

		Whole genome sequencing			RNA-Seq		
		2011 cost	output	2011 time	2011 cost	output	2011 time
Sample collection & experimental design		<i>from</i> blood samples (easy to collect) to brain tissue (hard to collect) ~\$100 onwards ~380M reads/lane; 1 individual; ~1140M total reads (~3 lanes for a 30x coverage); ~250Gb (intermediate files) <i>from</i> a few hours to several days			<i>same as for whole genome sequencing</i>		
Sequencing		<i>library preparation + running the sequencer (whole dual flow cell)</i> ~\$6500 = ~\$500 + ~\$6000	~380M reads/lane; 1 individual; ~1140M total reads (~3 lanes for a 30x coverage); ~250Gb (intermediate files)	~11-12 day	<i>library preparation + running the sequencer (whole dual flow cell)</i> ~\$3300 = ~\$300 + ~\$3000	~380M reads/lane	~12-14 day
Data reduction & management	Data storage, low-level processing	<i>Alignment (transfer* and storing raw data + mapping)</i> ~\$40 = ~\$33 + ~\$7	300Gb (BAM file)	~1/2 day *** (including transferring 250Gb FASTQ ~7.5 hrs)	<i>Alignment (transfer* and storing raw data + mapping)</i> ~\$5 = ~\$3 + ~\$2	~30Gb (BAM); ~22Gb (MRF)	< 2 hrs ***
		<i>(data transfer and storage for 10 days)*; **</i> ~\$40		~8.5 hrs	<i>(data transfer and storage for 10 days)*; **</i> <\$4		< 1hr
	High-level summaries**	<i>SNP calling (compute + transfer out)</i> <\$5 = ~\$4 + ~\$0.60	< 1Gb	~3 hrs	<i>Gene and exon expression quantification</i> <\$1	<1M	<1hr (1 CPU)
		<i>Indel calling (compute + transfer out)</i> <\$35 = ~\$32 + ~\$0.60	< 1Gb	~1 day	<i>Isoform quantification</i> ~\$6	<1M	~4h
		<i>SV calling (compute + transfer out)</i> <\$35 = ~\$32 + ~\$0.60	< 1Gb	~1 day			
Downstream analyses		>\$100K	~310Gb	months	>\$100K	~30Gb	months

Total of Sequencing and Data management & Reduction	~\$6500	~310Gb	~15 days		~3500	3~0Gb	~12-14 days
-----------------------------------------------------	---------	--------	----------	--	-------	-------	-------------

* Assuming a 10 Mbyte/sec transfer rate

** This is the cost of transferring 300Gb (BAM file), if the mapping is performed locally

*** 16 CPUs were used for all calculations, unless specified