**Supplemental Table Legends for "Linking transcriptional and genetic tumor heterogeneity through allele analysis of single-cell RNA-seq data"**

Jean Fan1,\*, Hae-Ock Lee2,\*, Soohyun Lee1, Da-eun Ryu2, Semin Lee1, Catherine Xue1, Seok Jin Kim5, Kihyun Kim5, Nikolaos Barkas1, Peter J. Park1, Woong-Yang Park2,§, Peter V. Kharchenko1,3,4,§

**Supplemental Tables**

Supplemental Table S1. CNV regions identified by HoneyBADGER and associated posterior probabilities for all cells for MGH31.

Supplemental Table S2. Mutation calling and WES results for BC09.

Supplemental Table S3. Karyotyping information and CNV regions identified by HoneyBADGER for MM135.

Supplemental Table S4. CNV regions identified by HoneyBADGER and associated posterior probabilities for all cells for MM34A.

Supplemental Table S5. Differential expression characterization of extramedullary-like subclone in MM34.

Supplemental Table S6. Gene set enrichment analysis to characterize the extramedullary-like subclone in MM34.

**Supplemental Tables**

**Supplemental Table S1. CNV regions identified by HoneyBADGER and associated posterior probabilities for all cells for MGH31.** Sheet 1) From allele-based model. Sheet 2) From expressed-based model. Genomic coordinates provided for each CNV along with posterior probabilities of having the CNV for each cell.

**Supplemental Table S2. Mutation calling and WES results for BC09.** Sheet 1) Summary of previous results from Chung *et al.* (Chung et al. 2017). Sheet 2) WES CNV calls. Sheet 3 and 4) WES mutation calls.

**Supplemental Table S3. Karyotyping information and CNV regions identified by HoneyBADGER for MM135.** Sheet 1) FISH and cytogenetic karyotyping results. Sheet 2) CNV regions identified by HoneyBADGER.

**Supplemental Table S4. CNV regions identified by HoneyBADGER and associated posterior probabilities for all cells for MM34A.**

**Supplemental Table S5. Differential expression characterization of extramedullary-like subclone in MM34.** Sheet 1) Genes in heatmap from Fig. 5B. Sheet 2) Significantly differentially expressed genes (Z < 1.96) identified using MM34 cells only. Genes in heatmap from Supp. Fig. 8A..Sheet 3) Significantly differentially expressed genes (Z < 1.96) identified in combination with MM34A. Genes in heatmap from Supp. Fig. 8B. lb, mle, ub represent the lower bound, maximum likelihood estimate, and upper bound of the 95% confidence interval for the expression fold change on log2 scale outputted from the SCDE package (Kharchenko et al. 2014).

**Supplemental Table S6. Gene set enrichment analysis to characterize the extramedullary-like subclone in MM34.** Sheet 1) Using gene sets from MSIGDB. Sheet 2) Using gene sets from GO.