Supporting Information

Ma et al. 10.1073/pnas.1221099110

Fig. S1. Plots for regions affected by copy number variation. Normalized log R ratio in tumor, normalized log R ratio in normal, log(tumor/normal R) and complete genomics tumor/normal normalized coverage with smoothing are plotted (*Upper Left*, *Upper Right*, *Lower Left*, *Lower Right*, respectively).

Fig. S1

Fig. S2. Schema for selection and annotation of high-confidence somatic SNVs.

Fig. S2

Table S1. Whole-genome sequencing-coverage summary

Table S1

Table S2. SNP-genotype concordance between whole-genome sequencing and genotyping array

Table S2

Table S3. Details of translocations

Table S3

Table S4. Copy number variation (*A*) and loss of heterozygozity events (*B*)

Table S4

Table S5. Genes affected by rare, damaging germ-line mutations (excluding missense)

Table S5

Table S6. Somatic mutation rates

Table S6

Table S7. Details of genes affected by somatic SNVs (*A*) and details of genes affected by loss of heterozygosity and copy number variation (*B*)

Table S7

Table S8. Details of SNVs that are identical in twin pairs

Table S8