Exome capture sequencing of 2 sets of paired metastatic tumors and their matched normal 384X coverage, 89.9% bases with high quality genotype calls

Number of potential somatic mutations: 2356

Assemble sequence data (genome build hg18) and filter putative somatic mutations

Number of mutations with a MPG/Coverage ratio>=0.5: 750

Missense/ nonsense/ splice site mutations: 486
Insertions/Deletions: 4
Synonymous mutations: 260

Search for mutations occurring in a single metastatic tumor

10 Nonsynonymous mutations occurring in only a single metastatic tumor comprising 2% of nonsynonymous mutations found

Search for conserved mutations between metastatic tumor pairs

480 Nonsynonymous mutations conserved between metastatic tumor pairs comprising 97.9% of nonsynonymous mutations found