

Figure S2: Single Cell RNA Sequencing Data Summary for *Pparg*<sup>-/-epi</sup> (KO) mouse skin.

10,228

Estimated Number of Cells

49,564

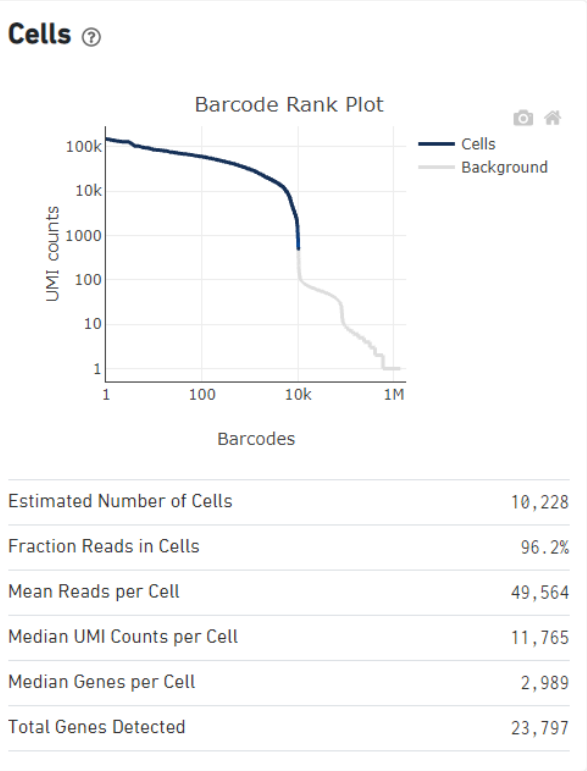
Mean Reads per Cell

2,989

Median Genes per Cell

Sequencing ?	
Number of Reads	506,940,549
Number of Short Reads Skipped	0
Valid Barcodes	97.7%
Valid UMIs	100.0%
Sequencing Saturation	52.5%
Q30 Bases in Barcode	95.8%
Q30 Bases in RNA Read	93.7%
Q30 Bases in UMI	95.3%

Mapping ?	
Reads Mapped to Genome	95.9%
Reads Mapped Confidently to Genome	92.5%
Reads Mapped Confidently to Intergenic Regions	4.9%
Reads Mapped Confidently to Intronic Regions	19.7%
Reads Mapped Confidently to Exonic Regions	67.9%
Reads Mapped Confidently to Transcriptome	65.1%
Reads Mapped Antisense to Gene	1.6%



Sample	
Sample ID	KO
Sample Description	
Chemistry	Single Cell 3' v3
Include introns	False
Reference Path	...index/v4.0.0/refdata-gex-mm10-2020-A
Transcriptome	mm10-2020-A
Pipeline Version	cellranger-6.1.1