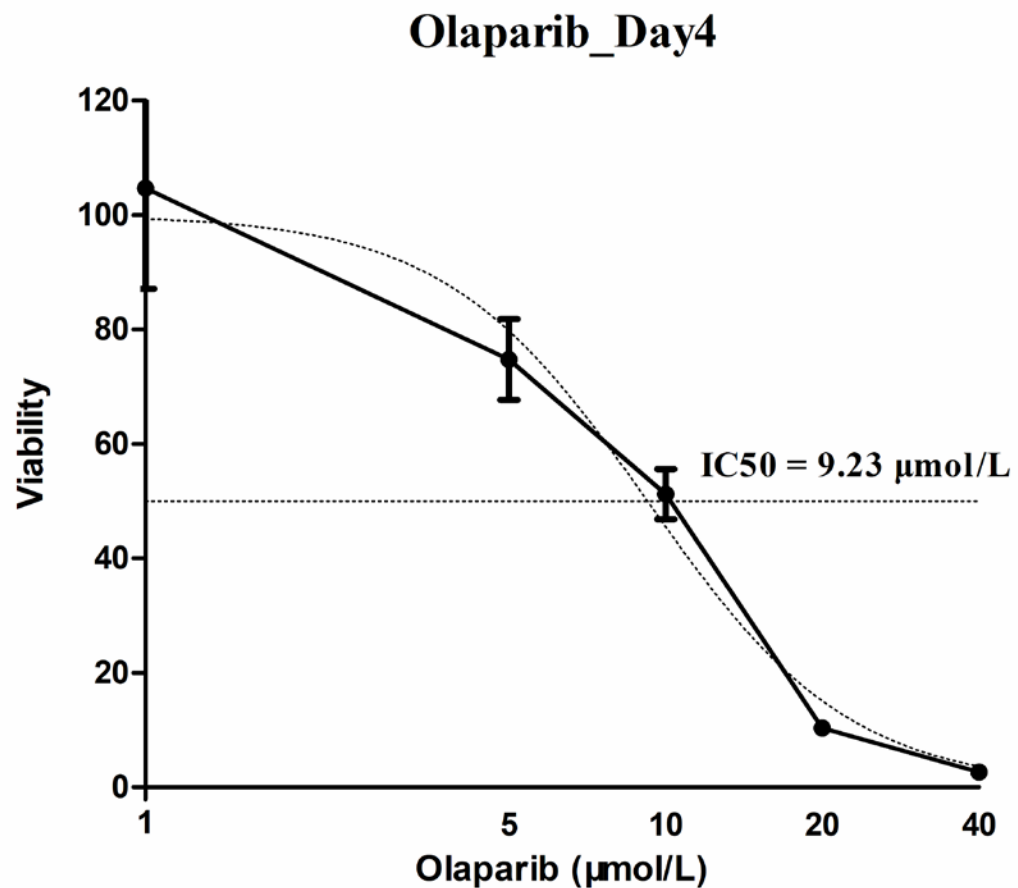
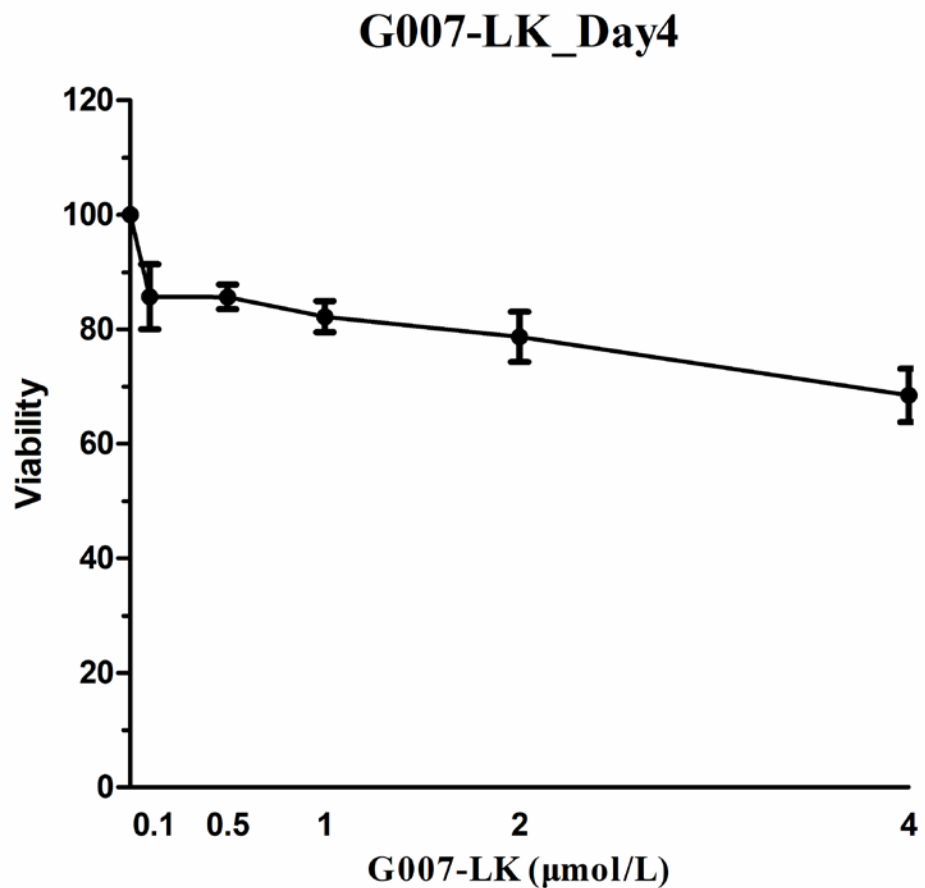


66~72<3n>,X,-X,der(Y;17)(q10;q10),+de(1)(q31q41),add(3)(p22),+add(3)(p12)-4,-5,-6,+7,9,der(10)t(10;14)(q26;q11.2),+i(11)(q10),add(12)(p11.2),i(13)(q10),-17,-18,+20,add(21)(p11.2),+mar3~6[cp15]

Supplementary Figure 5. Metaphase karyotype of H58. One representative karyotype is shown. Arrows indicate aberrant chromosomes. There are many structural aberrations, most of which are clonal. Many of the rearrangements could be partially characterized but some remained classified only as marker chromosomes (bottom). The modal number of chromosomes is in the triploid range.



Supplementary Figure 6. Diagrammatic representation of structural variant in BCAR4 – ZC3H7A genomic region. Duplication and resulting fusion gene product shown. A. Sequence of reference genome with breakpoints indicated in red. B. Predicted genome sequence of H58. C. Fusion transcript produced as a result of duplication.



Supplementary Figure 7. Drug sensitivity of H58 cells to G007-LK and Olaparib by MTT assay. Cell viability of H58 after treatment by G007 at concentration of 0, 0.1, 0.5, 1, 2, 4 μmol/L for 4 days (left), and after treatment by Olaparib at concentration of 0, 1, 5, 10, 20, 40 μmol/L for 4 days (right). H58 cell line is more sensitive to olaparib.