

Description of Additional Supplementary Files

File Name: Supplementary Data 1

Description: Clinical characteristics

File Name: Supplementary Data 2

Description: Sequencing depth and coverage

File Name: Supplementary Data 3

Description: Tumor purities and ploidies estimated

File Name: Supplementary Data 4

Description: Mutational burden and intertumor heterogeneity (mutations and SCNAs)

File Name: Supplementary Data 5

Description: Evolution models in MPMs

File Name: Supplementary Data 6

Description: dN/dS ratio across cohort

File Name: Supplementary Data 7

Description: Driver gene selectivity

File Name: Supplementary Data 8

Description: Per region segmented copy number data

File Name: Supplementary Data 9

Description: Clonal mutations detected in plasma circulating total DNA

File Name: Supplementary Data 10

Description: Variant allele frequencies (VAFs) per tumour region and circulating free DNA

File Name: Supplementary Data 11

Description: Primers used for clonal mutation detection in plasma

File Name: Supplementary Data 12

Description: High frequency copy number gains and losses

File Name: Supplementary Data 13

Description: Clonal versus subclonal copy number alterations with gene annotations

File Name: Supplementary Data 14

Description: Chromosome arm-level gains or losses

File Name: Supplementary Data 15

Description: UPD segmented data

File Name: Supplementary Data 16

Description: TCGA meso data clusters C1-C5

File Name: Supplementary Data 17

Description: Neoantigens predicted.

File Name: Supplementary Data 18

Description: Loss of heterozygosity in human leukocyte antigen (HLA LOH)