

**Table S1: GEO datasets included in the review.**

GSE identifier	Authors	Title	Structure	Platform	Link
<a href="https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE100797">GSE100797</a>	Lauss M, Jönsson G	Mutational and neoantigen load predict clinical benefit of adoptive T cell therapy in melanoma	25 melanoma samples	Illumina HiSeq 2000	<a href="https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE100797">https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE100797</a>
<a href="https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE131521">GSE131521</a>	Xu M, Sengupta S, Krummel D, Khan M	Radiation enhances melanoma response to immunotherapeutic and synergizes with benzodiazepines to promote improved anti-tumor activity	17 brain metastases	Illumina HiSeq 2500	<a href="https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE131521">https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE131521</a>
<a href="https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE133713">GSE133713</a>	Khan J, Wei JS	Immune Signatures and Tumor Biomarkers from Whole Transcriptome Sequencing Predict Outcome in Recurrent Resectable Stage III and IV Melanoma when Evaluated Following Treatment with Hu14.18-IL2	13 pre-treatment and 10 post-treatment samples	Illumina NextSeq 500	<a href="https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE133713">https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE133713</a>
<a href="https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE153388">GSE153388</a>	van Baren N, Mercier M, de Streel G	Inflammatory transcript signatures and activated regulatory T lymphocytes in melanoma metastases	19 cutaneous metastases	Illumina HiSeq 2000	<a href="https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE153388">https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE153388</a>
<a href="https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE168204">GSE168204</a>	Gao Z, Tian T	Pathway Signatures Derived from On-treatment Tumor Specimens Predict Response to Anti-PD1 Blockade in Metastatic Melanoma	27 melanoma samples	Illumina HiSeq 2000 / Illumina NextSeq 500	<a href="https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE168204">https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE168204</a>
<a href="https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE98394">GSE98394</a>	Badal B, Solovyov A, Di Cecilia S, Chan JM, Chang L et al	Transcriptional dissection of melanoma identifies a high-risk subtype underlying TP53 family genes and epigenome deregulation	27 benign melanocytic lesions and 51 melanoma samples	Illumina HiSeq 2500	<a href="https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE98394">https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE98394</a>
<a href="https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE100797">GSE100797</a>	Lauss M, Jönsson G	Mutational and neoantigen load predict clinical benefit of adoptive T cell therapy in melanoma	25 melanoma samples	Illumina HiSeq 2000	<a href="https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE100797">https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE100797</a>